

HELLENIC REPUBLIC
UNIVERSITY OF THESSALY
SCHOOL OF HEALTH SCIENCES
FACULTY OF MEDICINE

MSc in Public Health and Maritime Transport

Master Thesis

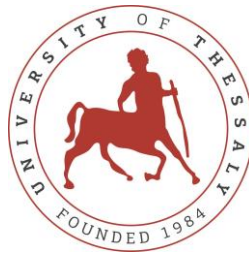
Title:

**Burden and Prevalence of Antimicrobial Resistance Bacteria among Maritime Human–
Environmental Interfaces: A Systematic Review and Meta-Analysis of Evidence from 2010 to 2024**

Submitted by: **OLALEKAN JOHN OKESANYA**

ID: M240623009

[FEBRUARY, 2026]



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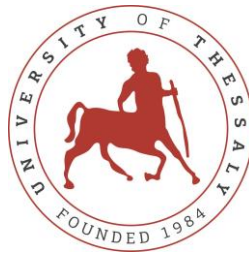
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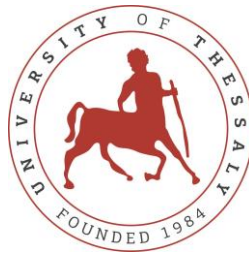
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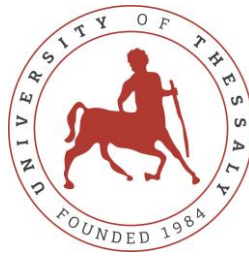
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Dedications

This work is dedicated to God Almighty for His grace, strength, and wisdom throughout this journey, and to my family, whose unwavering love, prayers, and support made this achievement possible.



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I give all glory and gratitude to God Almighty for His grace, strength, and guidance throughout the course of this Master's programme and the successful completion of this thesis. His wisdom and faithfulness sustained me through every challenge encountered along this journey.

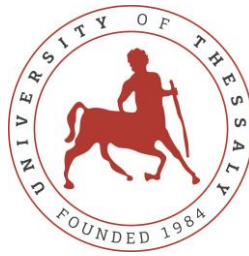
My sincere appreciation goes to the faculty and academic staff of the University of Thessaly, Volos, Greece, for providing an intellectually stimulating and supportive learning environment. The knowledge, training, and exposure gained throughout the Master of Public Health and Maritime Transport programme have profoundly shaped both my academic growth and professional outlook.

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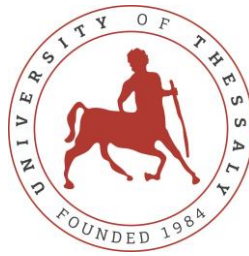
Finally, I express my heartfelt gratitude to my family for their unwavering love, prayers, sacrifices, and constant belief in me. Their support has been my greatest source of strength and motivation. This achievement would not have been possible without them.

To everyone who contributed directly or indirectly to the success of this thesis, I am sincerely thankful.



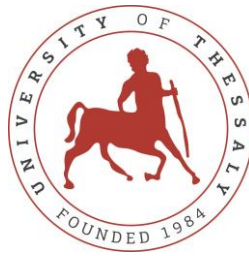
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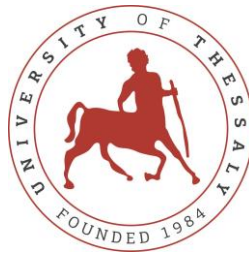
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Abstract

Antimicrobial resistance (AMR) continues to be a global health concern that extends to maritime ecosystems in addition to its increasing threat in clinical settings. The growth and spread of these resistant pathogens are facilitated by antibiotic abuse, exposure to contaminated waters, and special shipboard and coastal circumstances. This novel study systematically reviews and quantifies global evidence on AMR burden and prevalence in the maritime human-environmental interfaces. This systematic review and meta-analysis followed PRISMA guidelines and was registered in PROSPERO (CRD420251071827). Eligible studies were gathered from six databases between 2010 and 2024, which were screened using Rayyan software and evaluated using JBI tools to reduce bias. Data were both narratively synthesized thematically and quantitatively using random-effects meta-analysis in R, with heterogeneity assessed by I^2 statistics. A total of 14 eligible studies met the inclusion criteria, across maritime ecosystem in Asia, Europe, Africa and the Middle East. The study found the dominance of Gram-negative bacteria, especially *Escherichia coli*, *Vibrio* spp., *Klebsiella*, and *Pseudomonas* while key Gram-positive pathogens included *Staphylococcus aureus* and *Enterococcus* from ballast water, clinical samples, wastewater, human and environmental samples such as water sediment and seawater. AMR was prevalent with frequent multidrug resistance (MDR) to β -lactams, cephalosporins, aminoglycosides, and fluoroquinolones. Molecular analysis of the individual studies identified common resistance genes including *blaCTX-M*, *tetM*, *sul1*, and *intI1*, suggesting the possibility of horizontal gene transfer as also confirmed by the outbreaks of typhoid fever and foodborne disease on ships. The meta-analysis revealed significant regional and species-specific variation, with a high pooled AMR prevalence of 69% (95% CI: 36.4–89.7%) and great heterogeneity ($I^2 = 98.6\%$). Publication bias was identified, suggesting that the true frequency of AMR in maritime ecosystems may have been overstated. This study highlights marine habitats as emerging and novel AMR reservoirs through the quantitative pooled prevalence of AMR throughout maritime human–environmental interfaces. The findings of this study support the strengthening of surveillance systems, enhanced monitoring of wastewater and ballast water, and the implementation of robust public health measures to improve wastewater management within a One Health surveillance framework. Further genomic research and standardized monitoring are crucial to better quantify risks and reduce the global spread of AMR.

Keywords: Antimicrobial resistance, AMR, Bacterial resistance, Maritime ecosystem, Human-environmental interfaces, Marine body

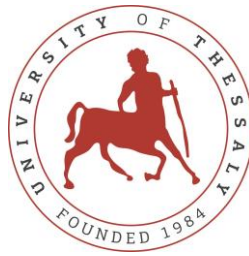


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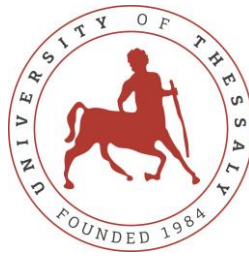
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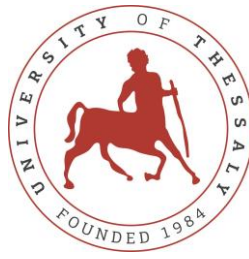


Burden and Prevalence of Antimicrobial Resistance Bacteria among Maritime Human–Environmental Interfaces: A Systematic Review and Meta-Analysis of Evidence from 2010 to 2024

1.0 INTRODUCTION

1.1 Background

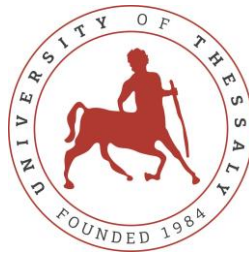
Antimicrobial-resistance (AMR) is a significant global public health challenge with implications that extend beyond clinical settings (Ahmed *et al.*, 2024). Marine communities may be increasingly at risk of the spread of AMR bacteria, as the unique conditions on board such as cramped quarters, shared amenities, and prolonged close contact can facilitate transmission, even if these environments are less likely to drive the development of resistance due to the relatively low-risk, non-immunocompromised populations and limited invasive medical procedures (Kusi *et al.*, 2022; Adebisi, Bamisaiye and Prisno, 2025). While routine testing for resistant pathogens on ships is uncommon, these unique living conditions could facilitate the undetected spread of resistant microorganisms highlighting a critical gap in current AMR surveillance and research (Lim *et al.*, 2021). AMR in aquatic systems is a result of some antibiotics ending up in sewage and wastewater that are not eliminated by treatment procedures. Research has shown that the presence of antibiotics in aquatic environments can promote the emergence and spread of antimicrobial resistance (AMR) by selecting for a resistance genes in microbial populations (Chokshi *et al.*, 2019; Singh *et al.*, 2022). Bacteria develop resistance to the most potent antibiotics because of horizontal gene transfer and mutagenesis influenced by sub-inhibitory antibiotic concentrations in aquatic systems, exposure of low drug level to the bacterial physiology such as genetic development, phenotypic differences, and the signaling efficacy of the antibiotics (Andersson and Hughes, 2014; Kusi *et al.*, 2022). Recent reports of methicillin-resistant *Staphylococcus aureus* (MRSA) outbreaks on navy ships demonstrate how susceptible these settings are to the spread of AMR (Lekkerkerk *et al.*, 2013; Bon *et al.*, 2017).



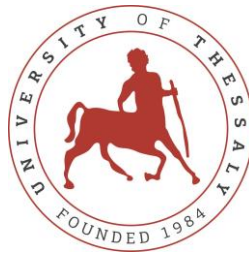
Maritime populations such as seafarers, coastal communities, and port workers are frequently exposed to certain risk factors, including close quarters, occasionally restricted access to healthcare, and exposure to marine habitats such as ballast water systems, contaminated coastal waters, and shipborne biofilms that may harbor AMR organisms (Herttua, Vork and Paljarvi, 2021). The prevalence of these risk factors necessitate the pressing need for focused intervention to address the challenges of the use and misuse of antibiotics in maritime settings and implementation of infection control measures and surveillance to alleviate the burden of AMR in maritime environments (Shao, Adebisi and Adeola, 2025). Maritime populations may be indirectly vulnerable because of occupational exposures like shared apartment, limited access to timely care, and likely exposure to environmental reservoirs of resistant pathogens (Tulchinsky and Varavikova, 2014; Salam *et al.*, 2023). Despite their vulnerability, these populations remain understudied even with the global nature of maritime operations increasing the risk of AMR spread (Coque *et al.*, 2023). The absence of systematic global data limits the ability to conduct effective surveillance, implement preventive strategies, and inform targeted policy interventions within this mobile and internationally connected demographic (Salam *et al.*, 2023). This study will focus on marine populations, which are frequently overlooked in most studies on AMR. It will provide insights about AMR trends and geographic distribution by synthesizing data from 2010 to 2024. To close this gap, this study will gather globally available data on the prevalence of AMR bacteria in marine health populations to improve global health security and safeguard vulnerable populations, while directing the creation of focused interventions, infection control guidelines, and surveillance initiatives.

1.2 Statement of the Problem

AMR continue to emerge as one of the top pressing health challenges globally which is halting years of progress in the treatment and management of infectious diseases. In 2024, the World Health Organization



(WHO) identified antimicrobial resistance (AMR) as one of the top ten global public health challenges, with resistant bacteria contributing to high morbidity, mortality and economic burden globally. The human–environmental interface within maritime ecosystems represents a crucial and emerging domain that remains understudied in AMR epidemic, even though the larger portion of research and policy attention has been focused in clinical and agricultural settings. The maritime environments, including ports, coastal waters, fishing villages, and ship-based waste disposal systems are unique ecological habitats where humans, animals and microbes interact together. These interfaces are frequently exposed to untreated sewage, ballast water discharges, aquaculture effluents, and pharmaceutical residues, creating conditions that facilitate the emergence, development, and spread of antimicrobial-resistant bacteria. Furthermore, human activities not limited to fishing, shipping, recreation, and consumption of seafood facilitate direct and indirect emergence and spread of transmission pathways of AMR from the marine environment to human populations. Concerns regarding the marine body's role as a pathogen reservoir and transmission pathway have been raised by the discovery that marine bacteria carry resistance genes such as blaCTX-M, mcr-1, and NDM-1. However, it is challenging to assess the global or regional burden of AMR in marine systems because most of the research is context-specific, methodologically diverse, and lack thorough synthesis. Another major problem in the research on AMR in marine environments is the dearth of recent systematic reviews and meta-analyses that integrate data across various geographic regions and study designs. Opportunities to spot patterns, pinpoint high-risk interfaces, and guide integrated One Health programs are lost due to the lack of cross-sectoral synthesis. Neglecting the field of AMR in marine environments has serious ramifications as it exposes populations dependent on these inter-related environments such as coastal urban dwellers, fishing communities, and sailors to potential resistant bacteria. The regulation of waste disposal in these marine bodies are challenging and difficult for health systems and politicians.



1.3 Aim and objectives

To determine the prevalence and burden of antimicrobial resistant bacteria among maritime human-environmental interfaces from 2010 to 2024.

With specific objectives to;

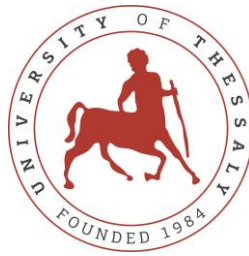
- Identify the most common AMR bacterial species in maritime human-environmental interfaces.
- Assess geographic and temporal trends in AMR prevalence.
- Identify key risk factors contributing to AMR in these populations

1.4 Research Questions

- What is the most common AMR bacterial species in maritime human-environmental interfaces?
- What is the geographic and temporal trends in AMR prevalence?
- What are the key risk factors contributing to AMR among these populations?

1.5 Justification of the Study

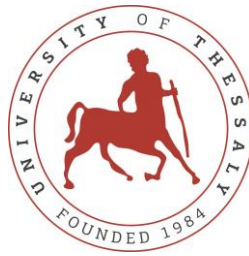
The long-standing pressing issue of AMR is addressed by this study by exploring the maritime human-environmental interface, which often has been largely neglected in global trade, fisheries, and human health. Conducting this systematic review and meta-analysis will fill a significant knowledge gap regarding the prevalence and burden of AMR in maritime settings. The dynamics of AMR are significantly influenced by the interdependence and inter-relationship of humans, animals, and the environment. Marine systems, where human consumption of seafood and interactions with coastal habitats are important, provide an example of this interdependence. This study reinforces and advances the One Health concept by focusing the conversation on the marine interface and emphasizing the need for multisectoral, integrated measures to effectively combat AMR. By documenting the prevalence and distribution of resistant bacteria in marine environments, data will be gathered to support public health initiatives that target high-risk populations and lessen health disparities. Future longitudinal monitoring, laboratory studies, and the



creation of innovative interventions like surveillance instruments or antimicrobial stewardship initiatives customized for maritime systems will use the results as a starting point. Specifically, this study supports sustainable development goals (SDG) 3 which addresses the threat of AMR to human health; SDG 6 addresses the effect of waste and effluents on marine contamination; SDG 14 protects aquatic ecosystems from pollution; and SDG 17 provides evidence for international and cross-sectoral partnerships.

1.6 Scope of the Study

This systematic review and meta-analysis will focus on the AMR data at the maritime human-environmental interfaces between 2010 and 2024. The marine environment will encompass human-related groups, including but not limited to seafarers, fishermen, and coastal communities, as well as environmental settings such as ballast water, aquaculture systems, and wastewater. The scope of AMR will be restricted to bacterial pathogens, with viral, fungal, and parasitic resistance excluded. We will gather evidence globally with data reported from port, coastal locations where AMR transmission is reported and known. The analysis will assess the pooled prevalence of AMR, the resistance gene burdens, and other variables responsible for resistance among the bacterial pathogens.



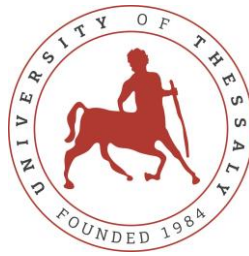
CHAPTER TWO

2.0 Literature Review

2.1 Overview of AMR

Antimicrobials are crucial medications used in the prevention and treatment of infections in humans, animals, and plants, which include antibiotics, antivirals, antifungals, and antiparasitics (Puvača, 2022). AMR is an important evolutionary response of microorganisms to therapeutic medicines. Pathogens such as bacteria, viruses, fungi, and parasites become resistant to these medications which ought to inhibit and prevent them, making these medications ineffective. Because of this resistance, Infections that were previously treatable are becoming increasingly difficult to manage and control, increasing the risk of disease spread, serious sickness, disability, and death. Although AMR is a natural phenomenon that can develop over time due to genetic alterations in bacteria, human activity, specifically the abuse and overuse of antibiotics in different settings has accelerated its onset and spread (Salam *et al.*, 2023) (World Health Organization., 2023a). Both chromosomal gene mutations and horizontal gene transfer (HGT), which inserts resistance determinants into bacterial DNA, are the two main evolutionary mechanisms by which bacteria adapt to antibiotics. Three important gene groups are frequently impacted by these mutations: those that encode transporters, antibiotic targets, and regulatory factors that govern the development of enzymes that change antibiotics and multidrug efflux pumps, all leading to heightened resistance (Tao *et al.*, 2022).

Studies indicates that commensal bacteria, especially those from the environmental sources are likely the origins of resistance genes that can be transferred to pathogenic bacteria through HGT. Environmental microorganisms produce a wide range of antibiotics, which necessitates the evolution of intrinsic resistance mechanisms to prevent self-destruction (Vivekanandan *et al.*, 2025). Bacteria can exhibit resistance either through intrinsic, acquired, or adaptive mechanisms. Intrinsic resistance is the natural ability of certain



bacteria to resist specific antibiotic classes due to pre-existing chromosomal genes, without mutations or gene acquisition. This form of resistance is inevitable when treating infections caused by these bacteria because of their inherent properties, particularly involving efflux pumps and alterations in membrane permeability (Solanki and Kumar Das, 2024). Acquired resistance involves previously susceptible bacteria developing resistance either through chromosomal mutations or through the introduction of foreign genetic material via HGT. The mechanisms for HGT include transformation, transposition, and conjugation, often resulting in resistance being spread via plasmids. This acquired resistance may be temporary or stable, depending on the nature of the genetic material transferred (Bobate *et al.*, 2023). Conversely, adaptive resistance is a transient phenotypic alteration brought on by environmental factors; depending on how long selection pressure lasts, it may last or reverse. When certain environmental stimuli, such as nutrition availability, stressors, pH changes, and ion concentrations, are combined with sub inhibitory antibiotic concentrations, bacteria may acquire adaptive resistance. High mutation rates, gene amplification, efflux pump activity, biofilm development, and the inherent population variability of bacterial communities are some of the variables that may contribute to the evolution of adaptive resistance, however this is not entirely understood. Since it usually reverts when the environmental variables causing it are eliminated, this resistance is usually temporary (Figure 1) (Wee *et al.*, 2023);(Belay *et al.*, 2024).

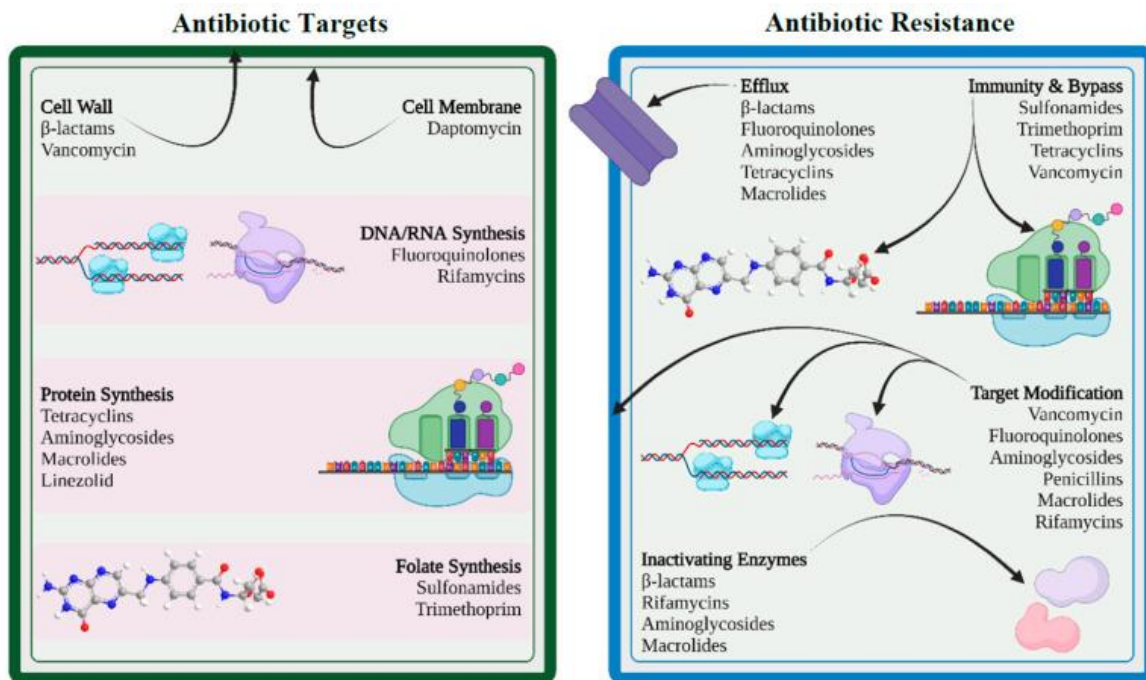
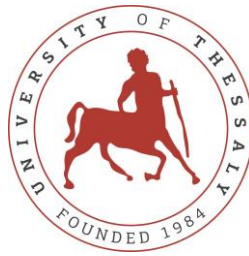
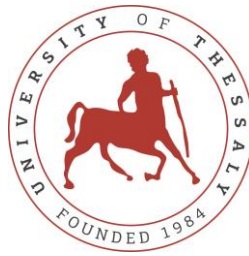


Figure 1: Antibiotic targets and drug resistance mechanisms (Salam *et al.*, 2023).

2.2 The Global Burden of AMR

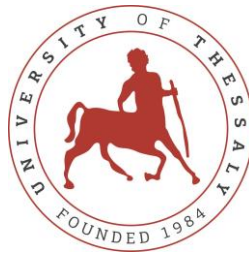
There is a concerning increase in AMR among microorganisms, according to recent statistics. With median AMR resistance rates of 42% for third-generation cephalosporin-resistant *E. coli* and 35% for methicillin-resistant *Staphylococcus aureus*, the 2022 Global Antimicrobial Resistance and Use Surveillance System (GLASS) report shows concerningly high resistance rates in a variety of bacterial strains across 76 countries (World Health Organization., 2023b). 20% of *E. coli* cases that caused urinary tract infections in 2020 showed decreased susceptibility to conventional medicines including ampicillin and fluoroquinolones, indicating a decline in treatment efficacy for common bacterial illnesses (Mouanga-Ndzime *et al.*, 2024). Another common gut bacterium, *Klebsiella pneumoniae*, has shown heightened resistance to necessary antibiotics, increasing the need for last-resort medications like carbapenems, which are also losing their effectiveness because of increased resistance. By 2035, resistance to these important antibiotics is expected



to double compare to 2005, according to OECD projections. This calls for the immediate deployment of strict antimicrobial stewardship and increased surveillance worldwide (Figure 1) (Li, Kumar and Zhang, 2024).

AMR is posing a significant epidemiological challenge in the maritime settings where restricted and communal living arrangements aboard ships facilitate the rapid transmission of resistant microorganisms. Significant outbreaks are not limited to methicillin-resistant *Staphylococcus aureus* (MRSA), demonstrating how susceptible these settings are to AMR. MRSA frequency was shown to be substantially greater (5.8%) than that of the general population (0.11%) in a study including 124 seafarers, with wound-related problems being identified as a critical risk factor (Lekkerkerk *et al.*, 2013). Other antimicrobial-resistant species such as vancomycin-resistant *Enterococcus* (VRE), multidrug-resistant *Pseudomonas aeruginosa*, Carbapenem-Resistant *Enterobacteriaceae* (CRE), Resistant *Salmonella typhi*, Resistant *Vibrio cholerae*, and *Escherichia coli* that produces Extended-Spectrum Beta-Lactamase (ESBL), and Multiple-antibiotic-resistant *Shigella flexneri* have been found to be prevalent on ships. These pathogens when present are frequently associated with suboptimal sanitation conditions, limited onboard medical devices, and ineffective infection-control procedures. AMR pathogen exposure is increased by the transient and heterogeneous population on board ships, which is made worse by the different geographic origins of personnel and passengers (Lv *et al.*, 2023) (Soleimani *et al.*, 2021)(Goh *et al.*, 2022) (Meena *et al.*, 2022) (Adebisi, Bamisaiye and Prisno, 2025).

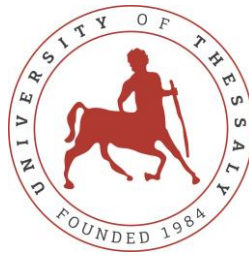
Furthermore, the global distribution and movement of vessels make containment measures more difficult by acting as a route for the cross-border spread of AMR. The operational challenges associated with the empirical use of broad-spectrum antibiotics and further promoting the development of resistant bacteria, were highlighted in a scoping assessment that recognized antimicrobial resistance as a significant concern in marine infection treatment (Anagnostopoulos *et al.*, 2025).



Long-distance travel contributes to the widespread spread of illnesses before they are discovered, and the release of untreated ship effluent into marine areas presents ecological hazards. AMR surveillance on ships is currently insufficient, making it difficult to determine its frequency and impact. Additionally, cases of resistant infections may go unreported. To build efficient surveillance and reporting systems and enable the implementation of focused treatments to manage AMR in maritime environments, it is imperative that maritime authorities, health organizations, and shipping firms work together. The operational and environmental aspects influencing AMR transmission must be considered in customized tactics addressing the particular difficulties of ship situations (Adebisi, Bamisaiye and Prisno, 2025) (O’Flaherty *et al.*, 2019) (Sellera *et al.*, 2024).

2.3 Factors influencing maritime AMR

Antimicrobial-resistant organisms can spread easily on ships due to their confined spaces and dense populations. As demonstrated by outbreaks of respiratory and gastrointestinal disorders, the close quarters shared by thousands of passengers and crew members allow infectious diseases to spread quickly. The risk of pathogen transmission is increased by communal settings like dining establishments and recreational areas as well as extended durations at sea. Control of AMR in these settings is further complicated by ship ventilation systems that recirculate air, potentially facilitating the spread of airborne pathogens (Salam *et al.*, 2023);(Jenkins *et al.*, 2021). Due to their frequent docking at international ports where passengers and crew interact with local populations, ships' global mobility exacerbates the AMR problem by serving as effective conduits for the spread of resistant bacteria. This ongoing mobility hampers public health intervention measures and jeopardizes spatially focused AMR containment initiatives. The rapid turnover of personnel on board may promote the creation of novel resistance mechanisms by facilitating genetic exchange among germs (Cotugno *et al.*, 2025). According to a study on medication usage onboard ships, antibiotics were found to be used extensively in maritime healthcare, accounting for more than 32% of



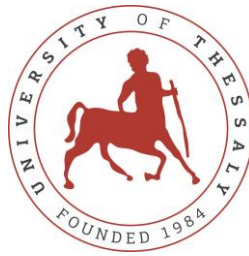
prescriptions.. Amoxicillin was the antibiotic most often prescribed. Antibiotics are empirically used, frequently without conclusive proof of bacterial infection since diagnostic skills are inadequate, which leads to the spread of resistant strains. The scarcity of medical professionals aboard certain ships and the widespread use of broad-spectrum antibiotics as a preventive measure worsen this problem. Further factors increasing the risk of AMR transmission include ineffective antibiotic stewardship programs and inadequate infection control measures, such as inadequate sanitation and hand hygiene (Shao, Adebisi and Adeola, 2025); (Adebisi *et al.*, 2022). Another significant obstacle to AMR control is environmental contamination from ship waste handling. When poorly processed or released directly into the ocean, large amounts of wastewater, such as sewage and ballast water with high bacterial counts and leftover antibiotics, can pollute marine ecosystems. By promoting the spread of resistance traits among microorganisms, these settings may end up serving as reservoirs for resistant bacteria, which could influence the health of people, animals, and the environment. In order to prevent the spread of AMR on ships and safeguard both public health and marine ecosystems, it is imperative that these challenges be addressed (Cheung *et al.*, 2025).

2.4 Maritime Environments as Reservoirs of AMR

The maritime environment is a novel setting that plays a key yet underexplored role in the emergence, and dissemination of AMR. The maritime ecosystems have developed into an intricate interface due to the continuous rapid expansion of global-international trade, shipping, and aquaculture where interactions between humans, animals, and the environment promote the spread of resistant genes and bacteria. These ecosystems pose an emerging significant risk to food security, workplace safety, and public health since they act as both AMR reservoirs and transmission channels (Sassi *et al.*, 2025).

2.4.1 Seawater

Seawater is one of the most significant environmental matrices for the accumulation of resistant bacteria and microbes. Seawater including coastal waterways are oftentimes contaminated by direct exposure to



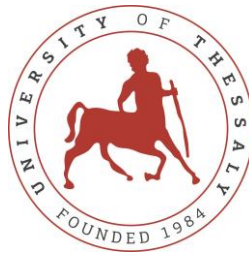
antibiotics and resistant microorganisms via the constant release of untreated or partially treated municipal wastewater, pharmaceutical residues and hospital effluents (Dasi *et al.*, 2024). Other factors include the run-off contaminations from agricultural lands, carrying resistant bacteria and antibiotics residues to marine environments. Several studies have shown that multidrug-resistant pathogen not limited to MDR *Escherichia coli*, *Klebsiella pneumoniae*, and *Enterococcus* species are present in coastal saltwater, highlighting the exchange of both anthropogenic inputs and natural microbial interaction (Adenaya *et al.*, 2025);(Meradji *et al.*, 2025);(Ho *et al.*, 2021). HGT across aquatic microbial communities further exacerbate the emergence and spread of resistant genes across aquatic microbial communities, contributing to the bulk and burden of persistent AMR in saltwater (Cheung *et al.*, 2025).

2.4.2 Ballast Water

Another major pathway through which ships contribute to the transboundary transport and spread of antimicrobial resistance is ballast water. These ballast waters are often loaded on ships from one geographical region and subsequently are discharged in another geographical region, inadvertently transmitting AMR bacteria and genetic material across continents (Guo *et al.*, 2022). For example, most of the ballast waters often contain MDR bacteria such as *Vibrio spp.*, and *E. coli* as well as other pathogenic bacteria, resulting in the spread and emergence of AMR in newly ecological niches. Although, reducing these bio invasions have been discussed and agreed by the Ballast Water Management Convention of the International Maritime Organization, however, regulatory and surveillance gaps persist in the understanding of ballast water's role in AMR spread (Soleimani *et al.*, 2021);(Meradji *et al.*, 2025).

2.4.3 Ports and Shipping Waste

Ports and ship waste are becoming an emerging hotspot for AMR contamination due to industrial discharge, garbage produced by vessels, and concentrated human activity. Antibiotic residues, resistant bacteria, and heavy metals that co-select for resistance are frequently found in shipping waste, which



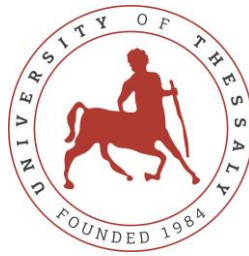
includes sewage, bilge water, and food waste (Balta *et al.*, 2025). The risks of these resistant bacteria infiltrating the maritime environments is further heightened by poor and inadequate waste management practices in many ports, especially in low- and middle-income countries (LMICs). Finally, the increase in maritime activities during this decade has resulted in the frequency of environmental contamination through an isolated resistant bacteria hotspot in port waters (Adenaya *et al.*, 2025);(Musoke *et al.*, 2021).

2.4.4 Fisheries and Aquaculture

The development of AMR in maritime settings is also dependent on important contributors such as fisheries and aquaculture. Aquaculture's extensive use of antibiotics for treatments, growth promotion, and disease prevention is resulting in high quantities of antimicrobial residues into nearby waters and sediments [(Milijasevic *et al.*, 2024);(Agbabiaka, Onwuzuruigbo and Jimoh, 2025)]. It has been reported that aquaculture systems have been found to harbor resistant bacteria including *Aeromonas* and *Vibrio* species, and resistance genes like *tet*, *sul*, and *bla* variants. Environmental channels, foodborne transmission, and direct exposure are several ways in which these organisms transfer resistance to humans. Fish and shellfish taken from contaminated habitats can serve as carriers of resistant bacteria that infiltrate the human food chain, posing risks to both domestic and foreign markets (Popoola, Adeyemi and Samson, 2025) ;(Deng *et al.*, 2025).

2.4.5 Occupational Exposures

At the human–environment interface of AMR, maritime workers not limited to fishermen, dock workers, and seafarers also represent vulnerable groups. The risk of the emergence of, and infection with, resistant bacteria is heightened among maritime workers due to continuous exposure to contaminated seawater, shipping waste, and aquaculture environments (Cheung *et al.*, 2025);(Singh *et al.*, 2022). For example, dock workers handling ballast water or fishermen handling aquaculture goods may come into contact with resistant infections through their skin, their lungs, or their food. Seafarers frequently operate in confined



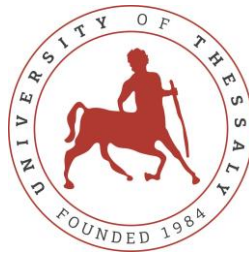
environment with little access to medical treatment, which can make resistant illness outbreaks on board ships worse. Moreover, underreporting and underestimation of occupational AMR risks are caused by inadequate health surveillance and poor occupational safety measures among maritime workers (Okeke *et al.*, 2022);(Almansour *et al.*, 2023).

2.5 Integrated Risks Across Maritime Systems

Integrated risks across maritime systems are increased by the dynamic network created by the interconnectedness of seawater, ballast water, ports, fisheries, shipping waste and aquaculture. Resistant bacteria are released from sources like seawater, ballast discharge and aquaculture effluents which navigate widely, contaminating distant regions. In a same vein, ports act as hubs for the convergence points of AMR determinants by bringing together garbage, shipping, and occupational exposures for humans. The significance of embracing an One Health viewpoint that views maritime settings as crucial nodes in the global AMR network as well as ecological systems is underscored by these linked dangers (Kurniawan *et al.*, 2026);(Outinen *et al.*, 2024).

2.6 AMR's Implications on Maritime Environments

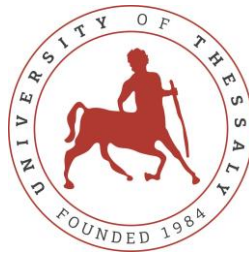
In maritime environments, AMR poses significant public health challenges, especially when outbreaks occur on board ships where passengers and personnel are confined in close quarters. The global transmission of AMR is facilitated by this environment, which raises the possibility of resistant illnesses spreading quickly and be brought back to home nations (Shao, Adebisi and Adeola, 2025). Documented outbreaks of MRSA and other resistant bacteria emphasize the potential role of cruise ships as amplifiers of AMR, while cruise ships are particularly vulnerable due to their huge international passenger base and frequent port visits (Bokhary *et al.*, 2021); (Cotugno *et al.*, 2025). Additionally, the transient nature of populations onboard makes it difficult to implement timely tracing and control measures, hindering public health interventions. AMR outbreaks aboard ships have the potential to cause operational and financial



disruptions for the whole maritime sector. Ships with confirmed resistant infections may be subject to quarantines, port entry denials, or expensive decontamination, which could result in shipping delays, financial losses, and reputational harm. These economic impacts are further amplified by effects that extend beyond maritime operations to supply chains reliant on timely shipping, port activities, and tourism (Adebisi, Bamisaiye and Priso, 2025); (Salam *et al.*, 2023).

There are also serious environmental issues associated with AMR in maritime environments. Untreated wastewater discharge that contains resistant bacteria and antibiotic residues can help spread resistance genes in marine environments, potentially making marine life a reservoir for these pathogens. Concerns over the long-term ecological implications on biodiversity and human health through the seafood supply chain have been raised by the discovery of multidrug-resistant *Escherichia coli* and *Enterococcus* species in maritime ecosystems affected by shipborne garbage (Popoola, Adeyemi and Samson, 2025). Additionally, this contamination may prolong a bacterial resistance gene transfer cycle, making mitigation efforts more difficult.

The problem of managing antimicrobial resistance at sea worsened by regulatory obstacles. Ship operators, port authorities, and international organizations like the IMO and WHO are all involved in effective governance; nevertheless, enforcement is hampered by the absence of standardized AMR management rules (Endale, Mathewos and Abdeta, 2023). The transboundary character of maritime operations, which calls for collaborative multinational initiatives, might exacerbate compliance inconsistencies caused by variations in port regulations. To address the underreported contributions of the maritime sector to the global AMR epidemic, a unified global framework, clear responsibility, and cooperative efforts between public health and maritime industry stakeholders are essential (Mahadeo and Del Savio, 2023).



CHAPTER THREE

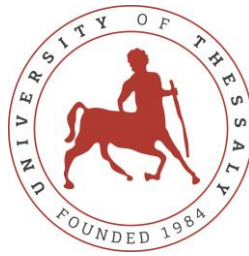
3.0 Methodology

3.1 Study Design

This systematic review and meta-analysis study was conducted strictly following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines. The PRIMA guideline included and guided all the components of this thesis which include but are not limited to the title, abstract, introduction, methodology, results and discussion to ensure the transparency and reproducibility. OJO registered this study review protocol in Prospero, detailing the research question, objectives, eligibility criteria and the methodological approach with the registration number CRD420251071827.

3.2 Eligibility Criteria

Criteria	Inclusion	Exclusion
Population	Human populations including seafarers, fishermen, port workers, coastal residents, crew, passengers and environmental interfaces such as seawater, sewage, sediments samples, wastewater, and ballast water.	General population not linked to maritime or coastal activities and maritime ecosystem
Intervention	Any assessment of AMR bacteria with laboratory confirmation, including surveillance studies. Eligible laboratory methods for identifying AMR bacteria include culture-based techniques, molecular methods, and metagenomics, for detection of resistance in mixed microbial	Studies without AMR data



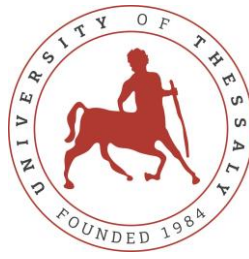
	communities through diverse specimen types including clinical samples such as blood, wound swabs, sputum, urine and stool and environmental samples such as hospital surfaces, medical equipment, wastewater, food, and drinking water.	
Outcome	Prevalence and burden of AMR bacteria as confirmed by the presence or absence of infection and reporting of AMR in human clinical samples and environmental samples.	Non-AMR-related bacterial infections
Study Design	Cross-sectional, cohort, case-control, surveillance reports	Reviews, editorials, commentaries, case reports
Language	English	Non-English
Time Frame	January 2010 – December 2024	Outside the specified period

3.3 Resources required

We conducted the search strategy on the following databases PubMed, Scopus, Web of Science, Embase, Science Direct, Cochrane Library. Manual Search from the reference lists of included studies was also conducted.

3.3.1 Search Strategy

The search strategy for this systematic review and meta-analysis was the combinations of Medical Subject Headings (MeSH) and keywords such as:



- "antimicrobial resistance" OR "antibiotic resistance" OR "drug-resistant bacteria"
- "maritime population" OR "seafarers" OR "coastal population" OR "fishermen" OR "port workers"
- "prevalence" OR "burden"

Using the Boolean “OR” and “AND”, the keywords were combined appropriately for each of the databases.

3.3.2 Structured search strategy

This strategy included Boolean logic, MeSH terms, keywords, and database-specific considerations tailored to each of the six databases:

1. PubMed (MEDLINE) Search Strategy

("Antimicrobial Resistance"[Mesh] OR "Drug Resistance, Bacterial"[Mesh] OR "antimicrobial resistance" OR "drug-resistant bacteria" OR "multidrug resistant" OR "resistant pathogens")

AND

("Seafarers"[Mesh] OR "Maritime Health"[Mesh] OR "Seafaring" OR "Fishermen" OR "Coastal population" OR "Port workers" OR "Maritime population" OR "Naval personnel" OR "Marine workers")

AND

("Prevalence"[Mesh] OR "Epidemiology"[Subheading] OR "Burden" OR "Occurrence" OR "Distribution")

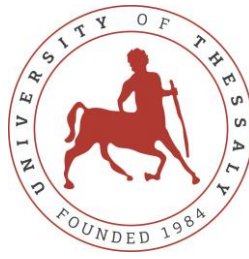
2. Scopus Search Strategy

(TITLE-ABS-KEY("antimicrobial resistance" OR "drug-resistant bacteria" OR "multidrug resistant" OR "resistant organisms"))

AND

(TITLE-ABS-KEY("maritime population" OR "seafarers" OR "fishermen" OR "naval personnel" OR "port workers" OR "marine workers" OR "coastal community"))

AND



(TITLE-ABS-KEY("prevalence" OR "burden" OR "epidemiology" OR "distribution"))

3. Web of Science Search Strategy

TS=("antimicrobial resistance" OR "drug-resistant bacteria" OR "resistant pathogens")

AND

TS=("seafarers" OR "maritime population" OR "fishermen" OR "naval personnel" OR "port workers" OR "coastal population")

AND

TS=("prevalence" OR "burden" OR "epidemiology" OR "distribution")

4. Embase Search Strategy

('antimicrobial resistance'/exp OR 'drug resistant bacteria'/exp OR 'antimicrobial resistance':ti,ab,kw OR 'drug-resistant bacteria':ti,ab,kw)

AND

('maritime health'/exp OR 'seafarer'/exp OR 'fishermen':ti,ab,kw OR 'coastal population':ti,ab,kw OR 'marine worker':ti,ab,kw OR 'port worker':ti,ab,kw)

AND

('prevalence'/exp OR 'epidemiology'/exp OR 'burden':ti,ab,kw OR 'distribution':ti,ab,kw)

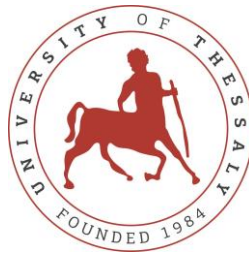
5. ScienceDirect Search Strategy

("antimicrobial resistance" OR "drug-resistant bacteria" OR "resistant organisms")

AND

("maritime population" OR "seafarers" OR "fishermen" OR "port workers" OR "marine personnel" OR "coastal dwellers")

AND



("prevalence" OR "epidemiology" OR "burden" OR "distribution")

6. Cochrane Library Search Strategy

("antimicrobial resistance" OR "drug-resistant bacteria" OR "resistant bacteria")

AND

("seafarers" OR "maritime workers" OR "fishermen" OR "coastal population")

AND

("prevalence" OR "epidemiology" OR "disease burden")

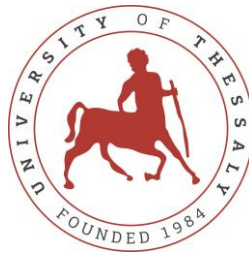
3.3.3 Study Selection Screening Process:

All included articles for this study were imported into a systematic review software manager (Rayyan) and duplicates were removed. Two reviewers (OJO and TAO) independently screened the titles and abstracts for eligibility using inclusion and exclusion criteria. Discrepancies were resolved by discussion with a third reviewer (UOA). Full texts of potentially eligible studies were obtained and screened by two reviewers independently (OJO and TAO). A PRISMA 2020 flowchart was used to document the study selection process.

3.4 Data Extraction

Data extraction was conducted by OJO using a standardized form including:

- Author(s), year, country/region
- Study design, sample size, study population description
- Type of AMR bacteria detected
- Diagnostic method used
- Antibiotics tested
- Prevalence/Resistance pattern/Genes detected



- Key Findings
- Limitations

3.5 Risk of Bias and Quality Assessment

The Joanna Briggs Institute (JBI) Critical Appraisal Tools was used to assess the eligible studies for quality assessment and bias mitigation. Each included study was scored appropriately with studies requiring a minimum of 50% to be included in the analysis as shown in Table 1. Assessments were performed by OJO and disagreements resolved by consensus.

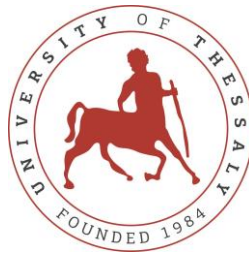
Table 1: JBI Critical Appraisal Result

S/N	AUTHORS	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	TOTAL
1	VICTORIA ET AL., 2022	Y	Y	Y	Y	N	N	Y	N	62.5%
2	VICENTE-CERA ET AL., 2019	Y	Y	Y	Y	N	N	Y	N	62.5%
3	CHAHOURI ET AL., 2020	Y	Y	Y	Y	N	N	Y	Y	75%
4	GIRIJAN AND PILLAI, 2021	Y	Y	Y	Y	N	N	Y	N	62.5%
5	LV ET AL., 2014	Y	Y	Y	Y	N	N	Y	Y	75%
6	BABU ET AL., 2018	Y	Y	Y	Y	N	N	Y	N	62.5%
7	LV ET AL., 2022	Y	Y	Y	Y	N	N	Y	Y	75%
8	SOLEIMANI ET AL., 2017	Y	Y	Y	Y	N	N	Y	N	62.5%
9	SOLEIMANI ET AL., 2021	Y	Y	Y	Y	N	N	Y	U	62.5%
10	MEENA ET AL., 2022	Y	Y	Y	Y	N	N	Y	Y	75%
11	PAVLI ET AL., 2016	Y	Y	Y	Y	N	N	Y	Y	75%
12	LV ET AL., 2021	Y	Y	Y	Y	N	N	Y	Y	75%
13	OOMS ET AL., 2022	Y	Y	Y	Y	N	N	Y	Y	75%
14	KIM AND SON ET AL., 2024	Y	Y	Y	Y	N	N	Y	Y	75%

Y= YES, N= NO U=UNCLEAR

JBI Critical Appraisal Checklist

1. Were the criteria for inclusion in the sample clearly defined?
2. Were the study subjects and the setting described in detail?



3. Was the exposure measured in a valid and reliable way?
4. Were objective, standard criteria used for measurement of the condition?
5. Were confounding factors identified?
6. Were strategies to deal with confounding factors stated?
7. Were the outcomes measured in a valid and reliable way?
8. Was appropriate statistical analysis used?

3.6 Data Synthesis and Statistical Analysis

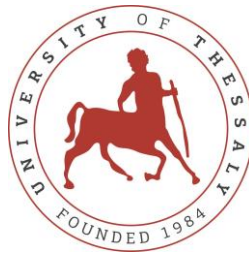
A systematic narrative qualitative synthesis and a quantitative analysis for all included studies was conducted. Where appropriate, we pooled the prevalence data in a meta-analysis using R software version (R 4.3.2) with meta and metafor packages. The random-effects model was adopted to account for heterogeneity between-study and across crops. Prevalence estimates were calculated along with 95% confidence intervals (CIs).

Heterogeneity among studies was assessed using the I^2 statistic, and interpreted as:

- 0% = no heterogeneity
- 25% = low
- 50% = moderate
- 75% = high

3.7 Ethics and Dissemination

No ethical approval was required as the study uses already published data.



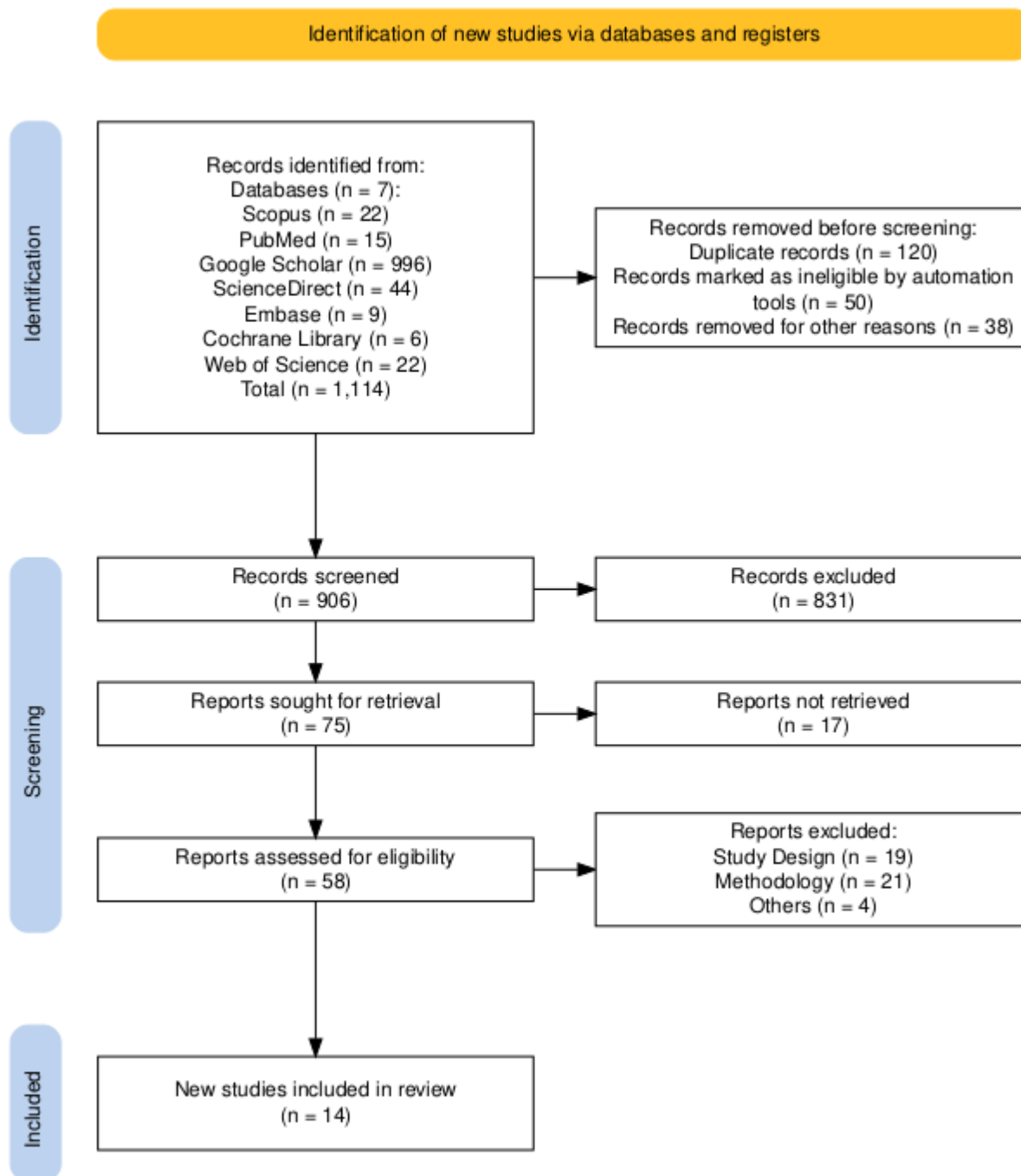
CHAPTER FOUR

4.0 RESULTS AND PRESENTATION

We present the findings of the systematic review and meta-analysis in this chapter, which was conducted to determine the pooled prevalence of AMR in bacterial isolates from maritime environments. The results are



structured to provide an overview of the included studies, the overall pooled prevalence, an assessment of heterogeneity, a detailed breakdown of study-specific and subgroup findings, and a critical evaluation of potential biases.



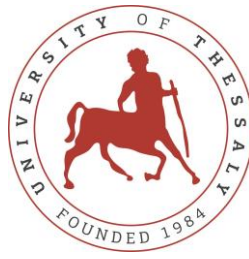
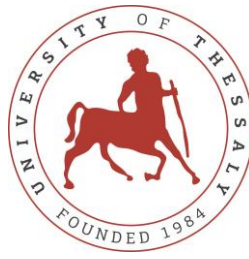


Figure 2: PRISMA Flowchart of the included studies (Haddaway *et al.*, 2022)

4.1. Characteristics of Included Studies

The comprehensive literature search across the included electronic databases found a total record of 1,114 articles including 22 from Scopus, 15 from PubMed, 996 from Google Scholar, 44 from ScienceDirect, 9 from Embase, 6 from Cochrane Library, and 22 from Web of Science (Figure 2). Finally, 14 studies published between 2010 and 2024 were included after the title and abstracts were screened and full-text assessment against eligibility criteria (Figure 2, PRISMA flow diagram). The included studies showed a broad geographic distribution, spanning Europe (Spain and Netherlands), the Middle East (Iran), Africa (Morocco), and Asia (India, China, Iran, South Korea, and Morocco). In terms of study design, the majority ($n = 9$) were cross-sectional observational studies that monitored the environment for wastewater, sediments, saltwater, and ballast water, outbreak investigations ($n = 1$), prospective or retrospective cohort studies ($n = 2$), and comparative ecological assessments ($n = 2$) (Table 2). Several study settings were reported varying from hospital effluent discharge sites (Kerala, India), shipyards and ports (Cádiz, Jiangyin, Bushehr, Andaman Islands), coastal beaches and estuaries (Cape Comorin, Agadir beach, Oued Souss), and human-focused maritime environments (wounded fishermen, asylum seekers housed on ships, cruise ship passengers and crew, and students on a training vessel). The included studies examined bacterial species in environmental samples (ballast water/sediment, wastewater, seawater, coastal sediments and bivalves) and Human/clinical samples (wounds of fishermen, stool/blood from outbreak investigations, cruise ship clinical reports, training-ship rectal samples). The meta-analysis screening process yielded 6 independent studies with homogenous data that are suitable for inclusion, for the quantitative analysis. From these



studies, a total of 15 individual effect sizes (logit-transformed prevalence values) were extracted, as several studies reported AMR data for multiple bacterial species. The forest plot in Figure 3 provides a detailed visualization of each effect size, its confidence interval, and its contribution to the overall model. The use of multiple effect sizes per study necessitated a multilevel meta-analytic model to account for the non-independence of data.

4.2. Bacterial spectrum identified

Gram-negative pathogens were predominant in environmental samples in the included studies and included *Escherichia coli*, *Vibrio* spp. (*V. cholerae*, *V. parahaemolyticus*, *V. alginolyticus*), *Salmonella* spp., *Pseudomonas aeruginosa*, *Shigella* spp., *Klebsiella* spp., *Aeromonas* spp., and other Enterobacterales (Soleimani *et al.*, 2021);(Meena *et al.*, 2022); (Lv *et al.*, 2023); (Chahouri *et al.*, 2022);(Babu *et al.*, 2018);(Victoria, Sree Devi Kumari and Lazarus, 2022). Several studies also detected fecal indicator organisms at high counts in ship wastewater and coastal waters (Vicente-Cera *et al.*, 2019);(Soleimani *et al.*, 2017). On the other hand, few gram positive bacteria were reported including *Staphylococcus aureus* (including MRSA and VRSA strains) and *Enterococcus* spp (Babu *et al.*, 2018);(Girijan and Pillai, 2021);(Lv *et al.*, 2023). Emerging and rare pathogens such as *Cronobacter sakazakii*, *Serratia nematodiphila*, *Bacillus anthracis*, and *Mycobacterium avium* were less reported as unexpected findings across several studies in the maritime interfaces (Chahouri *et al.*, 2022);(Lv *et al.*, 2021); (Lv *et al.*, 2018);(Lv *et al.*, 2023).

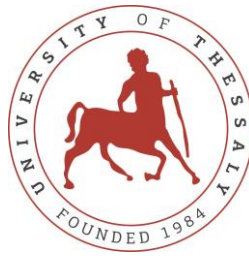
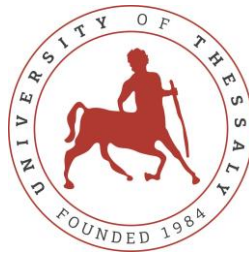
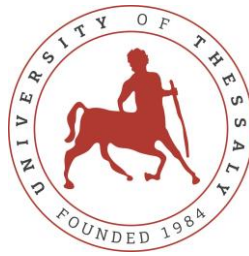


Table 2 – Characteristics of the Included Studies

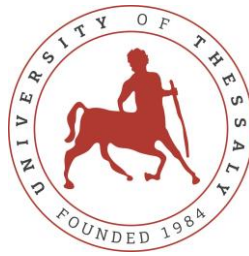
S/ N	Author and Year	Country/Region	Study Design	Study Settings	Sample Type	Sample Size	Population/ Source
1	(Victoria, Sree Devi Kumari and Lazarus, 2022)	Cape Comorin, India	A bacteriological survey	Conducted in coastal area impacted by untreated sewage from tourists and residents across three different seasons between December 2019 and November 2020.	Raw sewage, partially mixed sewage, seawater (0–20 cm depth), and surface sediment (0–5 cm depth)	36 water samples and 12 sediment samples were collected	Coastline of Kanyakumari, Tamil Nadu, India
2	(Vicente-Cera <i>et al.</i> , 2019)	Cádiz and Puerto Real (SW Spain)	Environmental monitoring and cross-sectional observational study	Shipyards of Cádiz and Puerto Real, Southwest Spain	5L of Wastewater samples were collected from four cruise ships	8 wastewater samples	Wastewater samples were obtained from cruise ships during repair works
3	(Chahouri <i>et al.</i> , 2022)	Morocco	Comparative ecological assessment	Conducted at two sites: the Oued Souss estuary and Agadir beach.	Seawater, bivalves (<i>Donax trunculus</i> and <i>Scrobicularia plana</i>), and surface sediment.	144 samples	Oued Souss estuary and Agadir beach
4.	(Girijan and Pillai, 2021)	India	Observational cross-sectional environmental study	Conducted in three hospitals in Kerala, India located near water bodies used for fishing	Water and sediment samples	6 samples yielding 162 isolates	3 hospitals discharge points



				between August-December 2018-2019.			
5.	(Lv <i>et al.</i> , 2018)	China	Observational cross-sectional molecular study	Environmental pollution in ballast tank sediments was analyzed for ARGs and HBPs	Ballast tank sediment samples	9 samples	Ballast tank sediments from ocean-going vessels in a shipyard in Jiangyin City, China
6.	(Babu <i>et al.</i> , 2018)	India	A cross-sectional study	Fishermen in coastal areas with any wounds, from 13 villages.	Pus/wound swabs collected from fishermen's wounds.	292 fishermen with wounds	Fishermen involved in fishing activities from coastal areas of Puducherry.
7.	(Lv <i>et al.</i> , 2023)	China	A cross-sectional, laboratory-based study	Samples were collected from cargo ships at Jiangyin Harbor, China, originating from various global regions, with ballast water and sediment analyzed for bacterial pathogens	Ballast water samples and Sediment samples	60 samples	Cargo ships docked at Jiangyin harbor, China, originated from various regions, including Southern China Sea and Mediterranean
8.	(Soleimani <i>et al.</i> , 2017)	Iran	A cross-sectional environmental study	Conducted between 15 February and 25 August 2016, in which ballast water samples from commercial ships arriving at Bushehr Port were	Ballast water samples	34 samples	Commercial ships entering Bushehr port, along the Persian Gulf from 34 ports around the world



				collected from vessels originating from 34 international ports.			
9.	(Soleimani <i>et al.</i> , 2021)	Iran	A cross-sectional study	Ballast water samples were collected from 34 commercial ships at Bushehr Port and transported to the laboratory within 2 hours for the detection of <i>E. coli</i> and <i>Vibrio cholerae</i>	Ballast water samples	34 samples	34 commercial ships entering Bushehr port from different ports around the world
10.	(Meena <i>et al.</i> , 2022)	India	A cross-sectional study assessing bacteriological risks	Ballast water and seawater samples were collected for <i>Vibrio cholerae</i> detection within 4 hours.	Ship's ballast water	30 samples yielding 72 isolates	10 Andaman Islands ships
11.	(Pavli <i>et al.</i> , 2016)	European Port	3-Study Prospective Study	Conducted from January 2011 to December 2013 on Cruise Ship A, departing from a European port depending on the itinerary	Clinical samples such as Oropharyngeal/rhinopharyngeal swabs (for ARI/ILI testing). Stool or vomit-related clinical reporting (for GI).	Not Reported	Patients, passengers, and crew members of Cruise Ship A presenting with ARI, ILI, or GI symptoms.
12.	(Lv <i>et al.</i> , 2021)	China	Cross-sectional laboratory-based study	Conducted at the Port of Jiangyin, Jiangsu Province,	Ballast water	30 samples	Ballast water from cargo ships arriving

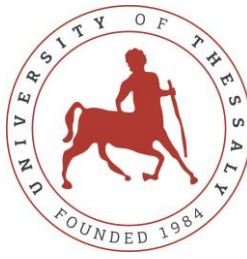


				China (Yangtze River) on Cargo ships originated from multiple ports to investigate ARB			at Jiangyin Port
13.	(Ooms <i>et al.</i> , 2024)	Netherland	Outbreak investigation using epidemiological survey, case register review, environmental/technical inspection, and water sample analysis	Investigated a typhoid fever outbreak among asylum seekers on two retired ships	Human and environmental samples	~200 asylum seekers	Male asylum seekers housed on Ship 1 and Ship 2, Employees working on the ships and environmental source
14.	(Kim and Son, 2024)	South Korea	A retrospective cohort study design	Conducted on a training ship from A High School during a training period	Human and environmental samples	38 Rectal samples 17 Environmental samples	Entire exposed group of 171 individuals on the training ship (students, staff, food handlers)

4.3. Detection methods

Several laboratory diagnostics methods were employed to detect the bacteria and the Antimicrobial resistance patterns and genes such as;

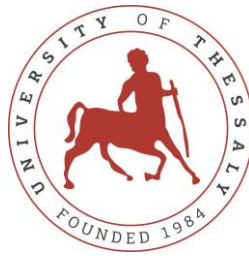
1. **Culture-based methods:** Such as API 20E, selective/chromogenic agars and conventional culture were used across early and many environmental studies for species identification and isolation as routine biochemical tests (Chahouri *et al.*, 2022);(Soleimani *et al.*, 2021).



2. **Molecular methods:** PCR, qPCR/real-time PCR, 16S rDNA sequencing and targeted gene amplification (e.g., *mdh*, *ompW* for *E. coli*/*V. cholerae*) were used increasingly from 2018 onward for both pathogen detection and ARG screening (Girijan and Pillai, 2021); (Lv *et al.*, 2018);(Lv *et al.*, 2023).
3. **Antimicrobial susceptibility testing (AST):** The most common phenotypic AST method used was the Disk diffusion (Kirby–Bauer); MIC/strip tests were used in some clinical/hospital studies. Genomic approaches (ResFinder/PointFinder and ARG panels) supplemented phenotypic AST in a subset of studies (Victoria, Sree Devi Kumari and Lazarus, 2022);(Babu *et al.*, 2018);(Girijan and Pillai, 2021);(Ooms *et al.*, 2024).

4.4. Antimicrobial resistance profiles

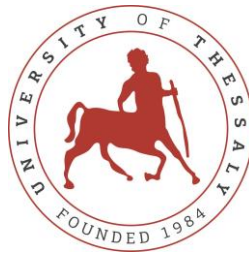
Human and environmental maritime interfaces consistently showed resistance to routinely tested antibiotics, including aminoglycosides, first- and second-generation cephalosporins, fluoroquinolones, carbapenems, and penicillins and related β -lactams across all the included studies. Class 1 integrons (*intI1*) and mobile genomic elements have been identified as significant predictors of ARG abundance and possible horizontal transmission. Nathini *et al* reported universal resistance to β -lactam antibiotics such as penicillin and piperacillin among isolates on a coastal survey with *E. coli* and *Proteus mirabilis* showing the highest resistance burdens (Victoria, Sree Devi Kumari and Lazarus, 2022). *Vibrio* spp. including *V. parahaemolyticus* and *V. alginolyticus* also demonstrated substantial resistance to ampicillin and cephalothin respectively in another study (Chahouri *et al.*, 2022). *Staphylococcus aureus* was identified in a hospital effluent study, where 76% of isolates exhibited multidrug resistance (MDR) and *vanA/vanB* genes were detected among vancomycin-resistant *S. aureus* (VRSA) isolates (Girijan and Pillai,



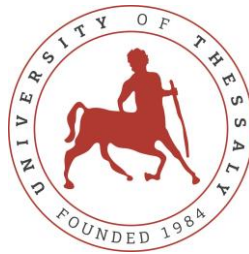
2021). High proportions of methicillin-resistant *S. aureus* (MRSA) were also reported among isolates from fishermen in a coastal occupational study (Babu *et al.*, 2018). The presence of carbapenemases was confirmed in maritime settings with the identification of MBL-producing *Pseudomonas* spp. reported in another occupational study (Babu *et al.*, 2018). Ballast-derived *V. cholerae* isolates showed high MDR rates and substantial ampicillin resistance (Soleimani *et al.*, 2021);(Meena *et al.*, 2022). Molecular ARGs including *aadA1*, *blaCTX-M*, *blaTEM*, *ermB*, *mefA*, *strB*, *sul1*, *sul2*, *tetM*, *tetQ* and a high prevalence of *intI1*, and plasmid-mediated resistance were also reported in the studies (Lv *et al.*, 2018). Lastly, MDR organisms were commonly reported from ballast water, sediments and wastewater, indicating maritime environments as reservoirs and transmission points (Babu *et al.*, 2018);(Meena *et al.*, 2022) (Table 3).

Table 3: Burden and Prevalence of Antimicrobial Resistance Bacteria among Maritime Human–Environmental Interfaces (2010–2024)

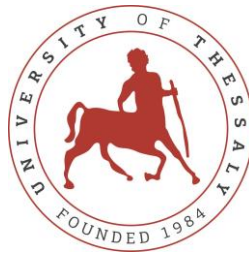
S/N	Bacterial Species	Bacteria detected	Detection Methods	Antibiotics Tested	Prevalence/Resistance pattern/Genes detected	Key Findings	Limitations
1	(Victoria, Sree Devi Kumari and	<i>Enterococcus faecalis</i> , <i>E. coli</i> , <i>Vibrio cholerae</i> ,	Biochemical tests identified gram-negative	Ten widely used antibiotics in India; Penicillin, Gentamycin,	<i>E. coli</i> and <i>Proteus mirabilis</i> showed the highest resistance. All	Kanyakumari coastal waters are plagued by	Not Reported



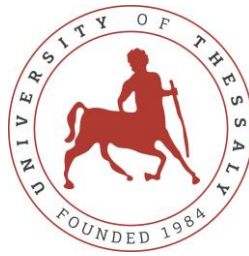
	Lazarus, 2022)	<i>Shigella</i> spp., <i>Klebsiella</i> spp., <i>Aeromonas</i> spp., <i>Proteus mirabilis</i> , <i>Flavobacterium</i> spp. and <i>Salmonella typhi</i>	organisms. Kirby-Bauer Disk Diffusion method	Norfloxacin, Ceftriaxone, Amoxicillin, Piperacillin, Chloramphenicol, Amikacin, Ofloxacin, and Meropenem.	isolates were resistant to Penicillin and Piperacillin. Resistance was mediated by mobile genetic elements like plasmids	pathogenic pollution indicators, sewage from various sources, fetal contamination, high levels of antibiotic- resistant bacteria, and community ignorance contributing to ongoing issues.	
2	(Vicente- Cera <i>et al.</i> , 2019)	<i>E. coli</i> and Enterococci were detected in all samples, with total coliforms present in significant amounts and fecal microorganisms consistently above 10 ⁴ CFU 100 mL ⁻¹ .	Not Reported	Not specified (only triclosan reported)	High fecal bacterial loads indicated potential spread of resistance. Presence of antibiotic compounds may contribute to ARB generation.	Cruise ship wastewater exhibited high pollution levels, fecal bacteria levels surpassing untreated domestic wastewater, and antibiotics present, posing a risk of resistance development, with AIS data aiding in tracking ship repair activities.	Not Reported
3.	(Chahouri <i>et al.</i> , 2022)	<i>Vibrio</i> pathogens, salmonella, <i>Cronobacter</i> <i>sakazakii</i> , <i>Pseudomonas</i> <i>fluorescens</i> , and <i>Aeromonas</i>	Biochemical tests were performed using API 20 E system. Antibiotic resistance	Nine antibiotics were tested including ampicillin, amoxicillin/clavulanic acid, imipenem, gentamicin, amikacin, norfloxacin,	<i>V. parahaemolyticus</i> showed high resistance to ampicillin (60%) and cephalothin (70%), with additional resistance to amikacin and evidence of	Fecal indicator bacteria, virio pathogens, and Salmonella strains in Agadir Bay ecosystems are causing	FIB alone may not reliably assess microbiological quality. Environmental surveys are



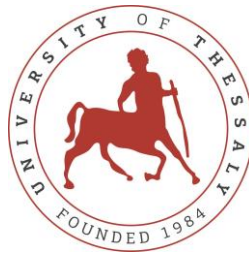
		<i>hydrophila</i>	profiles were determined using the Kirby-Bauer method.	Ciprofloxacin, chloramphenicol, cefotaxim, and cefalotin.	multidrug resistance. <i>V. alginolyticus</i> exhibited weaker resistance to ampicillin (52%) and cephalothin (57%). <i>Salmonella</i> strains were mostly sensitive, except for resistance to ampicillin and amoxicillin. Resistance genes contribute to the persistence of resistant bacteria in marine environments.	antimicrobial resistance, raising concerns for coastal water safety.	crucial for understanding pathogen distribution
4.	(Girijan and Pillai, 2021)	A total of 113 <i>S. aureus</i> isolates focusing on <i>vancomycin-resistant Staphylococcus aureus</i> (VRSA)	Disc diffusion tests for antibiotic susceptibility, MIC determination using strip method, plasmid curing and conjugation for plasmid-mediated resistance, and PCR for resistance gene detection.	Azithromycin (15 µg), Ampicillin (10 µg), Clindamycin (2 µg), Clarithromycin (15 µg), Chloramphenicol (30 µg), Ciprofloxacin (5 µg), Moxifloxacin (5 µg), Erythromycin (15 µg), Gentamicin (10 µg), Methicillin (5 µg), Oxacillin (1 µg), Streptomycin (10 µg), Trimethoprim (5 µg), and Vancomycin (30 µg).	76% of <i>S. aureus</i> isolates are resistant to multiple antibiotics, with high MAR index values. <i>vanA</i> and <i>vanB</i> genes were detected in VRSA isolates with <i>vanA</i> comprising 46.5% of the total isolates.	Hospital wastewater contains vancomycin-resistant <i>S. aureus</i> , with 76% of isolates resistant to multiple antibiotic classes. These isolates, encoding genes <i>vanA</i> and <i>vanB</i> , contaminate public water bodies.	Not Reported



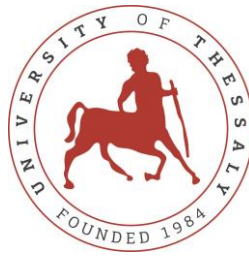
5.	(Lv <i>et al.</i> , 2018)	<i>Vibrio</i> parahaemolyticus was found in ballast tank sediments, with <i>Enterococcus hirae</i> as the dominant pathogen. <i>Bacillus anthracis</i> was the most prevalent, along with <i>Pseudomonas pseudoalcaligenes</i> , related <i>Vibrio</i> and <i>Escherichia</i> species.	Genomic DNA extraction, real-time PCR quantification of ten common ARGs, analysis of Class-I integron gene (intI1) and 16S rRNA gene, and correlation analysis to assess potential horizontal gene transfer.	Not reported	Ten ARGs (aadA1, blaCTX-M, blaTEM, ermB, mefA, strB, sul1, sul2, tetM, and tetQ) were found in ballast tank sediments, with sulfonamide resistance genes predominant in coastal areas. intI1 gene was more abundant, suggesting horizontal gene transfer.	Ballast tank sediments contain diverse ARGs and HBPs, including sul1, sul2, and intI1, with 44 bacterial pathogens identified, posing ecological and health risks due to strong correlations between intI1 and ARGs.	Indicator microbes may underestimate pathogenic bacteria diversity in sediments, and potential ARG transfer among human pathogens is not fully addressed, while management of ballast tank sediments is a concern.
6.	(Babu <i>et al.</i> , 2018)	<i>Staphylococcus aureus</i> , <i>Staphylococcus spp.</i> , <i>Pseudomonas spp.</i> , <i>Streptococcus pyogenes</i> , <i>E.coli</i> , <i>Klebsiella pneumoniae</i> , <i>Proteus spp.</i> , <i>Enterococcus spp.</i> , <i>Diphtheriods</i> , <i>Enterobacter spp.</i> and <i>Streptococcus spp.</i>	Kirby Bauer disk diffusion method	Amikacin (30 µg), Gentamycin (10 µg, 120 µg), Nitrofurantoin (300 µg), Ceftazidime (30 µg), Amoxycylav (30/10 µg), Cefepime (30 µg), Co-trimoxazole (25 µg), Ceftazidime-clavulanic acid (30/10 µg), Clindamycin (2 µg), Vancomycin (30 µg), Cefoxitin (30 µg), Imipenem (10 µg), Meropenem (10 µg), Imipenem + EDTA, Aztreonam (50 µg),	61.0% MRSA and 32.3% Methicillin-resistant CONS, 8.7% MBL producing <i>Pseudomonas spp.</i> and 5% MDR <i>E. coli</i> were isolated	30.5% of fishermen experienced lower extremity injuries, 92.1% did not receive first aid, and 25.3% reported gear injuries. High drug resistance in bacterial infections and modern fishing methods are noted.	The study was limited by lack of data on patient co-morbidities, absence of follow-up on 13.3% of CONS isolates, financial and logistical constraints, potential influence of self-medication on drug



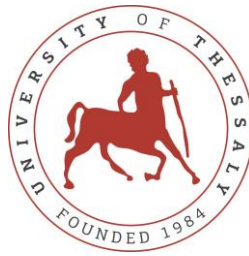
				Erythromycin (15 µg)			resistance, and restricted generalizability due to participants' limited access to medical services
7.	(Lv et al., 2023)	<i>Escherichia coli</i> <i>Enterococcus faecalis</i> <i>Salmonella</i> spp. <i>Shigella</i> spp. <i>Bacteroidetes</i> <i>Vibrio cholerae</i> <i>Staphylococcus aureus</i> <i>Acinetobacter lwoffii</i> <i>Pseudomonas aeruginosa</i> <i>Vibrio parahaemolyticus</i> <i>Vibrio alginolyticus</i> <i>Mycobacterium avium</i>	Quantitative PCR (qPCR) for pathogen detection using SYBR® Premix Ex Taq TM, Bio-Rad CFX96 Real-time PCR System, and <i>E. coli</i> plasmids with varying gene copies.	Not Reported	48 bacterial pathogens (<i>uidA</i> , <i>efaA</i> , <i>invA</i> , <i>ipaH</i> , <i>Bac32</i> , <i>hemM</i> , <i>nuc</i> , <i>blaOXA</i> , <i>oaa</i> , <i>tlh</i> , <i>toxR</i> , <i>V12-myav</i>), with <i>Rhodococcus erythropolis</i> and <i>Vibrio campbellii</i> being predominant, while <i>Shigella</i> sp. and <i>Staphylococcus aureus</i> were found in higher concentrations.	Ballast sediments have higher pathogen concentrations than water, with significant differences between communities. Indicator species may underestimate pathogen risks, posing ecological and health risks.	Not Reported



8.	(Soleimani <i>et al.</i> , 2017)	Total coliforms, fecal coliforms, <i>Pseudomonas aeruginosa</i> , <i>E. coli</i> and heterotrophic plate count (HPC) bacteria	Biochemical methods	Not Reported	Total coliforms: detected in 24/34 samples Fecal coliforms: detected in 13/34 samples <i>E. coli</i> : detected in 4/34 samples <i>Pseudomonas aeruginosa</i> and HPC detected in all samples	Ballast water contains harmful pathogenic bacteria, with coliform and fecal coliform levels lower than coastal waters. <i>Pseudomonas aeruginosa</i> levels exceed coastal standards.	Not Reported
9.	(Soleimani <i>et al.</i> , 2021)	<i>E. coli</i> and <i>Vibrio cholerae</i>	PCR techniques were utilized to detect <i>E. coli</i> Mdh gene and <i>Vibrio cholerae</i> OmpW gene, offering rapid, sensitive, and specific detection compared to conventional culture methods.	Not Reported	<i>E. coli</i> was detected in 19/34 samples, <i>Vibrio cholerae</i> 14/34 samples while Mdh gene was positive in 4 <i>E. coli</i> samples	PCR assays offer rapid and precise pathogen analysis in samples, including identifying <i>Vibrio cholerae</i> in ballast water and detecting <i>E. coli</i> O157:H7 in samples.	Lack of implementation of international guidelines for ballast water management, particularly in third world countries, and calls for better management and more efficient use of PCR techniques in future research.
10.	(Meena <i>et al.</i> , 2022)	<i>Vibrio cholerae</i> O1 and O139, other bacteria detected include <i>Listeria</i>	PCR amplification was used to detect	penicillin, ampicillin, oxacillin, amoxycylav, cefotaxime, cefpodoxime,	100% of <i>V. cholerae</i> isolates had the hlyA gene, 60% possessed the luxA gene.	<i>V. cholerae</i> was found in ballast water from various ships, with	Not Reported



		monocytogenes and <i>E. coli</i>	biomarker genes in <i>V. cholerae</i> , with a positive control and chromogenic agar used for isolating strains.	ceftazidime, cefoxitin, kanamycin, gentamycin, tobramycin, erythromycin, azithromycin, clindamycin, vancomycin, rifampicin, gatifloxacin, ciprofloxacin, gemifloxacin, nalidixic acid, tigecycline.	Resistance to Ampicillin was 54.16%. Most prevalent resistance type was antibiotic 11, 43.3%. 77.44% exhibited MDR phenotypes.	maximum count in GO ship ballast water. All isolates showed 100% antibiotic resistance, highlighting bacteriological risk in Andaman sea.	
11.	(Pavli <i>et al.</i> , 2016)	<i>Helicobacter</i> and <i>Streptococcus</i>	Rapid diagnostic tests, laboratory analyses, and imaging techniques	Not Reported	Not Reported	Respiratory and gastrointestinal infections were rare, with the majority of cruises to Northern Europe. The incidence rates were 1.970/1000 (ILI), 0.958/1000 (ARI), and 1.026/1000 (GI), respectively.	Limited sample size, insufficient evaluation of laboratory investigations, low sensitivity of influenza tests, and reliance on self-reported data, potentially causing bias.
12.	(Lv <i>et al.</i> , 2021)	<i>Serratia nematodiphila</i> and <i>Vibrio parahaemolyticus</i>	The 16S rDNA of MARB was amplified using specific primers, cultured in 2216E liquid medium, and PCR products	PEN, LEX, TET, CHL, OXY, VAN, ERY, GEN, CIP, and CEP	ARBs were detected in 83.3% of ballast water samples, with PEN-resistant bacteria having the highest detection rate at 73.3%. Five or more ARB types were found	ARB were found predominantly in ballast water samples, with PEN-resistant bacteria having the highest detection rate. AMARB index exceeded 200% in	Not Reported



			sequenced after quality control, using the Basic Local Alignment Search Tool for gene analysis.		in 20 samples.	five ships' ballast waters, with OXY-, CHL-, TET-, and VAN-resistant bacteria predominant.	
13.	(Ooms et al., 2024)	Enterobacterales, <i>Salmonella spp.</i> , and <i>S. Typhi</i>	Blood and stool culture. AMR markers were detected using ResFinder and PointFinder	Not Reported	Typhoid 72/200	Typhoid fever outbreak on ship was caused by construction defect, contaminated freshwater emphasizing the need for future inspections.	Incomplete participation, recall bias, lack of technical blueprints, and difficulty in determining the length of stay on ships and the transmission route of <i>S. Typhi</i> .
14.	(Kim and Son, 2024)	<i>C. perfringens</i>	Biochemical Testing	Not Reported	41/165 (24.8%)	A food-borne disease outbreak on a training ship in Busan, caused by <i>Clostridium perfringens</i> , occurred with a 24.8% attack rate and a significant relative risk in 11 food items.	Staff reluctance, confusion from non-symptomatic students, lack of food preservation, consumed ingredients, and poor ventilation on the ship hindered the



							investigation and spread of infectious diseases.
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4.5. Outbreak and case study findings and Risk factors & environmental burden

Ooms et al. reported an outbreak of typhoid among asylum seekers on a ship, affecting 72 of the approximately 200 occupants (Table 3). Freshwater contamination was linked to ship construction and maintenance flaws discovered during an environmental examination, demonstrating how water systems and ship architecture may contribute in the spread of disease (Ooms *et al.*, 2024). A foodborne outbreak of *Clostridium perfringens* was reported by Kim & Son on a training ship where the investigation implicated food handling/preservation failures and environmental contributors (poor ventilation, food storage) (Kim and Son, 2024). Monitoring of gastrointestinal and respiratory disorders on cruise ships highlight surveillance inadequacies and the significance of laboratory confirmation in constrained marine settings, despite the low yet detectable incidence rates for ILI/ARI/GI (Pavli *et al.*, 2016). In all outbreak cases, AMR exacerbated clinical care issues and the risk of long-term transmission in restricted marine environments (ships, asylum-housing), especially when food safety procedures or sewage/water systems were disrupted. Untreated sewage and coastal contamination are linked to elevated pathogen loads and AMR in coastal waters. Ballast water and sediments are consistent reservoirs of diverse pathogens and ARGs, with higher concentrations in ballast sediments than in waters. Mobile genetic elements are correlated with ARG abundance and interspecies ARG dissemination potential. Policy and management gaps, particularly in LMICs settings, contribute to the environmental spread of resistant organisms.



AMR Prevalence in Maritime Environments

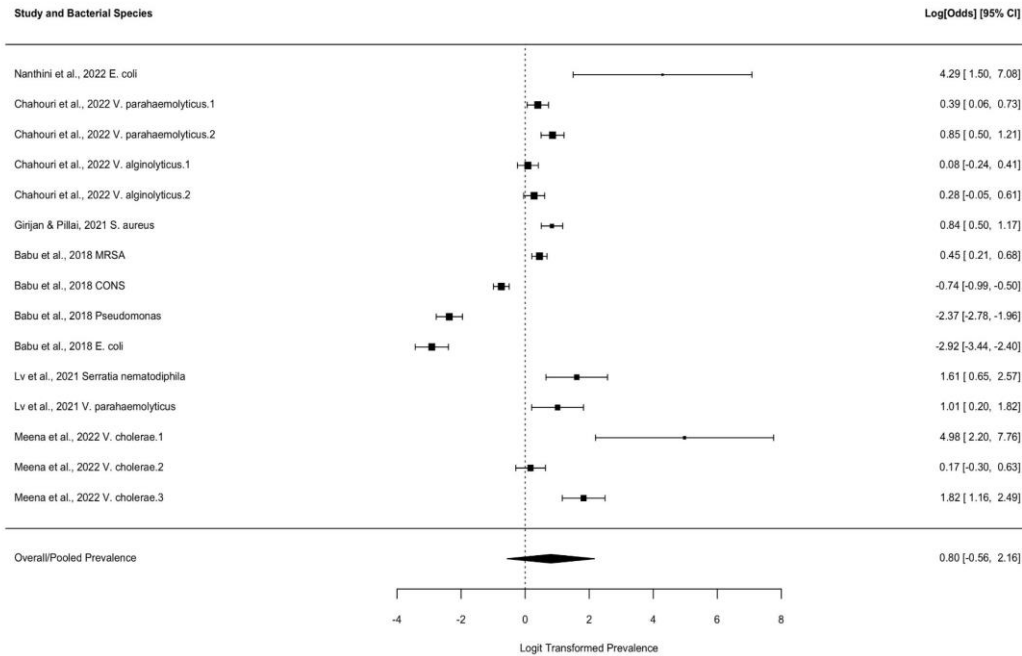


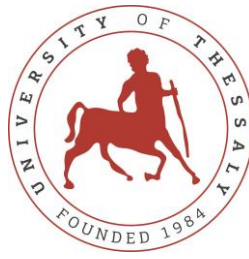
Figure 3: Forest Plot of Logit-Transformed AMR Prevalence in Maritime Environment

4.6 Overall Pooled Prevalence of Antimicrobial Resistance

The multilevel random-effects meta-analysis model was fitted to synthesize the data. The model revealed high pooled prevalence of AMR in maritime environments. The overall estimate was 69.0% (95% Confidence Interval [CI]: 36.4% to 89.7%). This overall effect was statistically significant ($p < 0.001$), indicating that the prevalence of AMR in these environments is substantially greater than zero. However, the exceptionally wide confidence interval reflects considerable uncertainty in this point estimate.

4.6.1 Assessment of Heterogeneity

The analysis revealed an extreme degree of heterogeneity among the effect sizes. The I^2 statistic, which quantifies the proportion of total variation due to heterogeneity rather than chance, was 98.6%. This value

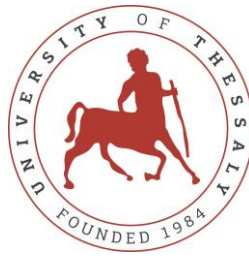


indicates that virtually all the variability in the observed effects is attributable to genuine differences between studies rather than sampling error. This finding was further supported by a highly significant Cochran's Q statistic ($Q = 419.91$, $df = 14$, $p < 0.0001$). The variance components were estimated as $\tau^2 = 1.595$ (between-study variance) and $\tau^2 = 1.267$ (within-study variance). This substantial heterogeneity precludes a simple interpretation of the pooled estimate and underscores the pronounced variation in AMR prevalence across different geographical locations, bacterial species, and methodological approaches.

4.6.2 Study-Specific and Subgroup Findings

The forest plot illustrates the extreme variation encapsulated by the heterogeneity statistics. The logit-transformed prevalences ranged from -2.37 (approximately 8.5% prevalence) for *Pseudomonas spp.* in Babu et al. (2018) to 4.98 (approximately 99.3% prevalence) for *V. cholerae* in Meena et al. (2022). A qualitative synthesis of the findings reveals distinct patterns:

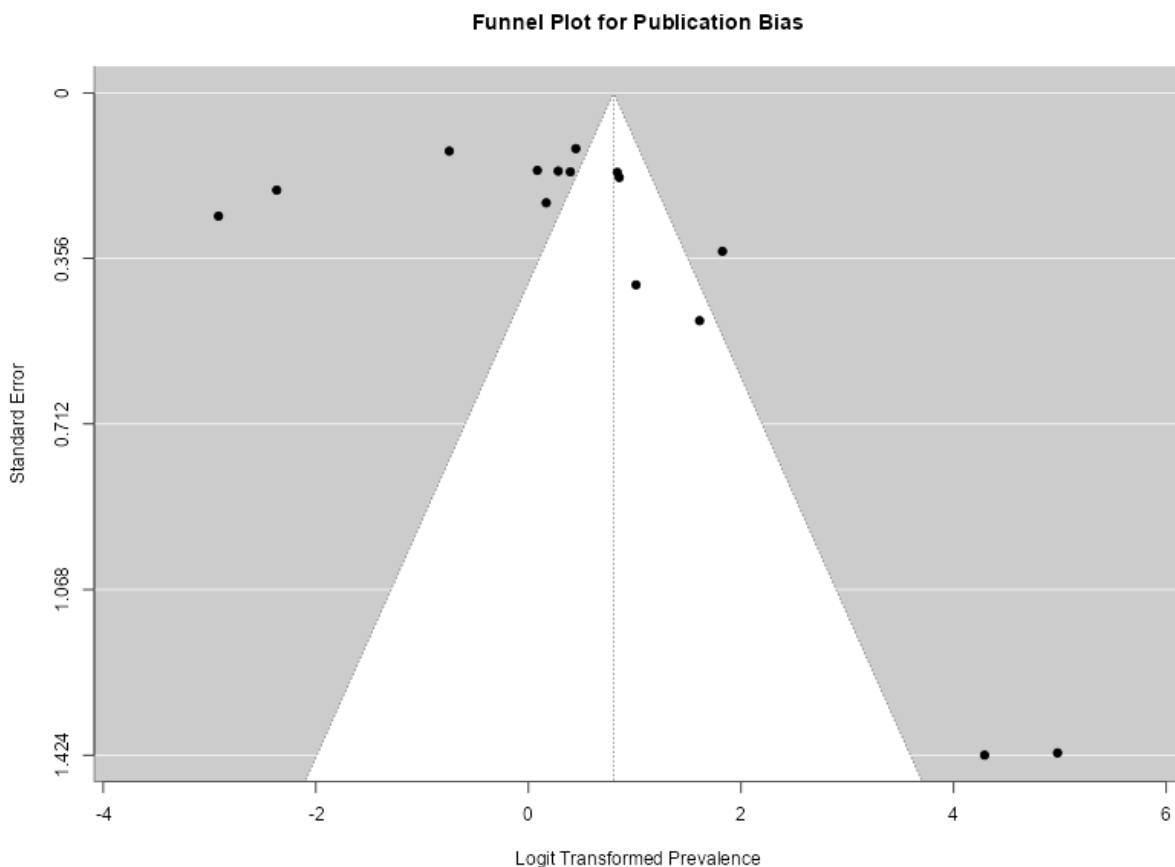
The prevalence of high resistance levels, categorized as greater than 70%, was notably alarming, particularly for *Vibrio* species and *E. coli* conducted by Nanthini et al. (2022) and Meena et al. (2022). In the moderate prevalence category, which ranges from 50% to 70%, bacteria such as *V. parahaemolyticus*, *V. alginolyticus*, and *S. aureus* exhibited resistance levels between 52% and 73%. Conversely, a lower prevalence of resistance, defined as less than 50%, was observed in several species investigated in the study by Babu et al. (2018). Specifically, CONS showed a resistance rate of 32.3%, *E. coli* had a much lower rate at 11.7%, and *Pseudomonas spp.* demonstrated an even lower rate of 8.5%. This data underscores that while resistance is predominantly high among certain bacterial species, especially *Vibrio* and *E. coli*, there exists considerable variability, indicating a clear need for more targeted interventions based on specific species susceptibility. While a formal statistical subgroup analysis by species was limited by the small number of studies, the data suggests that *Vibrio* species (particularly *V. cholerae*) and *E. coli* may represent



the highest-risk pathogens in terms of AMR prevalence in maritime settings. However, this finding is limited by the extreme heterogeneity of data and reflect a trend not a global burden of concern.

4.6.3 Assessment of Publication Bias

The observed funnel plot (Figure 4) displayed a notable asymmetry. There was a conspicuous absence of smaller studies (those with higher standard error, towards the top of the plot) in the region of low logit-transformed prevalence (left side). This pattern is indicative of potential publication bias, wherein smaller studies that found null or low AMR prevalence may be missing from the published literature. Consequently, the overall pooled prevalence of 69.0% may represent an overestimate of the true average prevalence across all maritime environments.



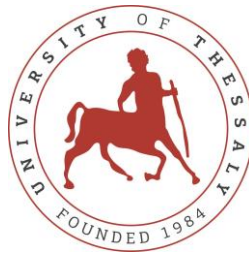
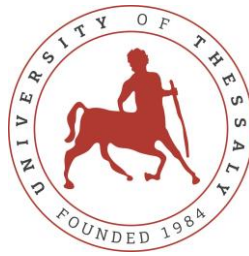


Figure 4: Funnel Plot for the Assessment of Publication Bias

4.7 Limitations and Summary of Findings

This meta-analysis provides evidence of a high point prevalence (69.0%) of AMR in maritime environments. However, this finding is tempered by two critical methodological observations; the evidence exhibits extreme heterogeneity ($I^2 = 98.6\%$), indicating that the pooled estimate is a summary of highly disparate results and that the true prevalence is context dependent. Also, there is visual evidence of funnel plot asymmetry, suggesting that the literature may be biased towards reporting higher AMR prevalences, potentially inflating the overall estimate. Therefore, the results are most reliably interpreted at the level of individual species and studies, which consistently identify specific pathogens like *V. cholerae* and *E. coli* as carrying particularly high resistance rates, highlighting a significant public and environmental health concern.

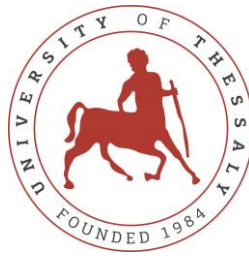


CHAPTER FIVE

5.0 DISCUSSION

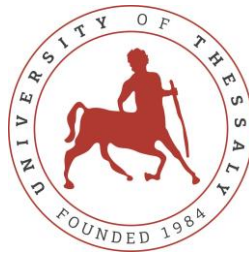
From our investigation and understanding, this systematic review and meta-analysis on both the quantitative and qualitative synthesis of AMR within the global maritime human-environmental interfaces is the first of its kind. Across the several maritime human-environmental interfaces such as ballast water, coastal sediments, ship wastewater and human cases linked to maritime activities, our meta-analysis found an alarmingly high pooled prevalence of AMR at 69.0% (95% CI: 36.4% to 89.7%). This high prevalence rate could likely be due to the unique confluence of anthropogenic pressures at maritime interfaces, including direct sewage discharge, agricultural runoff, and the concentrated waste from shipping activities. This finding reinforces that there is a substantial significant bacterial isolate that exhibited resistance to at least one of the classes of antibiotics agent within the studied environments (Ishwarya *et al.*, 2025).

Our analysis showed that Gram-negative bacteria—including *Escherichia coli*, *Vibrio cholerae*, *V. parahaemolyticus*, and *Klebsiella* spp.—were consistently identified as a spectrum of pathogens with high rates of antimicrobial resistance (AMR). In contrast, Gram-positive bacteria, such as methicillin-resistant *Staphylococcus aureus* (MRSA) and vancomycin-resistant *S. aureus* (VRSA), were also reported, particularly in studies involving hospital effluents and wound infections among fishermen (Babu *et al.*, 2018); (Lv *et al.*, 2023); (Chahouri *et al.*, 2022). The findings revealed a heterogeneous AMR risk profile, indicating that the burden of resistance was not uniform across the study settings. *Vibrio* species, particularly *V. cholerae*, and *E. coli*, consistently demonstrated the highest resistance prevalence, often exceeding 70%. This high burden among these pathogens is likely driven by the anthropogenic and environmental pressures at the maritime human-environmental interface (Hosseini and Ripanda, 2025). As further confirmed by Popoola *et al.* (2025), these microbes are exposed to antibiotic residues and resistant microbes from municipal, hospital, and aquaculture effluents, leading to horizontal gene transfer and



resistance accumulation (Popoola, Adeyemi and Samson, 2025). This is even compounded by the widespread confirmation of MDR phenotypes and diverse antimicrobial resistance genes (ARGs), such as *blaCTX-M*, *sul1*, *sul2*, *tetM*, and *vanA* among the studied environments. Importantly, the presence of the class I integron-integrase gene (*intI1*) points vividly to the fact that the environments are highly conducive and favoring mobile genetic materials through the horizontal transfer of resistance determinants among these bacterial populations (Shamsizadeh *et al.*, 2024). The case studies further illustrate that these environments serve as tangible reservoirs for public health challenges, as demonstrated with shipboard food and water systems acting as channels for disease outbreaks such as typhoid fever and *Clostridium perfringens* infection (Dargahi *et al.*, 2025); (Kanamori, Weber and Rutala, 2016). The role of coastal ecosystems as critical reservoirs and transmission pathways of AMR underscores the importance of monitoring these environments (Meradji *et al.*, 2025).

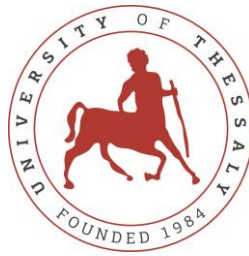
The public health importance of these findings aligns with and contribute to the existing body of knowledge on AMR in the environment. Previous studies and findings especially from Who and the O'Neill Review have consistently highlighted aquatic environments as major reservoirs and mixing pots for AMR (JIM O'NEILL, 2016);(Naznine *et al.*, 2025). By providing us with a robust, pooled prevalence of AMR, our study further strengthens the “One Health” approaches, linking human clinical outcomes such as wound infections among fishermen, and outbreaks on ships with environmental sources not limited to contaminated coastal and ballast waters. This highlights a significant gap beyond just examining and detecting ARGs in the environment to also evaluating and understanding their unique dynamic flow into the human populations through specific occupational and recreational pathways (Shao, Adebisi and Adeola, 2025). A must-to-do framework to address AMR is provided by One Health, which is crucial for achieving global health security, since resistant pathogens can now transcend borders and affect healthcare systems, food security and pandemic preparedness. In addition, this One Health approach becomes the backbone to



achieving several sustainable development goals (SDGs), not limited to Good Health and Well-being, Clean Water and Sanitation, Life below Water, and Life on Land, by informing a more coordinated antimicrobials stewardship, environmental safeguard including ocean health, and sustainable practices. Furthermore, the finding of ballast water and sediments in this study is significant, as it serves as a novel, long-distance translocation vector for bacterial pathogens and ARGs, further buttressing the long-held concerns of public health microbiologists (Shi *et al.*, 2025). The high heterogeneity observed in this study further underscores the complex and multifaceted nature of AMR emergence and spread, highlighting the critical role of local factors—such as antibiotic use patterns in nearby communities, sanitation infrastructure, and specific maritime activities—in shaping the local burden of AMR at human–environmental interfaces (Prestinaci, Pezzotti and Pantosti, 2015).

5.1 Implications for Public Health and Policy

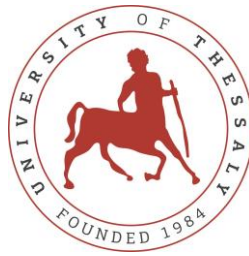
The findings of this study have profound implications, spanning local, national, and global scales. Looking through the public health perspective, certain populations face risks. Maritime Workers, not limited to ship crews, fishermen and dockworkers are at increased direct risk of infection with resistant bacteria through their daily and constant occupational exposure to contaminated water and surfaces as confirmed by the high rates of MRSA and MDR Gram-negative infections among infected fishermen (Salam *et al.*, 2023);(Babu *et al.*, 2018). Coastal Communities on the other hand are populations residing near ports or in areas with untreated coastal sewage discharge. These groups of people are also constantly exposed to contaminated seafood through recreational activities and consumption, which is confirmed through the high prevalence of resistant *Vibrio* species among populations with gastroenteritis and wound infections (Chahouri *et al.*, 2022).



The significant role of ballast water as a transboundary vector for AMR stand alone as a crucial challenge to global health security. This is made possible by ships departing from high-AMR prevalence regions, effectively releasing resistant bacteria and genetic materials into new ports, thereby, undermining local AMR containment efforts and globally, facilitating homogenization of resistance (Adebisi, Bamisaiye and Prisno, 2025). The findings of this study demand immediate action for policy practice. The International Maritime Organization's (IMO) Ballast Water Management Convention must be strengthened especially in the monitoring and evaluation of bacterial pathogens and ARGs, moving beyond just indicator species. Port states, especially those located in LMICs, require improved capacity for surveillance and enforcement, while integrated coastal zone management policies must prioritize wastewater treatment infrastructure to highly reduce the discharge of untreated sewage and clinically relevant antibiotics into coastal ecosystems (Chen *et al.*, 2025). Also, strengthening the development and implementation of rapid diagnostic tools at every port for health authorities could significantly help screen high-risk vessels, which are crucial components of a comprehensive One Health strategy to curb the global AMR crisis in an inextricably ecosystem of humans, animals and the environments and improve health at all levels (Salam *et al.*, 2023).

5.2 Strengths and Limitations

The key strength of this review is its methodological approach encompassing a systematic and comprehensive search strategy across several databases to reduce the chances of missing relevant studies. The systematic review included diverse range of study designs, from environmental monitoring to outbreak studies, thereby providing a holistic view of the AMR challenge across the human-environment interface. The combination of a multilevel meta-analytic model was a methodological strength, appropriately accounting for the non-independence of multiple effect sizes extracted from single studies, thereby providing a more statistically robust overall estimate. However, the findings of this study must be



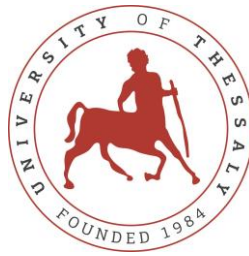
interpreted in light of significant limitations. Extreme variation in effect magnitude is revealed by the study, demonstrating the genuine diversity of AMR. Instead of being a precise number, the pooled prevalence estimate should be seen as a summary of a large range of values. The asymmetry of the funnel plot raises the possibility of publication bias, whereby low or nonexistent AMR can go unreported, resulting in overestimation. Direct comparisons are made more difficult using diverse laboratory techniques and the absence of standardized reporting. Finally, the few studies available for the meta-analysis (n=6 studies providing 15 effect sizes) limits the power for more nuanced subgroup analyses and calls for a cautious interpretation of the quantitative synthesis.

5.3 Future Research Directions

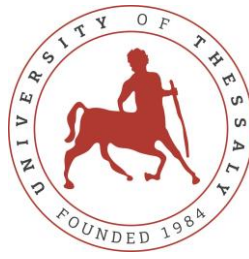
Future research should prioritize standardized surveillance in maritime environments, using harmonized protocols for sampling, bacterial identification, and AST/ARG detection. Tracking resistant bacteria and ARG plasmid designs through genomic elucidation may help identify pathways of transmission across human populations, animals, and environmental reservoirs. Research with an intervention focus should assess how well coastal sewage treatment, enhanced onboard wastewater management, and sophisticated ballast water treatment systems reduce AMR loads. The role of non-bacterial diseases and co-selecting heavy metals in under-sampled regions, especially in Africa and South America, should be investigated from a broader perspective.

5.4 Conclusion

The study finds that, with a high prevalence of 69%, global marine human-environmental interactions are important AMR hotspots. The shipping sector can pose a serious threat to global health since it is a transboundary vector for resistant bacteria and resistance genes, especially in ballast water and sediments. There is no denying the clear link between environmental contamination and human health, which impacts vulnerable populations including coastal villages and fishermen. A multifaceted strategy is advised to

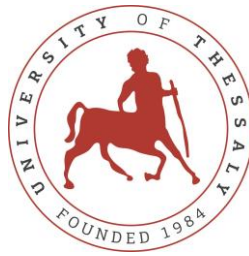


lessen this threat, which includes creating occupational health standards for maritime workers, investing in wastewater treatment facilities, and fortifying the Ballast Water Management Convention. To find and use efficient control methods, research should move from descriptive prevalence studies to genomic surveillance and intervention-based investigations. In the 21st century, protecting seas and coastal regions from AMR is not just an environmental objective but also a vital necessity for maintaining global health security and safeguarding human health.

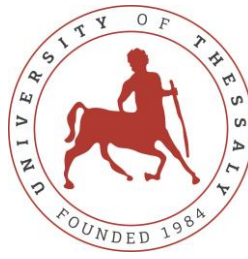


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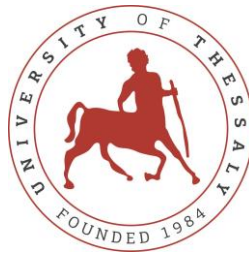
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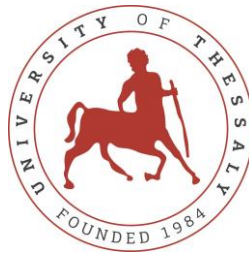


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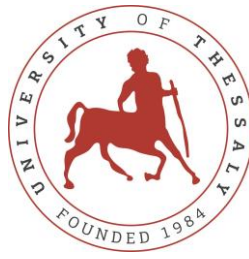


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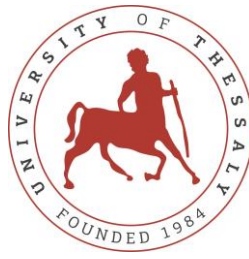


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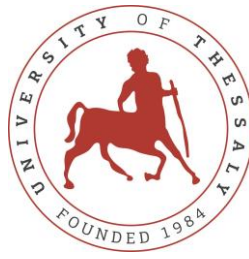


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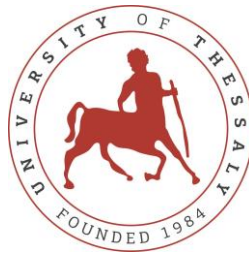
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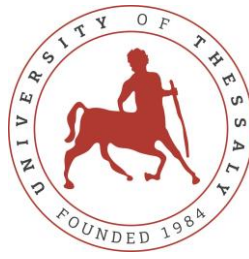
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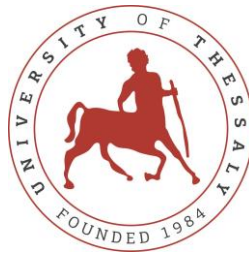


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Annexes

Not Applicable