

# Reopening the Strait of Hormuz: from a bioinvasion super-spreader warning to species–vessel–port prioritisation

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## Abstract

Prolonged vessel lay-up can create an exceptional biosecurity hazard by allowing fouling assemblages to accumulate before vessels re-enter shipping networks. A recent study highlighted this risk following closure of the Strait of Hormuz and recommended pre-departure biofouling assessment, route forecasting, early detection and rapid communication. These measures address vectors and pathways, but species-targeted preparedness also requires a geographically resolved donor-region species baseline. Here, we use the recently validated Regional Organization for the Protection of the Marine Environment (ROPME) Sea Area (RSA) biosecurity baseline and integrate it with vessel-, route- and recipient-related information to support species–vessel–port prioritisation. The RSA baseline re-examined 136 species, of which 24 required reassignment or exclusion; 130 were retained and 62 added, yielding 192 species: 123 extant and 69 horizon. Thirty-nine extant species entered the very-high-priority tier, including seven benthic fouling organisms associated with shipping and ports. A watch list based on previous extant classifications would omit four of these seven. We therefore propose integrating validated donor-region occurrence with vessel exposure, route conditions, recipient susceptibility and response capacity. This framework provides an operational basis for species-targeted inspection, surveillance and rapid response and is transferable to future mass vessel lay-ups and other disruptions of maritime trade.

*Keywords:* ROPME Sea Area; risk identification; vessel lay-up; ship biofouling; marine biosecurity

## 1 Introduction

When commercial vessels remain stationary for extended periods, biofouling can accumulate substantially because submerged surfaces become more susceptible to colonisation (Davidson et al. 2020; International Maritime Organization [IMO] 2023). Niche areas such as sea chests, chain lockers, rudders and other recessed or protected structures are particularly susceptible because they can be difficult to access, coat and manage effectively (de Castro et al. 2018; Hayes et al. 2019). Once vessels return to service, accumulated biofouling assemblages may be transported through highly connected shipping networks and released across multiple recipient ports (Seebens et al. 2016; Ruiz et al. 2022).

Against this background, in a recent paper Tamburri et al. (2026) drew attention to the unprecedented mass lay-up of vessels in the Gulf and Sea of Oman following the closure of the Strait of Hormuz during the ongoing conflict in West Asia, and warned that the eventual return to service of these vessels could trigger what they term a ‘bioinvasion super-spreader event’. In addition to in-water cleaning of ship biofouling, one of the most widely adopted intervention measures (Tamburri et al. 2021, 2025), their recommendations included: (i) estimation of biofouling before departure; (ii) forecasting of vessel routes and first ports of call; (iii) implementation of early detection and rapid response at high-risk ports; and (iv) establishment of rapid alert and knowledge-dissemination networks.

Collectively, these measures address the vector, transport pathway and network of potentially exposed recipient ports. However, they do not resolve the biological target. Marine biosecurity assessments have shown that pathway and vector information can identify exposure but cannot discriminate among the species responsible for that risk, whereas species-based analyses can provide targeted watch lists for surveillance and management (Barry et al. 2008; Azmi et al. 2015; Miralles et al. 2021). Without a reliable donor-region baseline, authorities and stakeholders therefore lack a scientifically defensible basis for determining

which species should shape inspection design, which diagnostic tools should be implemented, or which source–destination combinations deserve priority especially when resources are limited (Bishop and Hutchings 2011; Azmi et al. 2015; Miralles et al. 2021). This limitation does not diminish generic interventions such as in-water cleaning of heavily fouled vessels, which can be justified by fouling condition alone. It becomes important when authorities must decide which species to target in surveillance, which diagnostic capacity to prepare and which source–recipient combinations warrant priority.

Although prolonged vessel lay-up increases transport opportunity and propagule pressure, it does not by itself establish species-specific invasion risk. Biological invasion is a sequential process in which an organism must overcome barriers associated with transport, introduction, establishment and spread (Blackburn et al. 2011). In the present context, a non-native species (*sensu* Soto et al. 2024; Vilizzi et al. 2025a, 2026b) must occur at the source, reach or colonise the vessel, survive the stationary period and subsequent voyage, be released into the recipient environment, encounter suitable conditions, establish and ultimately spread, with impacts representing a further and distinct consequence of successful invasion (Haubrock et al. 2026a, 2026b). Vessel numbers, submerged surface area and network connectivity influence several steps in this sequence, but none identifies the species for which the complete sequence is biologically plausible.

Pathway analysis, as advocated by Tamburri et al. (2026), and species-level risk identification must therefore be used in conjunction. Here, we develop that missing biological component using the updated and validated regional baseline recently developed by Vilizzi et al. (2026a). We first examine the extent to which the regional evidence used by Tamburri et al. (2026) provides an adequate operational representation of the contemporary source-species pool. We then identify a concise set of very-high-priority extant fouling species from the validated baseline and show how these can be combined with vessel and route information.

The main contribution of the present study is to add a validated donor-region species layer to the vessel- and route-based recommendations of Tamburri et al. (2026), thereby expanding a general pathway and super-spreader warning into species-specific operational preparedness.

## **2 Why the validated donor-region baseline matters**

Pathway management is most useful when it is tied to a validated list of biological targets. A general instruction to monitor for (invasive) non-native species is unlikely to be adequate during an event involving hundreds or thousands of vessels, particularly where surveillance resources are constrained (Bishop and Hutchings 2011). Rapid visual surveys, scrape samples, settlement panels, conventional taxonomy, targeted molecular assays and metabarcoding differ in sensitivity, taxonomic coverage, cost and turnaround time (Hayes et al. 2005; Campbell et al. 2007; Chebaane et al. 2026). The choice among them also depends on the organisms expected and on the consequences of missed detection. The same applies to inspection and cleaning. The amount of biofouling can be estimated without identifying every organism, but its biosecurity significance depends on species composition and location. Biofouling assemblages, including colonial tunicates, serpulids, barnacles, mussels and macroalgae, can differ among exposed hull surfaces and vessel niche areas, which are often disproportionately fouled and may require different inspection and sampling approaches (Coutts and Dodgshun 2007; Peters et al. 2019; Georgiades et al. 2020, 2026). Although a regional baseline cannot replace direct vessel inspection, it can define the biological targets that an inspection programme should be prepared to identify, sample or diagnose.

The Regional Organization for the Protection of the Marine Environment (ROPME) Sea Area (RSA) comprises the Gulf, the Sea of Oman and adjacent parts of the Arabian Sea (Fig. 1). It is bordered by Bahrain, Iran, Iraq, Kuwait, Oman, Qatar, Saudi Arabia and the United Arab Emirates, which constitute the eight ROPME Member States (van Lavieren and Klaus 2013; Bailey and Munawar 2015). The RSA provides the transboundary spatial and

institutional framework within which regional marine environmental evidence, including marine biosecurity information, can be assembled, validated and translated into coordinated action. This regional framework is not adopted by Tamburri et al. (2026); instead, they use the term ‘Gulf region’, drawing principally on Clarke et al. (2020) and Chebaane et al. (2026) to characterise its non-native and biofouling biota.

Source occurrence must also be resolved below the scale of the entire RSA. A vessel laid up, for example, near Kuwait in the northern Gulf cannot automatically be assigned the same candidate species pool as a vessel that remained in Omani waters east of the Strait of Hormuz. This is because environmental conditions, species assemblages and introduction pathways may differ substantially across the region (Vilizzi et al. 2026a). Conversely, national inventories alone may underrepresent transboundary distributions where monitoring intensity, taxonomic capacity and reporting differ among Member States. The appropriate starting point is therefore a harmonised regional inventory that retains Member State-level occurrence. This is what Vilizzi et al. (2026a) recently provided through their first regional biosecurity baseline for the RSA, based on taxonomic validation, geographic verification, extended species categorisation (i.e. beyond the simplified native vs non-native dichotomy), Member State-level species status assignment, and systematic risk identification under present and projected climate conditions.

Clarke et al. (2020) represented the first structured risk screening of marine and brackish-water species for the Gulf and Sea of Oman. However, that study did not incorporate systematic cross-validation of species status across all ROPME Member States or the taxonomic and distributional verification subsequently undertaken by Vilizzi et al. (2026a). To address this gap, Vilizzi et al. (2026a) systematically re-examined all 136 species screened by Clarke et al. (2020) using current taxonomy, updated peer-reviewed and database records, geographic verification and Member State-level validation, and extended the scope of the

screening to the RSA (hence, including its Inner, Middle and Outer sections, represented respectively by the Gulf, the Sea of Oman and adjacent parts of the Arabian Sea along the coasts of Oman). Of those 136 species, 24 ( $\approx 18\%$ ) required reassignment or exclusion. Specifically, two species classified as extant (i.e. already present in the RSA) were reassigned as horizon (i.e. absent from the RSA but likely to be introduced in the near future), 16 classified as horizon were found to be extant (with only two of those species having effectively entered the RSA after 2019, that is the year before publication of that study), another five classified as horizon were excluded because the available evidence supported their native status in the RSA, and one horizon freshwater species was outside the marine and brackish-water scope. Six species were consequently excluded, leaving 130 validated species from the original screening exercise by Clarke et al. (2020), while 62 additional species, comprising 53 extant and nine horizon species, were identified and screened. The resulting regional baseline comprised 192 species of which 123 extant and 69 horizon (Vilizzi et al. 2026a).

The revision by Vilizzi et al. (2026a) therefore extended beyond a simple expansion of the original list by Clarke et al. (2020). It established which species were already present (extant) and potentially available for uptake or transfer, where their occurrence had been verified within the RSA at both the section and Member State level, how their regional status should be interpreted and which warranted highest management attention (i.e. the very-high-priority tier). The 192 screenings, which, similar to Clarke et al. (2020), relied on the Aquatic Species Invasiveness Screening Kit (AS-ISK: Copp et al. 2016; Vilizzi et al. 2025b), were updated or conducted by local assessors from all ROPME Member States with expertise in marine and brackish-water ecology in the RSA, and the resulting screening outcomes were recalibrated by organismal group (i.e. birds, plants, fishes, invertebrates and chromists). Thirty-nine extant species ultimately entered the very-high-priority tier and were identified for progression to

comprehensive risk assessment and management action at both the RSA and Member State level (Vilizzi et al. 2026b). Among these species, seven were explicitly characterised as benthic fouling organisms closely associated with shipping and port environments: the tunicates *Botrylloides niger*, *Didemnum psammotodes* and *Symplegma brakenhielmi*; the serpulid *Hydroides elegans*; the barnacle *Amphibalanus subalbidus*; and the bivalves *Brachidontes pharaonis* and *Perna perna* (Table 1). Their selection is not intended to rank the probability of vessel-mediated export, but to identify a precautionary subset that combines verified donor-region occurrence, high regional management priority and an established association with ship biofouling. Vessel-specific transfer likelihood must subsequently be determined from the exposure and route components of the prioritisation.

The comparison with Clarke et al. (2020) demonstrates why an updated donor-region baseline matters operationally. *Didemnum psammotodes* and *Hydroides elegans* were not screened in the earlier study but were subsequently confirmed as extant and were ranked as very-high-priority, whereas *Brachidontes pharaonis* and *Perna perna* had been treated as horizon species but were shown by the revised evidence to be extant in the RSA. A donor-region watch list based solely on the earlier classifications would therefore omit these four very-high-priority biofouling species despite their likelihood of uptake. Further, screening scores increased substantially for *Amphibalanus subalbidus* and *Symplegma brakenhielmi* (Table 1).

The significance of these species cannot, however, be generalised across recipient ports because their biogeographic status differs among recipient regions (Soto et al. 2024). A vessel-mediated transfer represents a potential new introduction where the transported species is absent and non-native to the recipient region. Where the species is native, its arrival is not a non-native species introduction, although transfer of non-local genotypes or associated pathogens may still have biosecurity implications (Georgiades et al. 2021); where it is already



established as non-native, additional arrivals may increase propagule pressure or genetic diversity (Touchard et al. 2023). Tamburri et al. (2026) recognise the potential importance of repeated introductions into established non-native populations; however, their geographically broad super-spreader scenario may not capture the local status of candidate species at individual recipient ports with the same resolution. Vessel movements and environmental similarity remain important determinants of transport and establishment opportunity (Seebens et al. 2016; Donelan et al. 2025), but the invasion significance of a movement is ultimately species- and recipient-specific (Leung et al. 2012). The super-spreader analogy is therefore strongest at the level of transport opportunity, whereas the resulting bioinvasion consequences must be evaluated for individual species–recipient port combinations.

Chebaane et al. (2026) provide an important complementary form of evidence. Combining DNA metabarcoding and photographic surveys of pontoons, docks and settlement panels at 12 sites along approximately 300 km of the Saudi Arabian Gulf coast, they detected 57 non-native or cryptogenic species, with particularly high richness and relative abundance in industrial and commercial ports. Their results therefore provide direct empirical support for the biofouling mechanism invoked by Tamburri et al. (2026) and also show species-level overlap with the validated RSA baseline. Direct comparison at the species level between the 57 non-native or cryptogenic species reported by Chebaane et al. (2026) and the RSA baseline identified eight matches: six classified as extant in the baseline (*Amathia verticillata*, *Botrylloides niger*, *Diplosoma listerianum*, *Hydroides elegans*, *Polyclinum constellatum* and *Symplegma brakenhielmi*) and two classified as horizon (*Botrylloides violaceus* and *Mytilus galloprovincialis*). Notably, three of the seven very-high-priority extant fouling species identified by Vilizzi et al. (2026a), namely *Botrylloides niger*, *Hydroides elegans* and *Symplegma brakenhielmi*, were detected in the Saudi biofouling surveys. However, Chebaane et al. (2026) was a spatially resolved ecological survey rather than an RSA-wide biosecurity

inventory or risk-prioritisation exercise. Its geographic coverage was restricted to part of the Saudi coast (i.e. Inner RSA), and the authors cautioned that species-level assignments from metabarcoding remain constrained by sparse regional reference libraries. Notably, Chebaane et al. (2026) reported *Botrylloides violaceus* and *Mytilus galloprovincialis*, both classified as horizon species in the validated RSA baseline. These detections constitute new occurrence evidence that warrants taxonomic and geographic verification before any change to their regional status, while illustrating the need for source-region baselines to remain responsive to independently validated new records.

The evidence supplied by Clarke et al. (2020), Chebaane et al. (2026) and Vilizzi et al. (2026a) is therefore complementary rather than interchangeable. Clarke et al. (2020) provided the original structured regional screening; Chebaane et al. (2026), the contemporary, site-resolved empirical evidence of Saudi Gulf coast (i.e. Inner RSA) biofouling communities; and Vilizzi et al. (2026a), the updated, taxonomically validated, Member State-resolved and risk-prioritised RSA baseline. Tamburri et al. (2026) drew on the first two evidence sources; integrating the third adds the geographically resolved source-species layer needed for species-targeted inspection, surveillance and rapid-response planning.

Operationalising the species-targeted elements of the recommendations made by Tamburri et al. (2026) requires linking species documented in the relevant donor area with their source-region priority status, vessel exposure history and the environmental characteristics and species status of the recipient port. Clarke et al. (2020) and Chebaane et al. (2026) provide important elements of this evidence, whereas the validated RSA baseline adds the geographically resolved source-species reference used here for operational prioritisation. A useful vessel lay-up watch list should also be narrower than the full set of 39 very-high-priority extant species many of which are associated primarily with ballast water, retained water, aquaculture, trade, natural dispersal or other pathways rather than external fouling

(Vilizzi et al. 2026a). The seven extant species identified in the validated RSA baseline as fouling organisms strongly associated with shipping and port environments (Table 1) do not imply occurrence on any particular vessel, but identify biological targets against which lay-up location, recent vessel movements, inspection findings and subsequent routes can be evaluated. In this way, the validated source-region baseline provides the biological component needed to translate a general bioinvasion warning into targeted inspection, surveillance and rapid-response planning.

### 3 Recommendations

#### 3.1 Species–vessel–port prioritisation

The recommendations of Tamburri et al. (2026) can be operationalised more specifically for species-targeted preparedness by treating the event as a set of species–vessel–port combinations rather than as a single regional threat. The relevant unit is a species that plausibly occurs at the source, can be transported by a particular vessel, is likely to survive the voyage and may encounter a susceptible recipient port where the consequences of the introduction justify intervention. This approach adapts established methods that integrate species, pathway and recipient-area information (Barry et al. 2008; Azmi et al. 2015; Hayes et al. 2019; Miralles et al. 2021) to the specific conditions created by prolonged vessel lay-up in the RSA. Its contribution lies in linking those components to a validated and geographically resolved source-species baseline. This is consistent with the sequential nature of biological invasions in which transport opportunity alone does not determine invasion risk (Blackburn et al. 2011; Leung et al. 2012).

The proposed species–vessel–port prioritisation comprises five linked components: source-region baseline, vessel exposure, route conditions, recipient port and response capacity (Fig. 2). The purpose is not to predict invasion but to prioritise species–vessel–port combinations for inspection, surveillance and response while retaining the uncertainty

associated with each component. The prioritisation is intentionally decision-structuring rather than predictive and does not prescribe numerical weights across components, because the availability and quality of vessel, route and recipient-port evidence will differ among events and jurisdictions. Five recommendations follow:

**1. *Source-region baseline.*** This component provides validated occurrence, Member State records and priority species. The validated RSA baseline supplies these elements (Vilizzi et al. 2026a); for operational use, this information should be related to actual vessel lay-up positions and recent movements. Absence of a Member State record should not be interpreted as demonstrated biological absence, because non-native species inventories remain sensitive to surveillance effort, taxonomic resolution and baseline quality (Latombe et al. 2017; Ojaveer et al. 2018; Tsiamis et al. 2019).

**2. *Vessel exposure.*** This component considers lay-up location and duration, vessel type and size, fouling condition, niche areas and cleaning history. Prolonged stationary periods can substantially increase biofouling accumulation, while vessel characteristics and niche areas influence where organisms are retained and transported (Davidson et al. 2020; IMO 2023; Georgiades et al. 2021).

**3. *Route conditions.*** This component comprises first port of call, voyage duration, temperature and salinity exposure, and freshwater exposure. Conditions experienced after departure can influence survival, reproduction and release during transport, and consequently modify the likelihood that organisms acquired during lay-up remain viable on arrival (Seebens et al. 2016; Donelan et al. 2025).

**4. *Recipient port.*** This component evaluates local species status, environmental suitability, habitats, and establishment and spread potential. Recipient conditions determine whether arrival translates into a meaningful biosecurity concern and should therefore be assessed

independently of donor-region screening outcomes (Leung et al. 2012; Carvalho et al. 2023).

**5. Response capacity.** The final component considers inspection capability, targeted sampling, cleaning options, surveillance infrastructure and rapid response measures. Ports differ substantially in these capacities, particularly in data-poor regions (Carvalho et al. 2023).

### 3.2 Translating the prioritisation into action

Before departure, or as early as possible before arrival, authorities should assemble vessel-specific information on lay-up history, hull and niche-area condition, in-water cleaning and maintenance, recent and planned ports, expected voyage conditions and the relevant donor-region taxa identified from the RSA baseline. Existing biofouling guidance already emphasises vessel-specific information, inspection history and management actions (IMO 2023; Tamburri et al. 2026). Adding the validated donor-region species layer allows recipient authorities to prepare species-targeted inspection and surveillance before berthing rather than responding only after release may have occurred.

Inspection and detection methods can then be selected according to the biological targets and vessel condition. Close-range imagery and scrape sampling may be appropriate for conspicuous external fouling, whereas targeted molecular assays can support confirmation of predefined non-native species and metabarcoding can broaden detection of cryptic assemblages (O'Shaughnessy et al. 2023; Sempere-Valverde et al. 2025; Chebaane et al. 2026). The purpose is not to prescribe a single surveillance method, but to ensure that available methods are informed by the species plausibly associated with the donor region and vessel.

Route and recipient information then refine priority. Environmentally similar first ports of call, as identified by Tamburri et al. (2026), provide an initial pathway screen, but source occurrence and recipient species status determine which species–vessel–port combinations warrant greatest attention. Priorities should therefore remain dynamic as routes change, vessels are cleaned, new source records become available or recipient status is clarified. At the regional level, ROPME could support this process by maintaining the validated species baseline, receiving Member State updates and communicating taxonomic or status revisions to relevant recipient authorities (e.g. Carvalho et al. 2023; Egawa et al. 2026).

### *3.3 Scope, limitations and refinement*

The RSA baseline should be used within its intended scope. AS-ISK scores calibrated for the RSA describe invasiveness risk within that risk assessment area and are not export-risk scores for European, African, South Asian or other recipient regions. Risk-screening outcomes are inherently context dependent, and calibrated scores and thresholds should be interpreted within the risk assessment area for which the application was undertaken (Vilizzi and Piria 2022; Vilizzi et al. 2022a, 2022b). The very-high-priority tier therefore identifies a source candidate pool of fouling species rather than determining risk at the destination, where environmental suitability, local species status, impacts and management consequences must still be considered. For many species and geographical regions, however, geographically explicit screening evidence based on the Invasiveness Screening Kit decision-support tools is already available (Vilizzi 2026). Where a relevant application overlaps a recipient region, such evidence can provide an independent, context-specific evidence layer for the recipient component of the prioritisation. Such screening outcomes should be used only within their respective risk assessment areas rather than transferred from the RSA or treated as universal species-level classifications. The RSA baseline addresses species available for uptake during lay-up within the RSA and it does not encompass organisms that individual vessels may have

retained from earlier voyages and source regions before entering the RSA. Vessel movement history and direct inspection therefore remain necessary to characterise this additional source pool. Accordingly, the present prioritisation does not itself assign destination-specific invasion risk to the individual first ports of call identified by Tamburri et al. (2026), but such prioritisation can incorporate existing recipient-region ISK applications, where available, together with validated local species-status and environmental evidence.

The seven very-high-priority fouling species identified in the baseline represent an operationally focused subset of the 39 very-high-priority extant species, not an exhaustive list of possible vessel-mediated transfers. Other species may be associated with ballast water, internal systems or alternative pathways, and lower-ranked species should not be excluded automatically where recipient conditions are more favourable. Uncertainty in source occurrence, taxonomic identification and monitoring coverage should therefore remain explicit in any species–vessel–port prioritisation (Latombe et al. 2017; Ojaveer et al. 2018).

The 2026 Gulf region lay-up also provides an opportunity to test and refine the proposed approach by linking vessel movements, source-region occurrence, inspection findings and subsequent detections in recipient regions. Such evaluation would move the discussion beyond whether a bioinvasion super-spreader event occurred and towards the more informative questions of which species–vessel–port combinations generated the greatest risk, which interventions reduced that risk and which forms of regional coordination enabled timely action.

## **4 Conclusions**

Tamburri et al. (2026) identified a credible biosecurity hazard arising from prolonged vessel lay-up and subsequent redistribution through global shipping. Inspection, route forecasting, early detection and rapid communication are appropriate responses. Their implementation,

however, requires a biological reference at the donor-region level. The consolidated RSA baseline supplies that reference and updates several previous species status assignments, expands taxonomic and geographic coverage, incorporates Member State validation and provides a transparent priority structure. The baseline is not an alternative to vessel inspection or recipient-port surveillance. It makes both more selective. Combining source records with vessel condition, route exposure, recipient status and response capacity yields decisions that can be explained, updated and tested against inspection results. The same problem may recur at different scales beyond the Strait of Hormuz. Trade disruption, corridor closure, port congestion and emergency lay-up can all produce atypical movements of vessels and organisms. Preparedness should therefore join real-time vector intelligence to curated regional species baselines before the next disruption. Pathway information indicates how organisms may move; source-region baselines indicate what authorities should be prepared to find.

#### **CRedit authorship contribution statement**

**Lorenzo Vilizzi:** Conceptualization, Writing – original draft, Writing – review & editing.

**Aisha F. Al-Marhoun:** Writing – review & editing. **Qusaie E. Karam:** Writing – review & editing. **Zainab Al-Wazzan:** Writing – review & editing.

#### **Declaration of competing interest**

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

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614 **Tables**

615 **Table 1.** Fouling species identified as very-high-priority in the updated ROPME Sea Area biosecurity baseline (Vilizzi et al. 2026a), with comparison against their treatment  
616 in Clarke et al. (2020). The seven taxa were explicitly identified by Vilizzi et al. (2026a) as benthic fouling organisms closely associated with shipping and port environments.  
617 For each species, the status in the RSA is provided according to Clarke et al. (2020) and revised in Vilizzi et al. (2026a): Extant = already present in the RSA; Horizon = not  
618 yet present in the RSA. Based on the Aquatic Species Invasiveness Screening Kit (AS-ISK: Copp et al. 2016; Vilizzi et al. 2025a), the following scores are provided for each  
619 species-specific screening record: BRA = Basic Risk Assessment; BRA+CCA = Basic Risk Assessment plus Climate Change Assessment. n.a. = not applicable because the  
620 species was not screened by Clarke et al. (2020). Scores  $\geq 50$  identify species in the very-high-priority tier (Vilizzi et al. 2026a). Member State occurrence indicates verified  
621 records in the updated RSA baseline and should not be interpreted as implying identical biogeographic status in each jurisdiction. Absence of a Member State from the table  
622 indicates absence of a verified record in the baseline rather than demonstrated biological absence.

| Taxon                          | Clarke et al. (2020) |               | Vilizzi et al. (2026a) |               | Member State occurrence                 | Operational significance                                                                                                                                         |
|--------------------------------|----------------------|---------------|------------------------|---------------|-----------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|                                | RSA status           | BRA / BRA+CCA | RSA status             | BRA / BRA+CCA |                                         |                                                                                                                                                                  |
| <i>Amphibalanus subalbidus</i> | Extant               | 32.0 / 24.0   | Extant                 | 41.0 / 53.0   | Iran, Iraq                              | Climate-adjusted score increased, changing operational interpretation and ranking it as very-high-priority.                                                      |
| <i>Botrylloides niger</i>      | Extant               | 36.0 / 36.0   | Extant                 | 42.5 / 54.5   | Bahrain, UAE                            | Retained from Clarke et al. (2020), but its updated BRA+CCA score places it in the very-high-priority tier.                                                      |
| <i>Brachidontes pharaonis</i>  | Horizon              | 36.0 / 48.0   | Extant                 | 39.0 / 51.0   | Kuwait, Oman, Saudi Arabia              | Treated as horizon (i.e. absent in the donor region) by Clarke et al. (2020), but recorded as extant (i.e. present in the donor region) in the updated baseline. |
| <i>Didemnum psammotodes</i>    | Not screened         | n.a.          | Extant                 | 52.0 / 64.0   | Iran, Oman                              | Absent from Clarke et al. (2020) despite being confirmed as extant and very-high-priority in the updated baseline.                                               |
| <i>Hydroides elegans</i>       | Not screened         | n.a.          | Extant                 | 43.0 / 53.0   | Iran, Kuwait, Oman, Qatar, Saudi Arabia | Absent from Clarke et al. (2020) despite being confirmed as extant and very-high-priority in the updated baseline.                                               |
| <i>Perna perna</i>             | Horizon              | 23.0 / 29.0   | Extant                 | 38.0 / 50.0   | Oman                                    | Treated as horizon (i.e. absent in the donor region) by Clarke et al. (2020), but                                                                                |

| Taxon                         | Clarke et al. (2020) |               | Vilizzi et al. (2026a) |               | Member State occurrence | Operational significance                                                                                                                                                                                                 |
|-------------------------------|----------------------|---------------|------------------------|---------------|-------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|                               | RSA status           | BRA / BRA+CCA | RSA status             | BRA / BRA+CCA |                         |                                                                                                                                                                                                                          |
| <i>Symplegma brakenhielmi</i> | Extant               | 31.0 / 31.0   | Extant                 | 46.0 / 58.0   | Bahrain                 | recorded as extant (i.e. present in the donor region) in the updated baseline.<br>Substantial increase in the assessed scores, particularly under climate change, resulting in placement in the very-high-priority tier. |

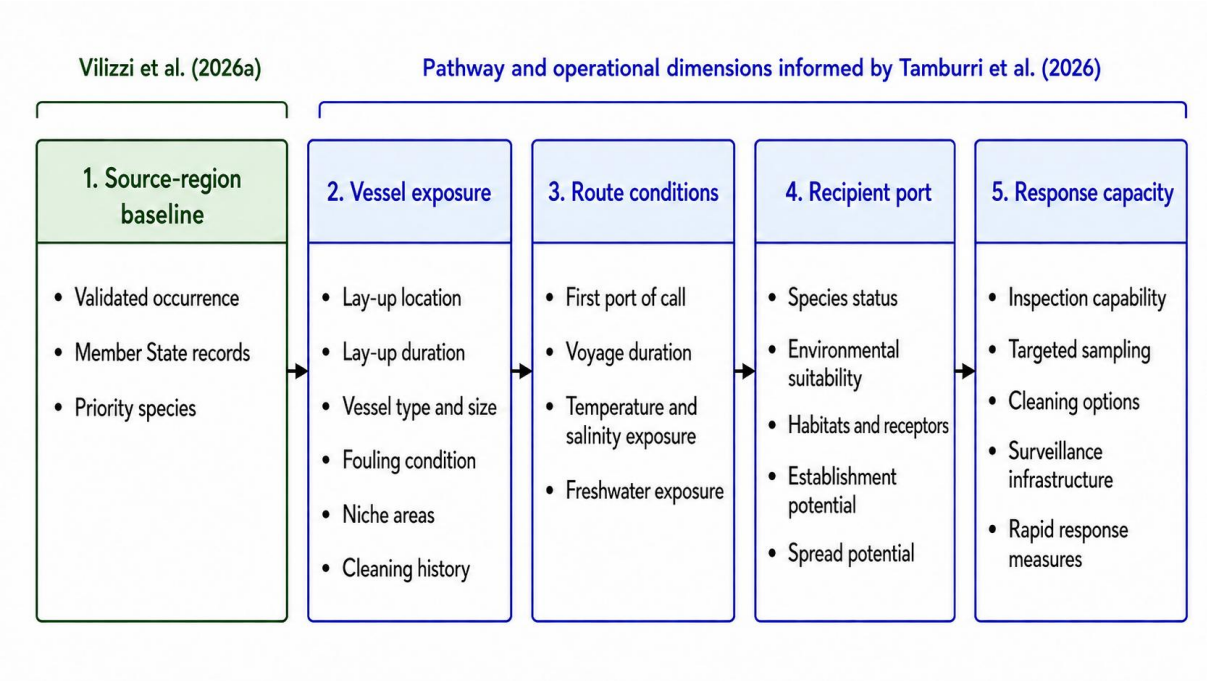
## Figure legends

**Fig. 1** Map of the study and risk assessment area: the Regional Organization for the Protection of the Marine Environment (ROPME) Sea Area (RSA) encompassing the Gulf, the Sea of Oman, and parts of the Arabian Sea, and subdivided into Inner, Middle, and Outer regions.

**Fig. 2** Conceptual integration of the validated RSA source-region species baseline from Vilizzi et al. (2026a) with pathway and operational dimensions informed by Tamburri et al. (2026). The present study integrates these evidence layers to support species–vessel–port prioritisation following prolonged vessel lay-up.



633 Fig. 1



634 **Fig. 2**