

I. INTRODUCTION

1.1 Background

Antimicrobial resistance (AMR) is currently one of the greatest global health challenges of the 21st century. In 2019, antimicrobial resistance in bacteria was estimated to contribute to 4.95 million deaths worldwide, with approximately 1.27 million deaths directly attributable to bacterial AMR (Murray *et al.*, 2022). This resistance arises due to the ability of microorganisms to adapt so that they are no longer affected by antibiotics, especially in the β -lactam group which is most widely used in infection therapy. This global concern is strongly linked to the misuse and overuse of antibiotics in various sectors, particularly in clinical medicine, veterinary and agricultural settings, food production systems, and even in crisis situations such as armed conflicts (Ahmed *et al.*, 2024). AMR not only affects human health, but also animals and the environment, making it a cross-sectoral issue that requires a One Health approach. If not addressed seriously, antibiotic resistance is projected to impose significant economic and social burdens and threaten the effectiveness of modern medicine in the future.

The ocean is one ecosystem that has the potential to become a reservoir of resistance due to pollution from human activities, such as domestic, industrial, and agricultural waste, which can introduce resistant bacteria into the aquatic environment. This condition allows marine animals, including mammals like bottlenose dolphins (*Tursiops truncatus*), to be exposed to bacteria containing resistance genes (Thiagarajan & Devarajan, 2025). As a species that lives in coastal waters and frequently interacts with environments close to human activity, dolphins are vulnerable to exposure to resistant bacterial contamination (Barratclough *et al.*, 2019). Although it is not yet certain whether the bacteria truly originate from dolphins as natural hosts or are simply the result of environmental contamination, their presence remains important to study. Dolphins also serve as bioindicators of marine ecosystem health, so research on resistance in this species can provide an initial overview of the relationship between the marine environment, wildlife,

and the issue of antibiotic resistance within the One Health framework (Barratclough *et al.*, 2019; RandallS. Wells *et al.*, 2004).

In the treatment of bacterial infections in humans and animals, β -lactam antibiotics are often the choice and are the most commonly used class of antibiotics in clinical practice (Vilvanathan, 2021). However, their widespread use has led to the emergence of resistance, primarily through the production of β -lactamase enzymes capable of inactivating these antibiotics. (Bush & Jacoby, 2010). Genes encoding β -lactamases such as blaTEM, blaSHV, blaCTX-M, and blaOXA are found in many bacteria of the *Enterobacteriaceae* family and are now widespread in various environments. The presence of these genes contributes significantly to the increasing number of antibiotic resistance cases worldwide (Ahmed *et al.*, 2024; Paterson & Bonomo, 2005) .

The *Enterobacteriaceae* family is a group of opportunistic pathogens because they are frequently involved in various infections, including urinary tract infections, sepsis, and pneumonia, and are a leading cause of nosocomial infections (Pitout & Laupland, 2008). These bacteria are highly adaptable and readily acquire resistance genes through plasmids and other genetic elements, thus playing a significant role in the spread of AMR (Muteeb *et al.*, 2025). *Enterobacteriaceae* are widely found in humans, animals, and aquatic environments, including the ocean. (Wellington *et al.*, 2013). The presence of resistant *Enterobacteriaceae* in aquatic environments indicates the potential for resistance reservoirs that can transfer across species and ecosystems, thereby increasing the risk of widespread dissemination of β -lactamase genes (Farkas *et al.*, 2025).

Based on the background, this study on the detection of beta-lactamase genes in *Enterobacteriaceae* isolated from bottlenose dolphins (*Tursiops truncatus*) is important. This analysis not only provides insight into the potential for antibiotic resistance in marine bacteria but can also contribute to wildlife conservation efforts and an understanding of the spread of resistance genes in aquatic environments.

1.2 Problem Statement

- 1.2.1 Are there *Enterobacteriaceae* bacteria in swab samples from bottlenose dolphins (*Tursiops truncatus*)?
- 1.2.2 Is there any β -lactamase antibiotic resistance observed in the isolated *Enterobacteriaceae*?
- 1.2.3 Can some anti- β -lactamase encoding genes be detected in *Enterobacteriaceae* that have been successfully isolated?

1.3 Research Objective

- 1.3.1 Isolate and identify bacteria isolated from bottlenose dolphins (*Tursiops truncatus*).
- 1.3.2 Perform antimicrobial resistance testing of *Enterobacteriaceae* using the disc diffusion method.
- 1.3.3 Detecting the genetic presence of β -lactamase resistance in *Enterobacteriaceae* with PCR.

1.4 Research Benefit

The research conducted is expected to provide theoretical benefits and practical benefits, namely as follows:

- 1.4.1 This study provides scientific insights in the field of environmental microbiology, particularly regarding antibiotic resistance in marine bacteria. In addition, the results of this study can be used as a reference in molecular studies of β -lactamase resistance genes in marine ecosystems that have not been widely studied in Indonesia.
- 1.4.2 This study provides preliminary data that can be used in monitoring and controlling antibiotic resistance in coastal environments. The information obtained can also support marine mammal conservation efforts and serve as a basis for evidence-based policy making related to marine ecosystem health in Indonesia. This study can serve as basic data and a reference for further research on the potential role of bottlenose dolphins (*Tursiops truncatus*) as carries of various *Enterobacteriaceae* species.