Veterinary Integrative Sciences 2026; 24(2): e2026052-1-21. DOI: 10.12982/VIS.2026.052

Veterinary Integrative Sciences
ISSN; 2629-9968 (online)

Research article

Bacterial infections and antibiotic resistance in stranded dugongs (*Dugong dugon*) from the Andaman Sea, Thailand

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Abstract

Bacterial infections are recognized as important contributors to mortality in dugongs (*Dugong dugon*), endangered marine mammals inhabiting Thai coastal waters, yet information on their pathogenic bacteria, pathological findings, and antibiotic resistance remains limited. This study investigated the occurrence of bacterial infections and antibiotic resistance profiles in samples collected during necropsy examinations of freshly stranded dugong carcasses recovered from the Andaman Sea, Thailand, between 2024 and 2025. Necropsy, histopathology, bacterial culture, antimicrobial susceptibility testing, and PCR detection of antibiotic resistance genes (ARGs) were performed. Ten bacterial isolates representing eight species were identified, predominantly Vibrio spp. and *Photobacterium damselae*, associated with lesions consistent with septicemia. Members of the family *Vibrionaceae* were predominant (60%), while other isolates included *Achromobacter xylosoxidans*, Shewanella putrefaciens, *Sphingomonas paucimobilis*, and Enterococcus *faecalis*. Lesions were characterized by inflammation, congestion, and hemorrhage, consistent with systemic bacterial infection. Antibiotic susceptibility testing in Gram-negative bacteria revealed variable resistance to amikacin (AK), cefazolin (KZ), *ceftazidime* (CAZ), *oxytetracycline* (OT), and *enrofloxacin* (ENR), whereas all isolates were susceptible to amoxicillin–clavulanic acid (AMC), imipenem (IPM), and sulfamethoxazole/ trimethoprim (SXT). In contrast, E. *faecalis* exhibited resistance to OT and ENR. PCR screening demonstrated that 90% of isolates carried one or more ARGs, most frequently *blaCTX-M* (60%), blaOXA-1 (40%), and *tetM* (40%), with *aac(3)-IIa*, *ant(2'')-Ia*, *sul1, sul2, gyrA, blaTEM*, and *blaSHV* also detected. Notably, some resistance genes were identified in phenotypically susceptible isolates, suggesting a latent resistance reservoir. These findings establish baseline data on bacterial pathogens and antibiotic resistance in Thai dugongs, emphasizing the need for antibiotic resistance monitoring in marine ecosystems and supporting improved therapeutic management of stranded marine mammals.

Keywords: Andaman Sea, Antibiotic susceptibility, ARGs, Bacteria, Pathology.

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Funding; *This research was funded by the Prince of Songkla University, Thailand (Contract No. VET6702022S).*

Article history; *received manuscript: 4 September 2025,*
revised manuscript: 10 October 2025,
accepted manuscript: 28 October 2025,
published online: 31 October 2025,
Academic editor; *Korakot Nganvongpanit*

INTRODUCTION

Dugongs (*Dugong dugon*) are the sole extant species of the family Dugongidae within the order Sirenia, a group of large, herbivorous, entirely aquatic mammals inhabiting tropical and subtropical regions (Wirsing et al., 2022). Unlike manatees (*Trichechus* spp.), which are typically found in rivers and coastal regions of the Atlantic Ocean basin, dugongs are predominantly distributed in nearshore coastal waters of the Indo-Pacific region and are classified as a protected species on the International Union for Conservation of Nature's Red List of Endangered Species (Wang et al., 2025). In Southeast Asia, dugongs are generally scattered throughout shallow island and coastal waters and have been reported in Brunei Darussalam, Cambodia, Indonesia, Malaysia, the Philippines, Thailand, and Vietnam (Panyawai and Prathep, 2022). In Thailand, notable dugong populations are particularly found around Trang, Satun, and some areas of Krabi, located in the Andaman Sea, which serve as important habitats for this endangered species (Poommouang et al., 2022).

Cetacean and sirenian strandings are complex events influenced by both natural and anthropogenic factors. Between 2018 and 2023, dugongs in Thailand faced multiple anthropogenic threats, including targeted or incidental captures, vessel collisions, and habitat degradation, as well as non-anthropogenic challenges such as infections by pathogenic organisms (Daochai et al., 2024). Infectious diseases are considered major contributors to the mortality of both wild and captive sirenians, with bacterial infections identified as one of the leading natural causes of death (Dunn et al., 2001). Documented bacterial pathogens include *Clostridium* spp. (Landsberg et al., 2022), *Brucella* spp. (de Sousa et al., 2021), *Mycobacterium* spp. (Sato et al., 2003), *Salmonella Panama* (Vergara-Parente et al., 2003), as well as *Streptococcus faecium*, *Plesiomonas shigelloides*, *Pseudomonas putrefaciens*, and *Escherichia coli* (Walsh et al., 1987). Although bacterial infections may not always represent the primary cause of strandings, they can act opportunistically or as secondary infections in immunocompromised hosts (Owen et al., 2013). Importantly, marine mammals are increasingly recognized as sentinels of ocean health, particularly for monitoring the emergence of pathogenic microorganisms and antimicrobial resistance (AMR) (Obusan et al., 2018). AMR arises when microorganisms such as bacteria develop mechanisms to withstand antimicrobial agents, including antibiotics, that are intended to eliminate them (Tang et al., 2023). This resistance makes infections increasingly difficult or even impossible to treat, leading to higher risks of disease transmission, severe illness, disability, and mortality. A major contributor to AMR is the inappropriate and excessive use of antibiotics in human and veterinary medicine, as well as in agriculture, aquaculture, and the food industry (Milijasevic et al., 2024). Antibiotic resistance may occur through spontaneous genetic mutations or through the acquisition of antibiotic resistance genes (ARGs) (Amarasiri et al., 2020). Aquatic environments act as important reservoirs and transmission pathways for ARGs, posing a substantial threat to public health (Liguori et al., 2022; Lajqi Berisha et al., 2024). Consequently, marine mammals inhabiting these environments are at high risk of exposure to resistant bacteria and ARGs, reflecting the growing burden of AMR in marine ecosystems. Despite this concern, information on the status of antibiotic susceptibility and ARGs in marine mammals remains limited. Furthermore, the potential zoonotic transmission of antimicrobial-resistant bacteria between marine mammals and humans during stranding responses, rehabilitation, captive care, or research activities emphasizes the significance of a One Health approach in marine conservation and public health efforts (Obusan et al., 2021).

Within the order *Sirenia*, most microbiological studies have been conducted on manatees, with comparatively few reports available for dugongs, particularly in Australia (Owen et al., 2012; Nielsen et al., 2013). Both Gram-positive and Gram-negative bacteria have been implicated in dugong mortality, including *Aeromonas* spp., *Clostridium* spp., *Vibrio* spp., *Enterococcus faecalis*, and *Pseudomonas* spp.

However, data on bacterial pathogens and their antibiotic susceptibility profiles to drugs commonly administered by field veterinarians for stranded dugongs in Thailand remains scarce. Consequently, the status of ARGs within the dugong-associated marine ecosystem are still poorly understood. Therefore, the aim of this study was to identify bacterial pathogens isolated from stranded dugongs in the Andaman Sea, Thailand; to assess their antibiotic susceptibility profiles, which may serve as a reference for improving therapeutic guidelines and monitoring antibiotic resistance in marine mammal health management; and to screen for the presence of ARGs.

MATERIALS AND METHODS

Ethical approval

The experimental protocol was reviewed and approved by the Institutional Animal Care and Use Committee (IACUC) of Prince of Songkla University (Approval No. MHESI 68014/1236). The committee determined that the submitted protocol qualified for exemption under the criteria for Exempt Determination Research.

Dugong samples, necropsy, and bacteriological sampling

This study was conducted using freshly stranded carcasses of dugongs (*Dugong dugon*) recovered along the coastlines of Trang (Kantang and Sikao districts), Krabi (Mueang and Nuea Khlong districts), and Phuket (Mueang district) provinces, Thailand, between March 2024 and June 2025 (Table 1). The stranding response, rehabilitation, necropsy, and collection of biological materials were conducted by trained veterinarians from the Andaman Coastal Research Center, Department of Marine and Coastal Resources (DMCR). After the death of dugongs, necropsy was performed following the standardized marine mammal necropsy procedures (Pugliares et al., 2007). Carcass decomposition stages were evaluated following the criteria of Eros et al. (Eros et al., 2007), ranging from 1 (freshly dead) to 5 (mummified or skeletal remains). For each suitable carcass, basic morphometric and health parameters were recorded, including estimated age class and body condition score (BCS). Age class was determined based on body length and chest girth according to Marsh (1980), and BCS was assessed on a five-point scale (1 = very thin to 5 = obese) following the Dugong Necropsy Manual of Thailand (Department of Marine and Coastal Resources, 2013). Gross pathological findings were documented in detail, and organs showing visible lesions were collected for histopathological examination. Bacterial sampling procedures were performed under strict aseptic conditions. Internal organs were sampled immediately upon exposure. The external surfaces of organs were disinfected by wiping with 75% ethanol and briefly flaming the intended incision site for 1–2 seconds. A new sterile stainless-steel scalpel blade was then used to make a single incision through the flamed area, and the exposed tissue or cavity was swabbed using a sterile culture swab (Pugliares et al., 2007). These procedures ensured that the isolates most likely represented bacteria present within the tissues rather than surface contaminants. Swab samples were collected from the spleen, liver, lung, kidney, brain, and heart of stage 1 carcasses (Figure 1) and transported in Stuart transport medium (Difco™, Becton, Dickinson and Company, MD, USA) to the Unit of Veterinary Pathology, Faculty of Veterinary Science, Prince of Songkla University. For anaerobic culture, tissue specimens were submitted in anaerobic transport medium (ATM) tube (Difco™). All samples were processed within 12 hours of collection. The results from histopathology and bacteriological analyses were integrated to confirm bacterial involvement in the observed lesions, and the confirmed bacterial isolates were subsequently used for further analysis.

Table 1 Distribution of bacterial species, antibiotic resistance profiles, and antibiotic resistance genes identified in isolates recovered from stranded dugongs in this study

Strander code	Stranding location	Date of isolation	Source of swab sample	Isolated bacteria	Resistance profiles	Antibiotic resistance genes
TRDU090	Nuea Khlong, Krabi	26 Mar 2024	Lung	*Photobacterium damselae*	AK	*aac(3)-IIa*, *ant(2′′)-Ia*, bla_{CTX-M}, bla_{OXA-1}
			Lung	*Shewanella putrefaciens*	OT	*tetM*, bla_{OXA-1}, *sul1*
TRDU099	Mueang, Krabi	30 Aug 2024	Lung	*Achromobacter xylosoxidans*	AK, KZ, CAZ, ENR, OT	*aac(3)-IIa*, bla_{OXA-1}
TRDU114	Mueang, Phuket	1 Sept 2024	Lung	*Vibrio alginolyticus*	KZ, CAZ, OT	*tet*M, bla_{CTX-M}, *sul2*, *gyr*A
TRDU109	Sikao, Trang	23 Oct 2024	Spleen	*Vibrio parahaemolyticus*	KZ	bla_{CTX-M}, *sul2*
			Lung	*Sphingomonas paucimobilis*	OT	ND
TRDU117	Kantang, Trang	6 Dec 2024	Lung	*Vibrio vulnificus*	AK	*aac(3)-IIa*, *ant(2′′)-Ia*, *sul1*
TRDU132	Nuea Khlong, Krabi	1 Jun 2025	Heart	*Photobacterium damselae*	–	bla_{CTX-M}
			Lung	*Vibrio parahaemolyticus*	–	*tet*M, bla_{OXA-1}, bla_{TEM}, bla_{CTX-M}, *sul2*
			Lung	*Enterococcus faecalis*	ENR, OT	*tet*M, bla_{TEM}, bla_{SHV}, bla_{CTX-M}, *sul*1, *gyr*A

AK = amikacin; OT = oxytetracycline; KZ = cefazolin; CAZ = ceftazidime; ENR = enrofloxacin; – = no resistance to tested antibiotics; ND = Not detected

Figure 1 Photographs of some fresh carcasses of stranded dugongs examined in this study. (a) TRDU109, (b) TRDU117, (c) and (d) TRDU132

Histopathology

Organ specimens were processed according to standard histological protocols (Sornying et al., 2025). Briefly, samples were fixed in 10% buffered formalin, dehydrated through a graded ethanol series, cleared in xylene, and embedded in paraffin wax. Sections of 4 µm thickness were cut and stained with hematoxylin and eosin (H&E) for routine histopathological evaluation. Stained slides were mounted with coverslips and examined microscopically for morphological assessment.

Bacterial identification

Bacterial isolation from swab samples was performed by aseptic streaking onto tryptic soy agar (TSA; Difco™) supplemented with 5% sheep blood (SBA). Tissues for anaerobic culture were inoculated onto SBA and incubated in anaerobic jars under anaerobic condition. All bacterial cultures were incubated at 35 ± 2°C for 24 h. A single bacterial colony from each sample was further analyzed using gram staining, catalase and oxidase tests, and enzymatic profiling using the VITEK® 2 (bioMérieux, Marcy-l'Étoile, France), following the manufacturer's instructions. Isolates were then stored in 20% glycerol tryptic soy broth (TSB; Difco™) at –80°C until use.

Antibiotic susceptibility testing

Antibiotic susceptibility testing of all bacterial isolates was performed using the disk diffusion method according to the guidelines of the Clinical and Laboratory Standard Institute protocols in VET-03 (CLSI, 2020). The following antibiotic disks were used for susceptibility testing of Gram-negative bacteria: amikacin (AK, 30 µg), amoxicillin with clavulanic acid (AMC, 30 µg), imipenem (IPM, 10 µg), cefazolin (KZ, 30 µg), ceftazidime (CAZ, 30 µg), enrofloxacin (ENR, 5 µg), oxytetracycline (OT, 30 µg), and sulfamethoxazole/ trimethoprim (SXT, 25 µg). For Gram-positive bacteria, the disks tested included AK, AMC, IPM, ENR, OT, ampicillin (AMP, 10 µg), doxycycline (DO, 30 µg), and erythromycin (E, 15 µg) (Oxoid, Basingstoke, UK). The antibiotic panel used in this study was selected based on the practical requirements and treatment protocols commonly implemented by field veterinarians from the DMCR during clinical interventions and emergency responses involving stranded dugongs. This approach aimed to establish a preliminary antibiotic susceptibility database that accurately represents the drugs readily available and routinely employed in Thai marine mammal rescue and rehabilitation operations. Pure bacterial colonies were collected and suspended in sterile saline solution (0.85 % NaCl), and the concentration of bacterial cells was adjusted to 0.5 of the McFarland standards. The bacterial suspension was then evenly swabbed onto Mueller-Hinton agar (Oxoid), and antibiotic disks were applied to the surface of the inoculated agar plate using an antimicrobial susceptibility disk dispenser (Thermo Fisher Scientific, Dartford, UK). The diameters of the inhibition zones after 24 h of incubation at 35 ± 2°C were measured in millimeters (mm) and interpreted as susceptible, intermediate, or resistant according to the CLSI documents (CLSI, 2002; CLSI, 2015a; CLSI, 2015b; CLSI, 2021). Interpretations were further supported by relevant literature (Huang et al., 2022; Tae Seon Cha et al., 2025; Harris et al., 2025) (Table 2). *Escherichia coli* ATCC 25922 and *Staphylococcus aureus* ATCC 25923 were used as quality control isolates. The isolates that presented resistance to three or more classes of antibiotics will be considered as multidrug-resistant isolates (El-Gohary et al., 2020).

Table 2 Antibiotic susceptibility test breakpoints used in this study.

Antibiotics	Zone diameter interpretive criteria (mm)			Reference
	S	I	R	
	Vibrio spp. and *Photobacterium damselae*[1]			
AK (30 µg)	≥17	15–16	≤14	CLSI (2015a)
AMC (30 µg)	≥18	14–17	≤13	CLSI (2015a)
IPM (10 µg)	≥23	20–22	≤19	CLSI (2015a)
KZ (30 µg)	≥18	15–17	≤14	CLSI (2002)
CAZ (30 µg)	≥21	18–20	≤17	CLSI (2015a)
ENR (5 µg)	≥23	17–22	≤16	CLSI (2002)
OT (30 µg)	≥15	12–14	≤11	CLSI (2015a)
SXT (25 µg)	≥16	11–15	≤10	CLSI (2002)
	Shewanella putrefaciens and *Sphingomonas paucimobilis*[2]			
AK (30 µg)	≥17	15-16	≤14	CLSI (2015b)
AMC (30 µg)	≥18	14–17	≤13	CLSI (2002)
IPM (10 µg)	≥19	16-18	≤15	CLSI (2021)
KZ (30 µg)	≥18	15–17	≤14	CLSI (2002)
CAZ (30 µg)	≥18	15–17	≤14	CLSI (2021)
ENR (5 µg)	≥23	17–22	≤16	CLSI (2015b)
OT (30 µg)	≥15	12–14	≤11	CLSI (2015b)
SXT (25 µg)	≥16	11–15	≤10	CLSI (2002)
	Achromobacter xylosoxidans[3]			
AK (30 µg)	≥17	15–16	≤14	CLSI (2021)
AMC (30 µg)	≥18	14–17	≤13	CLSI (2002)
IPM (10 µg)	≥24	18–23	≤17	Harris et al. (2025)
KZ (30 µg)	≥18	15–17	≤14	CLSI (2002)
CAZ (30 µg)	≥18	15–17	≤14	CLSI (2021)
ENR (5 µg)	≥23	17–22	≤16	CLSI (2015b)
OT (30 µg)	≥19	15–18	≤14	CLSI (2002)
SXT (25 µg)	≥28	21–27	≤20	Harris et al. (2025)
	Enterococcus faecalis			
AK (30 µg)	≥17	15–16	≤14	CLSI (2002)
AMP (10 µg)	≥17	–	≤16	CLSI (2021)
AMC (30 µg)[4]	≥17	–	≤16	CLSI (2021)
IPM (10 µg)	≥16	14–15	≤13	CLSI (2002)
ENR (5 µg)	≥23	17–22	≤16	CLSI (2002)
OT (30 µg)	≥19	15–18	≤14	CLSI (2021)
DO (30 µg)	≥16	13–15	≤12	CLSI (2021)
E (15 µg)	≥23	14–22	≤13	CLSI (2021)

S = susceptible; I = intermediate; R = resistance; AK = amikacin; AMC = amoxicillin with clavulanic acid; IPM = imipenem; KZ = cefazolin; CAZ = ceftazidime; ENR = enrofloxacin; OT = oxytetracycline; SXT = sulfamethoxazole/ trimethoprim; AMP = ampicillin; DO = doxycycline; E = erythromycin

[1)]Interpretive criteria for *Photobacterium damselae* is evaluated according to interpretive breakpoints for *Vibrio* spp. (Tae Seon Cha et al., 2025).

[2)]Interpretive criteria for *Shewanella putrefaciens* and *Sphingomonas paucimobilis* are not provided in CLSI; therefore, results were interpreted using *Pseudomonas spp.* breakpoints as surrogate references (Prasad et al., 2019), except for oxytetracycline, which was interpreted according to the *Enterobacteriaceae* standards of CLSI M100 (Huang et al., 2022).

[3)]Interpretive criteria for *Achromobacter xylosoxidans* are not provided in CLSI; therefore, results were interpreted using *non-Enterobacterales* and *Pseudomonas spp.* breakpoints as a surrogate reference (Harris et al., 2025).

[4)]The results of ampicillin susceptibility tests should be used to predict the activity of amoxicillin–clavulanate (CLSI, 2021); therefore, the interpretive criteria for AMC were applied from ampicillin.

PCR based screening of selected antibiotic resistance genes

Genomic DNA was extracted from bacterial colonies using the E.Z.N.A.® Bacterial DNA Kit (Omega Bio-tek, Norcross, GA, USA) according to the manufacturer's instructions. Polymerase chain reaction (PCR) was performed to amplify selected antibiotic resistance genes (ARGs), including four genes encoding extended-spectrum beta-lactamases (ESBL; bla_{TEM}, bla_{SHV}, bla_{OXA-1}, bla_{CTX-M}), two genes encoding tetracycline resistance (*tetO* and *tetM)*, two genes encoding sulfonamide resistance (*sul1* and *sul2)*, two genes associated with fluoroquinolone resistance (*gyrA* and *gyrB), and two genes* encoding aminoglycoside modifying

enzymes (*aac(3)-IIa* and *ant(2′′)-Ia*) (Table 3), using a PCR thermal cycler (Eppendorf, Hamburg, Germany). Each PCR reaction (25 µL total volume) contained 25–40 ng of DNA template, 0.2 µM of each forward and reverse primer, 12.5 µL of OnePCR Ultra Master Mix (Bio-Helix, New Taipei City, Taiwan), and nuclease-free water. The PCR cycling conditions consisted of an initial denaturation at 94 °C for 3 min, followed by 35 cycles of denaturation at 94 °C for 30 s, annealing at primer-specific temperatures (Table 3) for 1 min, and extension at 72 °C for 2 min, with a final extension at 72 °C for 5 min. PCR amplicons from ARG-positive *Vibrio* spp. and *E. coli* reference strains provided by the Veterinary Microbiology Unit, Faculty of Veterinary Science, Prince of Songkla University, served as positive controls, while distilled water was used as the negative control.

PCR products obtained from the samples were visualized by electrophoresis on a 1.5% agarose gel (Invitrogen™) and observed under UV transillumination (E-Box VXII, Vilber, Marne-la-Vallée, France). All PCR-positive products were purified utilizing the GenepHlow™ Gel/PCR kit (Geneaid Biotech Ltd., New Taipei City, Taiwan) and subjected to sequencing using the Big Dye™ Terminator v3.1 Cycle Sequencing kit (Applied Biosystems, Foster City, CA, USA) on an Applied Biosystems 3730 DNA Analyzer instrument (ATCG, Bangkok, Thailand). Nucleotide sequences were analysed using the BioEdit v.7.2 software and were cross-referenced with available sequences in the GenBank database using the BLASTN tool provided by the National Centre for Biotechnology Information (NCBI; https://blast.ncbi.nlm.nih.gov/Blast.cgi) to verify nucleotide identity.

Table 3 List of oligonucleotide sequences and their annealing temperature used in this study.

Target gene	Primer sequences (5' – 3')	Amplicon (bp)	Annealing temperature (°C)	Reference
bla$_{TEM}$	5' – AAAATTCTTGAAGACG – 3' 3' – TTACCAATGCTTAATCA – 5'	1,080	42	Sharma et al. (2010)
bla$_{SHV}$	5' – TTAACTCCCTGTTAGCCA – 3' 3' – GATTTGCTGATTTCGCCC – 5'	768	52	
bla$_{OXA-1}$	5' – ACACAATACATATCAACTTCGC – 3' 3' – AGTGTGTTTAGAATGGTGATC – 5'	813	52	Steward et al. (2001)
bla$_{CTX-M}$	5' – GCAGCACCAGTAAAGTGATGG – 3' 3' – GCGATATCGTTGGTGGTACC – 5'	534	60	
*tet*O	5' – AACTTAGGCATTCTGGCTCAC – 3' 3' – TCCCACTGTTCCATATCGTCA – 5'	515	55	Abdi-Hachesoo et al. (2014)
*tet*M	5' – GTGGACAAAGGTACAACGAG – 3' 3' – CGGTAAAGTTCGTCACACAC – 5'	405	62	Warsa et al. (1996)
*sul*1	5' – GGCCGATGAGATCAGACGTA – 3' 3' – TTTGAAGGTTCGACAGCACG – 5'	413	62	Grape et al. (2003)
*sul*2	5' – GCAGGCGCGTAAGCTGA – 3' 3' – GGCTCGTGTGTGCGGATG – 5'	657	58	
*gyr*A	5' – GGTTTAAACCTGTTCATCGTCGT – 3' 3' – GCAATACCAGTTGCACCCATTGACT – 5'	626	57	Hossain et al. (2017)
*gyr*B	5' – TGCGGTGGAACAGGAGATGGGCAAGTAC – 3' 3' –CTGGCGGAAGAAGAAGGTCAACAGCAGGGT – 5'	483	55	Akasaka et al. (2001)
aac(3)-IIa	5' – CGGAAGGCAATAACGGAG – 3' 3' – TCGAACAGGTAGCACTGAG – 5'	740	62	Soleimani et al. (2014)
ant(2′′)-Ia	5' – TCCAGAACCTTGACCGAAC – 3' 3' – GCAAGACCTCAACCTTTTCC – 5'	700	62	

RESULTS

Bacterial identification

Ten bacterial isolates representing eight species (*Achromobacter xylosoxidans*, *Photobacterium damselae*, *Vibrio vulnificus*, *V. alginolyticus*, *V. parahaemolyticus*, *Shewanella putrefaciens*, *Sphingomonas paucimobilis*, and *Enterococcus faecalis*) were recovered from the lungs (n = 8), spleen (n = 1), and heart (n = 1) of six dugongs (Table 1). The bacterial species isolated from stranded

dugongs varied among the three provinces (Figure 2). Members of the family *Vibrionaceae* (n = 6, 60%) were the predominant pathogens, with *V. parahaemolyticus and P. damselae* each identified in two separate carcasses, while the other bacterial species were detected only once. Bacterial culture revealed that one to three species could be isolated from each dugong, sometimes within the same organ, such as the lungs. No anaerobic bacteria were isolated from any of the tested organs.

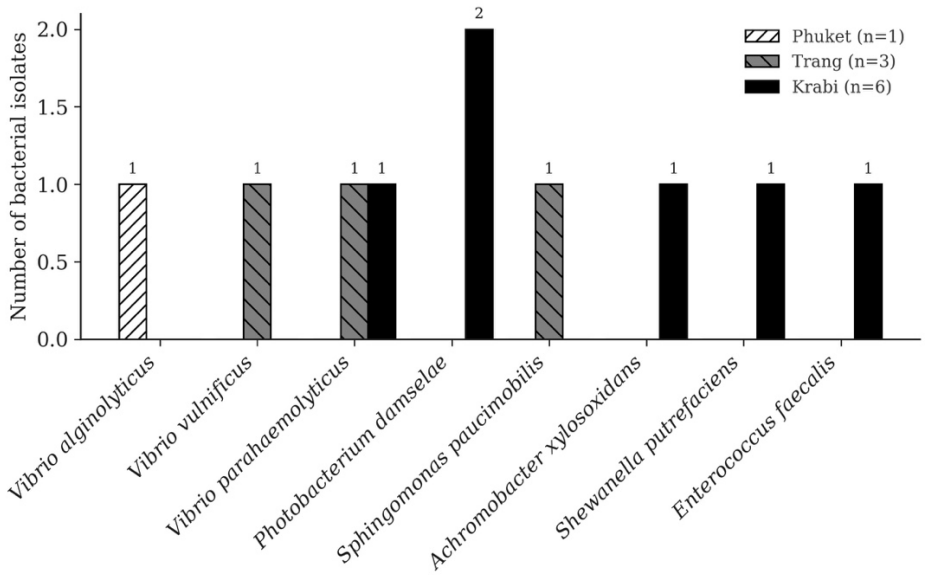

Figure 2 Distribution of bacterial species isolated from different organs of stranded dugongs in this study.

Occurrence of bacterial infections and pathological findings in stranded dugongs

A total of six dugong carcasses were included in this study based on the criteria of being freshly stranded and exhibiting gross pathological changes suggestive of bacterial infection. Among these, three (50%) were males and three (50%) were females. The age distribution comprised one newborn calf (16.67%), three juveniles (50%), one subadult (16.67%), and one adult (16.67%). Body condition scores (BCS) ranged from 2/5 to 3/5, with the majority of individuals (66.67%) exhibiting a BCS of 2/5, indicative of a thin condition, whereas two cases (33.33%) showed a BCS of 3/5, representing moderate condition.

Gross and histopathological examinations revealed lesions consistent with bacterial infection in all dugongs included in the study. The pathological patterns varied depending on the bacterial species isolated and whether the infection involved a single or multiple pathogens. Overall, the typical lesions observed across affected dugongs were characterized by inflammation, vascular congestion, and hemorrhage, indicating a systemic septicemic process.

Single bacterial infections (n = 3) were associated with organ-specific inflammatory and degenerative changes. Infection by *A. xylosoxidans* (TRDU099) caused multisystemic lesions, including pancreatic necrosis, lymphadenitis, splenitis, bronchopneumonia, and thromboembolic vasculopathy (Figure 3a), indicating a disseminated septicemic process. In contrast, *V. alginolyticus* (TRDU114) infection produced systemic circulatory and hepatobiliary disorders, with subcutaneous edema, icterus, reactive lymphadenopathy, pulmonary congestion and pneumonitis, hepatic cholestasis, and pericardial fat edema. Microscopically, lesions corresponded to chronic enteritis, gastroenteritis

(Figure 3b), hepatic congestion and hemosiderosis, splenitis, and mild interstitial pneumonitis (Figure 3c), suggesting a chronic systemic inflammatory response. *Vibrio vulnificus* (TRDU117) infection was characterized by bronchopneumonia, enteritis, gastritis, pancreatitis with trematode association, adrenal gland hemorrhage (Figure 3d) and renal congestion, suggesting acute septicemia with concurrent parasitic involvement. In the adult male (TRDU090) infected with *P. damselae* and *S. putrefaciens*, severe cutaneous erosion and congestion were evident, with hepatic lipofuscin and ferritin accumulation (Figure 3e), suggestive of oxidative stress and systemic compromise.

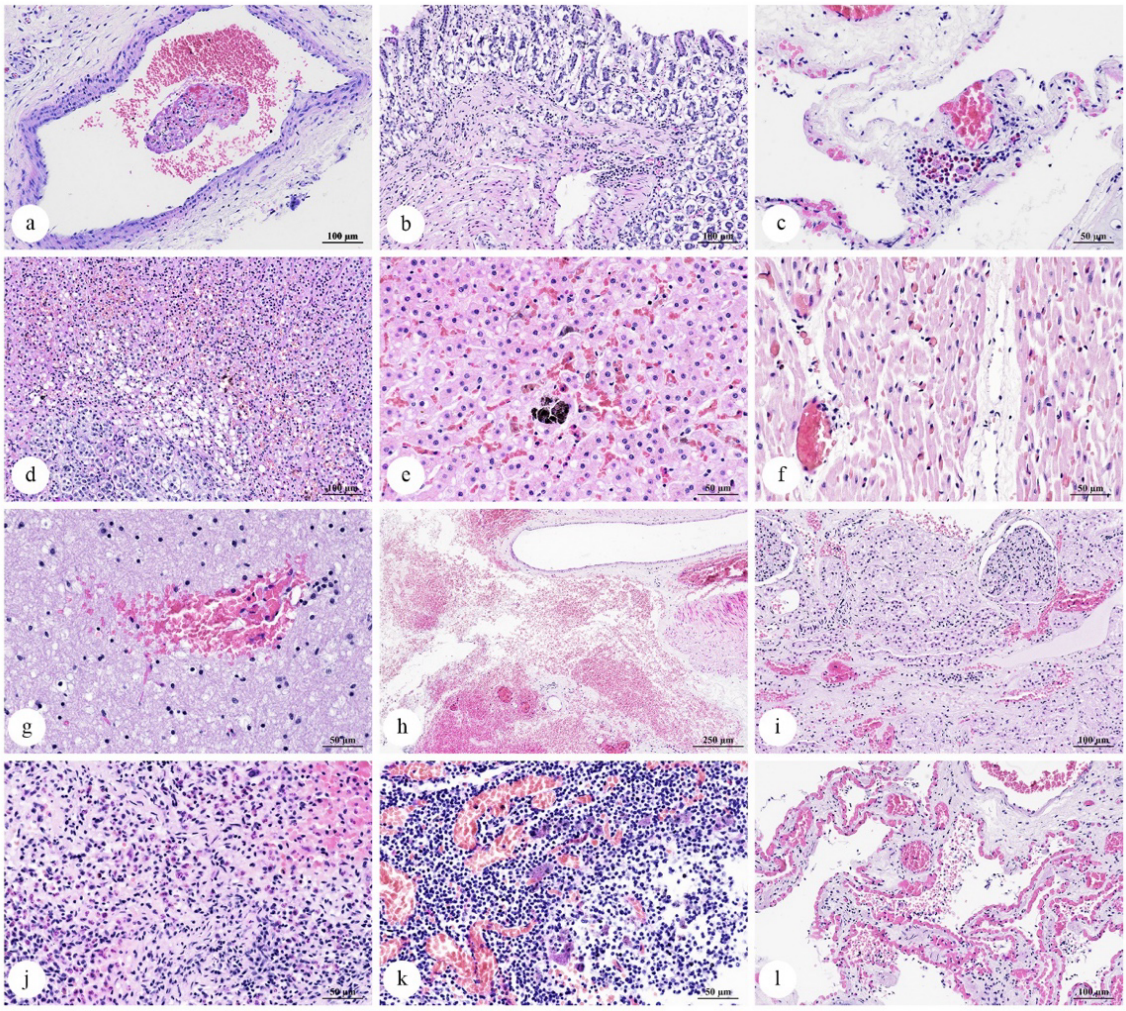

Figure 3 Representative microscopic lesions in dugongs infected with pathogenic and opportunistic bacteria. (a) Thromboembolic vasculopathy in a newborn infected with *Achromobacter xylosoxidans* (TRDU099). (b) Chronic enteritis and (c) interstitial pneumonitis associated with *Vibrio alginolyticus* infection (TRDU114). (d) Adrenal gland hemorrhage in *V. vulnificus* infection (TRDU117). (e) Hepatic lipofuscin and ferritin pigmentation in *Photobacterium damselae* and *Shewanella putrefaciens* infection (TRDU090). (f) Myocardial hemorrhage, (g) intracerebral hemorrhage, (h) gastroenteritis with suffusive hemorrhage, (i) renal congestion and hemorrhage, and (j) splenitis in polymicrobial infection with *P. damselae*, *V. parahaemolyticus*, and *Enterococcus faecalis* (TRDU132). (k) Reactive lymph node and (l) pulmonary hemorrhage associated with *V. parahaemolyticus* and *Sphingomonas paucimobilis* infection (TRDU109). (a–l = H&E, h, original magnification ×10, scale bar = 250 μm; a, b, d, i, l, original magnification ×20, scale bar = 100 μm; c, e, f, g, j, k, original magnification ×40, scale bar = 50 μm).

Mixed bacterial infections (n = 3) exhibited multiorgan involvement, including subcutaneous edema, icterus, reactive lymphadenopathy, hepatic cholestasis, pulmonary congestion, emphysema, and pericardial fat edema. The most complex polymicrobial case (TRDU132) involved *P. damselae*, *V. parahaemolyticus*, and *E. faecalis*, producing hepatic congestion, myocardial hemorrhage (Figure 3f), intracerebral hemorrhage (Figure 3g), interstitial pneumonitis, chronic gastroenteritis and suffusive hemorrhage (Figure 3h), renal congestion and hemorrhage (Figure 3i) and splenitis (Figure 3j). Similarly, *V. parahaemolyticus* together with *S. paucimobilis* (TRDU109) were associated with mild hemorrhagic enteritis, reactive lymph node (Figure 3k) and pulmonary hemorrhage (Figure 3l), consistent with acute vascular injury.

Overall, the lesions most frequently identified across infected dugongs included subcutaneous edema, hepatic congestion, enteritis, splenitis, pulmonary congestion and hemorrhage or pneumonia, and pericardial fat edema. These findings collectively indicate that both single and mixed bacterial infections, predominantly by *Vibrio* spp., *P. damselae*, and *A. xylosoxidans*, were associated with systemic and multiorgan pathology suggestive of septicemia and circulatory dysfunction. The detailed pathological findings for each case are presented in Table 4.

Antibiotic susceptibility profiling

Among the Gram-negative bacteria, nine isolates were susceptible to AMC, IPM, and SXT. Two isolates (*P. damselae* and *V. parahaemolyticus*) recovered from the stranded dugong TRDU 132 were also susceptible to AK, KZ, CAZ, ENR, and OT. The remaining isolates exhibited single or multiple resistance patterns to AK, KZ, CAZ, ENR, and OT. Resistance was most frequently observed to OT in 4 of 9 isolates, followed by AK and KZ in 3 isolates each, CAZ in 2 isolates, and ENR in 1 isolate. Different antibiotic resistance patterns were identified, with no association observed between antibiotic resistance profiles and bacterial species. *A. xylosoxidans obtained from Krabi* was classified as multidrug-resistant (MDR), exhibiting resistance to four classes of antibiotics: aminoglycosides, cephalosporins, tetracyclines, and fluoroquinolones. For Gram-positive bacteria, only one isolate of *E. faecalis* exhibited resistance to OT and ENR (Table 5).

Antimicrobial resistance genes screening

Several representative antibiotic resistance genes (ARGs) were selected based on previous reports in aquatic animals and hospitalized patients, and their distribution was analyzed in all bacterial isolates (Table 1, Figure 4). The results revealed that 90% (9/10) of the isolates carried one or more resistance genes. Among these, six isolates (60%) were positive for $bla_{\text{CTX-M}}$, four isolates (40%) for $bla_{\text{OXA-1}}$ *and tet*M, three isolates (30%) for *sul*1, *sul*2, and *aac(3)-IIa*, two isolates (20%) for *gyr*A, bla_{TEM} *and ant(2′′)-Ia*, and one isolate (10%) for bla_{SHV}. None of the isolates harbored *tet*O or *gyr*B. Regarding ESBL genes, one or more of the four targeted ESBL genes were detected in all isolates except *V. vulnificus* and *S. paucimobilis*. Notably, *V. parahaemolyticus* and *E. faecalis* harbored the highest number of ESBL genes (three each): bla_{TEM}, $bla_{\text{OXA-1}}$, and $bla_{\text{CTX-M}}$ in *V. parahaemolyticus*; and bla_{TEM}, bla_{SHV}, and $bla_{\text{CTX-M}}$ in *E. faecalis*. In addition, *Vibrio* spp. and *P. damselae* carried a variable number of ARGs, ranging from one to five genes, while the highest diversity was found in *E. faecalis*, which harbored six ARGs. By contrast, *S. paucimobilis* did not carry any of the targeted ARGs. Notably, the presence of amplified ARGs in this study did not correlate with bacterial species, geographical location, or phenotypic resistance profiles

Table 4 Summary of bacterial isolates and associated gross and histopathological lesions in stranded dugongs in this study.

	Strander code	Isolated bacteria	Infection type	Major gross lesions	Major histopathological lesions	Interpre tation
Newborn	TRDU099 Female BCS=3/5	*Achromobacter xylosoxidans*	Single	Multiple organs hemorrhage	Pancreatic necrosis, lymphadenitis, splenitis, bronchopneumonia, thromboembolic vasculopathy	Disseminated septicemia
Juvenile	TRDU114 Female BCS=2/5	*Vibrio alginolyticus*	Single	Subcutaneous edema, icterus, reactive lymph nodes, pulmonary congestion, hepatic cholestasis, pericardial fat edema	Chronic enteritis, gastroenteritis, hepatic congestion and hemosiderosis, mild interstitial pneumonitis, eosinophilic splenitis	Systemic inflammatory response with hepatic dysfunction
	TRDU109 Female BCS=2/5	*Vibrio parahaemolyticus*, *Sphingomonas paucimobilis*	Mixed	Subcutaneous edema, icterus, reactive lymph nodes, pulmonary congestion, hepatic cholestasis	Mild hemorrhagic enteritis, locally extensive pulmonary hemorrhage	Acute vascular injury and septicemia
	TRDU117 Male BCS=2/5	*Vibrio vulnificus*	Single	Pulmonary emphysema, pneumonia, pericardial and subcutaneous edema	Enteritis, gastritis, bronchopneumonia, hepatic and renal congestion, pancreatitis with trematodes	Mixed bacterial–parasitic infection causing septicemia
Subadult	TRDU132 Male BCS=3/5	*Photobacterium damselae*, *Vibrio parahaemolyticus*, *Enterococcus faecalis*	Mixed	Subcutaneous edema, icterus, reactive lymph nodes, pulmonary congestion, hepatic cholestasis, brain hemorrahge	Chronic enteritis, gastroenteritis, hepatic congestion, eosinophilic splenitis, renal congestion, interstitial pneumonitis, intracerebral hemorrhage, myocardial hemorrahge	Polymicrobial septicemia with multiorgan involvement
Adult	TRDU090 Male BCS=2/5	*Photobacterium damselae*, *Shewan ella putrefaciens*	Mixed	Severe generalized skin erosion, congestion	Hepatic lipofuscin and ferritin pigmentation	Systemic stress and early septicemia

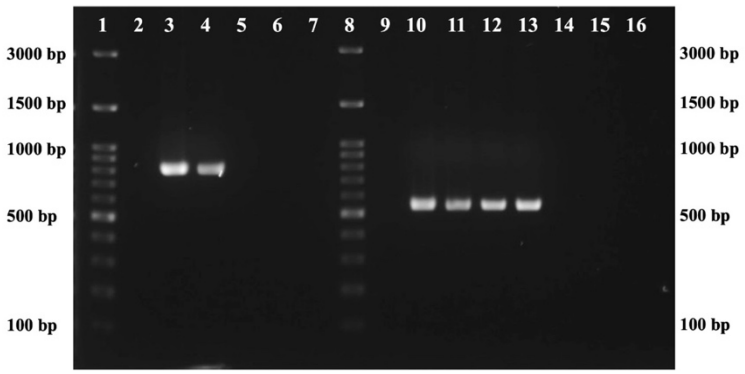

Figure 4 Representative PCR products of antimicrobial resistance genes (ARGs) analyzed in this study: Lanes 1–7 included PCR amplification of *blaSHV* gene (768 bp) and Lanes 8–16 included PCR amplification of *blaCTX*-M gene (534 bp). Lanes: (1) 100 bp DNA marker; (2) negative control (distilled water); (3) positive control; (4–7) dugong isolates; (8) 100 bp DNA marker; (9) negative control (distilled water); (10) positive control; (11–16) dugong isolates.

Table 5 Antibiotic susceptibility profiles (diameter of inhibition zones in mm) of bacterial isolates obtained from stranded dugongs in this study.

Strander code	Isolated bacteria	Antibiotics							
		AK	AMC	IPM	KZ	CAZ	ENR	OT	SXT
TRDU090	*Photobacterium damselae*	R(12)	S(19)	S(24)	S(21)	S(27)	S(25)	S(28)	S(19)
	Shewanella putrefaciens	S(21)	S(19)	S(21)	S(20)	S(29)	S(24)	R(10)	S(18)
TRDU099	*Achromobacter xylosoxidans*	R(12)	S(19)	S(26)	R(10)	R(14)	R(13)	R(11)	S(29)
TRDU114	*Vibrio alginolyticus*	S(22)	S(23)	S(25)	R(0)	R(0)	S(25)	R(0)	S(17)
TRDU109	*Vibrio parahaemolyticus*	S(19)	S(19)	S(27)	R(9)	S(27)	S(24)	S(27)	S(25)
	Sphingomonas paucimobilis	S(18)	S(21)	S(25)	S(19)	S(28)	S(24)	R(9)	S(18)
TRDU117	*Vibrio vulnificus*	R(13)	S(20)	S(26)	S(20)	S(29)	S(25)	S(26)	S(24)
TRDU132	*Photobacterium damselae*	S(22)	S(19)	S(25)	S(21)	S(28)	S(23)	S(29)	S(24)
	Vibrio parahaemolyticus	S(21)	S(19)	S(25)	S(22)	S(30)	S(23)	S(28)	S(23)
Strander code	Isolated bacteria	Antibiotics							
		AK	AMP	AMC	IPM	ENR	OT	DO	E
TRDU132	*Enterococcus faecalis*	S(20)	S(19)	S(21)	S(27)	R(11)	R(12)	S(18)	S(26)

S = susceptible; R = resistance; AK = amikacin; AMC = amoxicillin with clavulanic acid; IPM = imipenem; KZ = cefazolin; CAZ = ceftazidime; ENR = enrofloxacin; OT = oxytetracycline; SXT = sulfamethoxazole/ trimethoprim; AMP = ampicillin; DO = doxycycline; E = erythromycin

DISCUSSION

Microbiological studies in cetaceans provide several important benefits. They serve as a foundation for guiding medical treatment during the rehabilitation of stranded animals, highlight concerns regarding the zoonotic transmission of potentially pathogenic or antibiotic-resistant bacteria from cetaceans to humans, and offer valuable insights into bacterial pathogens affecting marine mammals in their natural oceanic environments (Obusan et al., 2018). This study is the first to investigate the occurrence of bacterial agents and their associated antibiotic resistance in stranded dugongs, an endangered species in Thailand. Although the detection of these bacteria and resistance traits does not directly explain the cause of stranding, the findings suggest potential sources of biological pollution and highlight environmental factors to which dugongs in the Andaman Sea may be exposed. Due to the limited sample size, the findings should be interpreted with caution, as they cannot be statistically generalized to the broader dugong population and provide preliminary insight into bacterial infections in Thai dugongs.

In the present study, members of the family *Vibrionaceae were identified as the main bacterial pathogens, including P. damsalae, V. parahaemolyticus, V. alginolyticus, and V. vulnificus. These species were detected either as single infections or in mixed infections with other bacteria, such as S. putrefaciens*, *S. paucimobilis*, and *E. faecalis*. *Vibrio* species are well-recognized as primary or opportunistic pathogens in marine environments and are frequently isolated from aquatic mammals (Sanches-Fernandes et al., 2022). The predominance of the *Vibrionaceae* aligns with previous findings in tropical marine mammals and teleost where warm, nutrient-rich waters promote bacterial growth (Suzzi et al., 2022; Mahieddine et al., 2025). The low to moderate body condition scores (BCS 2/5–3/5) observed among infected dugongs suggest that nutritional or physiological stress may predispose individuals to opportunistic infections, consistent with previous reports linking dugong mortality to cachexia and natural causes (Daochai et al., 2024). Pathological examinations revealed lesions typical of septicemia, including congestion, inflammation, and hemorrhage. In the case of *A. xylosoxidans* infection caused multisystemic necrosis and thromboembolic vasculopathy, indicating a severe septicemic process (Eiamcharoen et al., 2025). *V. alginolyticus* produced hepatobiliary and intestinal lesions similar to those previously reported in bottlenose dolphins (*Tursiops truncatus*) (Schroeder et al., 1985; Di Renzo et al., 2017), and rough-toothed dolphins *(Steno bredanensis)*

(Ewing et al., 2020). In contrast, *V. vulnificus* infection caused acute pneumonia, gastritis, and pancreatitis accompanied by parasitic involvement, suggesting a synergistic interaction between bacterial and parasitic agents during disease progression. The most common gastrointestinal parasite of dugongs, *Paradujardinia halicoris*, has previously been associated with enteritis and intestinal ulceration (Sornying et al., 2025), which could predispose the host to secondary bacterial invasion. *V. vulnificus* is known to cause severe fulminant septicemia and hemorrhagic lesions (Jones and Oliver, 2009; Candelli et al., 2025), with similar pathologies reported in marine mammals (Fujioka et al., 1987; Li et al., 2018). *S. paucimobilis* has also been reported in a clinically ill captive Antillean manatee in Brazil, although its clinical significance in manatees remains unclear (Silva et al., 2017).

Mixed bacterial infections, particularly those involving *P. damselae*, *V. parahaemolyticus*, and *E. faecalis*, caused more extensive and severe pathology than single infections, with diffuse congestion, hemorrhage, and degeneration across multiple organs including the liver, kidney, spleen, lungs, and myocardium. These bacteria are well-documented opportunistic and pathogenic agents in marine mammals, such as *P. damselae* in pinnipeds and cetaceans (Battistini et al., 2024; Cha et al., 2025), *V. parahaemolyticus* in bottlenose and Fraser's dolphins (*Lagenodelphis hosei*) (Lo et al., 2016; Di Renzo et al., 2017), and *E. faecalis* in seals and dolphins, where it has been associated with dermatitis, peritonitis, and septicemia (Sanches-Fernandez et al., 2022; Wu et al., 2023). Similar polymicrobial sepsis involving *Escherichia fergusonii*, *Shewanella haliotis*, *E. faecalis*, and *S. schleiferi* has also been reported in a fatal neonatal bottlenose dolphin (Baek et al., 2023). Mixed infections produced more severe multisystemic lesions, characterized by vascular congestion, edema, and hemorrhage consistent with bacterial endotoxemia. The isolated bacteria appear capable of inducing systemic septicemia, indicating bacterial infection as a significant cause of morbidity and mortality in Thai dugongs and emphasizing the need for ongoing health monitoring in this threatened species.

To evaluate the efficacy of antibiotics routinely used by veterinarians from the DMCR for the treatment and rescue of stranded dugongs in the Andaman Sea, we assessed the antibiotic susceptibility profiles of bacteria that cause infectious diseases in dugongs. Half of the isolates collected from the three provinces (*S. putrefaciens*, *S. paucimobilis*, *V. alginolyticus*, *A. xylosoxidans*, and *E. faecalis)* were resistant to OT, a Thai Food and Drug Administration (FDA)-approved drug that widely applied in aquaculture (Raharjo et al., 2022). This may suggest possible contamination of aquaculture-derived antimicrobials, particularly from coastal farming, into the marine environment. OT-resistant bacteria have also been abundantly reported in white-leg shrimp (*Litopenaeus vannamei*) and black tiger shrimp (*Penaeus monodon*) cultured in Thailand (Yano et al., 2011). Although reports on the antibiotic susceptibility of bacteria isolated from sirenians to tetracyclines remain scarce, Obusan et al. (2018) reported that *Proteus mirabilis* isolated from a pygmy sperm whale (*Kogia breviceps*) and *Vibrio* sp. isolated from a pantropical spotted dolphin (*Stenella attenuata*) exhibited resistance to tetracycline. Resistance to AK, a third-generation aminoglycosides, was observed in *A. xylosoxidans, P. damselae, and V. vulnificus.* This finding is comparable to that reported in Gram-negative bacteria such as *Acinetobacter* sp. and *Aeromonas* sp., as well as in Gram-positive *Enterococcus* sp. isolated from cetaceans in the Philippines (Obusan et al., 2018). Although cephalosporins, are commonly used to treat Gram-positive and Gram-negative bacteria such as *Staphylococcus* spp. and *E. coli*, *Vibrio* species are intrinsically resistant to first-generation cephalosporins (KZ) due to chromosomally encoded β-lactamases that inactivate these antibiotics. Likewise, *Enterococcus* species exhibit intrinsic resistance to all generations of cephalosporins (Bourque et al., 1976; Trinh et al., 2017). Therefore, the use of cephalosporins for medical treatment in Thai stranded dugongs may not be considered a first-line therapeutic option. In this study, *A. xylosoxidans* and *E.*

faecalis obtained from Krabi exhibited resistance to ENR, a fluoroquinolone commonly used in veterinary and aquaculture practices. In contrast, Norman et al. (2021) reported that only one isolate of *E. coli* recovered from harbor seals (*P. vitulina*) was resistant to ENR, whereas nine isolates (one *E. coli* and eight *Streptococcus* spp.) showed resistance to marbofloxacin. Multidrug-resistant bacterial pathogens resistant to fluoroquinolones have also been reported in stranded pinnipeds, suggesting the widespread environmental dissemination of quinolone-resistant bacteria in marine ecosystems (Wallace et al., 2013). Our isolates were fully susceptible to AMC, IPM and SXT, whereas some *Vibrio* spp. and *A. xylosoxidans* isolated from stranded cetaceans in the Philippines exhibited resistance to these antibiotics (Obusan et al., 2018). *A. xylosoxidans* was the only MDR isolate identified in this study, whereas *Enterococcus* spp. and *Vibrio* spp. have previously been reported in short-finned pilot whales (*Globicephala macrorhynchus*) and pantropical spotted dolphins (Obusan et al., 2018).

The emergence of AMR in human and animal microbiota is a global concern, suggesting the input of large amounts of ARGs into the environment (Grenni, 2022). The correlation between the presence of ARGs and phenotypic antibiotic resistance has been suggested, with increased resistance to β-lactam antibiotics in aquatic bacteria being associated with the occurrence of β-lactamase genes (Vega-Sanchez et al., 2014). Nevertheless, resistance genes are highly diverse (Yano et al., 2014), and to date, there have been no reports of ARG detection in marine mammals. In our study, several resistance genotypes were detected; however, the ARGs identified were not consistently associated with phenotypic antibiotic resistance patterns. Despite the limited number of isolates analyzed, a high proportion (40–60%) carried genes encoding extended-spectrum β-lactamases ($bla_{\text{CTX-M}}$, $bla_{\text{OXA-1}}$) or tetracycline resistance (*tet*M), even though some isolates remained phenotypically susceptible to these drugs. Similarly, sulfonamide resistance genes (*sul*1, *sul*2) were detected in our isolates despite high susceptibility to SXT, suggesting the potential for future resistance development. Variation in *tet* genes distribution was also observed in this study, including OT-resistant isolates with *tetM* (n = 3), OT-resistant isolates without *tetM* or *tetO* (n = 2), and an OT-susceptible isolate carrying *tetM*. These discrepancies may result from the presence of additional *tet* variants not amplified by the primers used, as over 40 *tet* genes have been characterized to date. Although *tetM* and *tetO* are commonly reported in aquaculture bacteria (Hedayatianfard et al., 2014), other untested determinants may contribute. The detection of *tetM* in OT-susceptible isolates likely reflects silent or non-expressed genes, possibly due to weak promoter activity or regulatory mutations, as similarly reported in *E. coli* isolates from swine carrying inactive resistance genes ($bla_{\text{OXA-2}}$, *aadA1*, *sul1*, *tetA*) (Enne et al., 2006; Georgi et al., 2012). Resistance to AK observed in Gram-negative bacteria in this study may be mediated by aminoglycoside-modifying enzymes encoded by the *aac(3)-IIa* and *ant(2'')-Ia* genes, as these isolates harbored either *aac(3)-IIa* or *ant(2'')-Ia*. This association has previously been demonstrated in *E. coli* isolates from human patients, where a high prevalence of these genes correlated with resistance to aminoglycosides such as gentamicin, amikacin, tobramycin, and kanamycin (Soleimani et al., 2014). Among the two ENR-resistant isolates, *gyr*A was only detected in *E. faecalis*, indicating that mutations in genes encoding DNA gyrase may not represent the primary mechanism of fluoroquinolone resistance in these bacteria. As aquatic ecosystems have been recognized as key reservoirs and transmission routes for AMR bacteria and ARGs (La Rosa et al., 2025), the detection of resistant bacteria or ARGs in stranded dugongs may be attributed to prolonged or repeated exposure to AMR bacteria present in the coastal environment. Dugongs are long-lived, slow-moving herbivorous marine mammals that inhabit shallow seagrass meadows close to shore, areas often influenced by anthropogenic activities such as aquaculture, wastewater and effluent discharges, and agricultural runoff (Ng et al., 2022). These coastal inputs can introduce antimicrobial residues and resistant bacteria into the marine ecosystem, creating

selective pressure that facilitates the persistence of AMR determinants (Lajqi Berisha et al., 2024). Consequently, dugongs may acquire AMR bacteria from the surrounding marine environment via ingestion of contaminated water, sediment, or seagrass biofilms harboring AMR bacteria or ARGs associated with extracellular DNA or plasmids. Such exposure may facilitate colonization of the oral cavity, gastrointestinal tract, or wounds, resulting in transient or chronic bacterial persistence. This situation is conceptually similar to nosocomial infections in humans, where prolonged exposure to hospital environments increases the risk of acquiring opportunistic or multidrug-resistant pathogens (Freitas and Werner, 2023). The accumulation of AMR and ARGs in marine sediments within near-shore habitats may therefore represent an ecological analogue to hospital reservoirs, serving as a continuous source of infection and reinfection in marine wildlife populations.

Several bacterial species identified in this study, including *V. alginolyticus*, *V. parahaemolyticus*, *V. vulnificus*, *P. damselae*, and *E. faecalis*, are recognized zoonotic pathogens capable of causing infections in humans (Abat et al., 2016; Hasan et al., 2018; Norman et al., 2021; Sheikh et al., 2024), while *A. xylosoxidans* is classified as an opportunistic pathogen (Rajni et al., 2023). These bacteria are of considerable public health significance. Although zoonotic transmission of these pathogens from marine mammals to humans has not yet been documented (Norman et al., 2021), marine mammals are known reservoirs of various pathogens that can pose potential health risks to humans, particularly those with occupational exposure (Waltzek et al., 2012). The detection of these bacteria in dugongs suggests possible transmission pathways linking marine environments, animals, and humans, and indicates the importance of antibiotic resistance surveillance in marine ecosystems.

CONCLUSIONS

This study provides the first evidence of bacterial infections and antibiotic resistance in stranded dugongs from the Andaman Sea, Thailand. Eight bacterial species were identified, predominantly *Vibrio* spp. and *P. damselae*, associated with lesions indicative of septicemia. The bacterial isolates exhibited variable resistance to several antibiotics (AK, KZ, CAZ, OT, and ENR) commonly used by veterinarians from the DMCR during clinical rescue and rehabilitation of stranded dugongs. In contrast, all isolates were susceptible to AMC and IPM, indicating that these drugs remain effective therapeutic options for stranded dugongs. Most of the isolates harbored one or more resistance genes, with some genes detected even in phenotypically susceptible isolates. The coexistence of potentially zoonotic and resistant bacteria supports the importance of continuous antibiotic resistance surveillance in marine mammal rescue programs to minimize risks to both animal and public health.

ACKNOWLEDGEMENTS

We express our gratitude to Dr. Pornphutthachat Sota of the School of Animal Technology and Innovation, Institute of Agricultural Technology, Suranaree University of Technology, Nakhon Ratchasima, Thailand, for her invaluable assistance.

CONFLICT OF INTEREST

The authors declare no conflict of interest with any financial organization regarding the material discussed in the manuscript.

AUTHOR CONTRIBUTIONS

Narissara Keawchana: Formal Analysis; Investigation; Methodology; Validation.
Sareepah Manmoo: Methodology.
Saowakon Indoung: Methodology.
Piyarat Khumraksa: Methodology; Resources. Santi
Ninwat: Methodology: Resources.
Watcharapol Suyapoh: Conceptualization; Investigation; Validation; Formal analysis.
Sasibha Jantrakajorn: Conceptualization; Formal analysis; Investigation; Validation; Writing – original draft; Writing – review and editing.

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How to cite this article;
Narissara Keawchana, Sareepah Manmoo, Saowakon Indoung, Piyarat Khumraksa, Santi Ninwat, Watcharapol Suyapoh and Sasibha Jantrakajorn. Bacterial infections and antibiotic resistance in stranded dugongs (*Dugong dugon*) from the Andaman Sea, Thailand. Veterinary Integrative Sciences. 2026; 24(2): e2026052-1-21.