

PREVALENCE OF BACTERIAL CONTAMINATION ON SEAFOODS PRODUCTS COLLECTED FROM TRADITIONAL FISH MARKET IN BALI PROVINCE DURING 2023

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Abstract

Seafood provides essential nutrients beneficial for human health; however, it is highly vulnerable to harmful bacterial infections that pose significant public health risks. This research seeks to assess the prevalence of five categories of seafood obtained from various traditional fish markets in Bali Province. A total of 108 tuna samples, 78 pelagic fish samples, 37 cephalopod samples, 14 sardine samples, and 53 demersal fish samples were collected from various traditional markets in Bali Province. This research evaluated the prevalence of *E. coli*, coliforms, *Salmonella*, *V. cholerae*, and *V. parahaemolyticus*. The study revealed that the highest prevalence of *E. coli*, coliform, and *V. parahaemolyticus* contamination in tuna samples was 95 (87%), 95 (87%), and 103 (95%), respectively. The study indicated that *E. coli* and coliforms were present in 73 of the 78 pelagic fish samples, representing 93% contamination. Sardine samples exhibited the lowest prevalence of bacteria. All seafood samples, however, tested negative for *Salmonella* and *V. cholera*. PCR products from *E. coli* and *V. parahaemolyticus* isolates were effectively amplified for the target genes utilized in this study. Local seafood markets should adopt appropriate handling and storage practices to enhance seafood quality. This study emphasizes the significant presence of *E. coli*, coliforms, and *V. parahaemolyticus* in seafood, along with the potential health risks posed by specific strains and their antibiotic resistance.
Keywords: coliforms, *E. coli*, *Salmonella*, *V. cholerae*, *V. parahaemolyticus*

Prevalensi Kontaminasi Bakteri pada Produk Hasil Ikan Laut yang dikumpulkan dari Pasar Ikan Tradisional di Provinsi Bali selama Tahun 2023

Abstrak

Makanan laut merupakan sumber zat gizi penting yang menunjang kesehatan manusia, namun sangat rentan terhadap infeksi bakteri berbahaya yang menimbulkan masalah serius bagi kesehatan masyarakat.

Penelitian ini bertujuan untuk menentukan prevalensi lima kelompok makanan laut yang dikumpulkan dari pasar ikan tradisional di Provinsi Bali. Sampel makanan laut berupa 108 sampel ikan tuna, 78 sampel ikan pelagis, 37 sampel sefalopoda, 14 sampel ikan sarden dan 53 sampel ikan demersal dikumpulkan dari berbagai pasar tradisional di Provinsi Bali. Prevalensi (%) *E. coli*, koliform, *Salmonella*, *V. cholerae*, dan *V. parahaemolyticus* dinilai dalam penelitian ini. Hasil penelitian menunjukkan bahwa prevalensi kontaminasi *E. coli*, koliform dan *V. parahaemolyticus* tertinggi ditemukan pada sampel ikan tuna masing-masing sebesar 95 (87%), 95 (87%), dan 103 (95%). Selanjutnya, pada sampel ikan pelagis, 73 dari 78 sampel (93%) ditemukan terkontaminasi *E. coli* dan koliform. Prevalensi bakteri terendah ditunjukkan pada sampel ikan sarden. Namun, *Salmonella* dan *V. cholerae* tidak terdeteksi (hasil negatif) pada semua sampel makanan laut tersebut. Produk PCR dari isolat *E. coli* dan *V. parahaemolyticus* beramplifikasi dengan baik pada gen target yang digunakan dalam penelitian ini. Upaya peningkatan kualitas makanan laut dapat dilakukan melalui praktik penanganan dan penyimpanan yang tepat dan harus diterapkan di pasar makanan laut lokal. Penelitian ini menyoroti prevalensi *E. coli*, koliform, dan *V. parahaemolyticus* yang meluas pada makanan laut serta potensi bahwa galur tertentu dan resistensinya terhadap antibiotik dapat mengancam kesehatan manusia.

Kata kunci: *E. coli*, koliform, *Salmonella*, *V. cholerae*, *V. parahaemolyticus*

INTRODUCTION

Seafood is one dietary stuff with significant nutritional benefits, particularly due to its high animal protein content (Maulu *et al.,* 2021). Yellowfin tuna *(Thunnus albacares)* is a marine product with excellent nutritional content and commercial value (Oktariani *et al.,* 2023). Yellowfin tuna is also supported by the abundance of minerals and other substances that may be used, one of which is collagen (Nurilmala *et al.,* 2019; Nurjanah *et al*., 2021; Wirayudha *et al*., 2022). Apart from tuna, fish in the demersal and pelagic classifications have a relatively high protein content, approximately 16.85%, and a low fat content, around 2.2% (Nordhagen *et al.,* 2020). Squid, which belong to the cephalopod group, include protein, essential amino acids, and minerals such as selenium, sodium, potassium, phosphorus, calcium, magnesium, and selenium. Squid includes vitamins B1 (thiamine), B2 (riboflavin), B12, niacin, folic acid, and fat-soluble vitamins (A, D, E, and K) (Schmidt *et al.,* 2024).

The global consumption of meat and fish products was projected at 209.20 million tons in 2010 and climbed to 248.73 million tons in 2019, representing an average rise of 3.9% (González *et al.,* 2020). Consumption is predicted to rise annually, in tandem with population and income growth (Fukase & Martin, 2020). In Indonesia, seafood has become a key source of revenue, particularly in terms of meeting national food security goals, as well as a downstream product (Nugroho *et al.,* 2022). The national downstream program prioritizes six marine and fisheries sector goods, including shrimp, tuna, skipjack tuna, crab, and tilapia. The export value of each commodity, such as yellowfin tuna, is USD 927.2 million, or 114.7 trillion, in 2023. Pelagic fish exports in Indonesia reached USD 4.81 billion between January and October 2024, while demersal fish exports reached IDR 4.21 billion. In 2020, the export value of cephalopod capture commodities such as squid in Indonesia was USD 10.2 billion, accounting for 6.8% of total fisheries product exports. Bali is one of the islands in Indonesia that is a priority in producing marine fish, besides being a tourist destination. Seeing the importance of this, traditional markets play an important role as the backbone in providing quality seafood sources to support the regional economy.

However, the reduction in the quality of marine products is frequently neglected by some groups, particularly those that engage in fishing and poor treatment, particularly during post-harvest activities (Torell *et al.,* 2020). Food-borne diseases are the primary cause of the reduction in the quality of seafood sold in traditional markets (Todd, 2014). *Vibrio* spp., *Salmonella* spp., *Shigella* spp., and *Listeria* spp. are examples of microorganisms that have been linked to foodborne illnesses in humans (Mumpuni & Hasibuan, 2018; Kabiraz *et al.,* 2023). According to previous research, seafood spoils more quickly than other foods due to biochemical degradation processes and the presence of food spoilage bacteria after being caught in the sea *(Karanth et al.,* 2023). Interestingly, these food spoilage bacteria can form biofilms and are known to be the main source of disease outbreaks spread through seafood intake as well as an early characteristic of antibiotic resistance mechanisms (Toushik *et al.,* 2021).

Gram-negative bacteria like *V. parahaemolyticus* frequently infect freshwater and seafoods (Mahmoud, 2014). Previous research has found that *V. parahaemolyticus* is prevalent in several fish products, with tilapia fillets having the largest percentage of positive findings (76%) among other fish products in various fish markets and restaurants in Alexandria governorate, Egypt (Hamad *et al.,* 2024). The overall prevalence of *Salmonella* spp. in seafood sold in Phnom Penh, Cambodia was 64% (32/50), with an average *Salmonella* count ranging from 1.2 to 7.40 log 10 CFU/g (Huoy *et al.,* 2024). Antimicrobial-resistant *E. coli* and *Staphylococcus* spp. were more prevalent in local fish products (18.6%; 32.6%) than in imported fish (5.3%; 24.6%) isolated from local markets in Mfoundi Division, Central Region of Cameroon (Moffo *et al.,* 2024). The identification results of Ihsan (2021) are that there is bacterial contamination of *Vibrio* spp. and *Salmonella* spp. in fishery products sold in the traditional market of Tarakan city.

The high frequency in fishing products may imply that fish's natural environment is extremely sensitive to contamination from home, industrial, and agricultural waste (Cabello *et al.*, 2016; Ferri *et al.,* 2022). Contamination of pathogenic microbes may be due to lack of personal hygiene, poor handling of materials and inadequate environmental sanitation (Yennie *et al.*, 2022). Interestingly, harmful microorganisms contaminate fish goods more frequently in traditional marketplaces (Belleggia & Osimani, 2023; Novoslavskij *et al.,* 2016; Siddiqui *et al.,* 2024). Concerns regarding the safety of fish items in traditional marketplaces are growing as zoonotic infections proliferate (Chandimali *et al.,* 2024; Ghatak *et al.,* 2023; Grema *et al.,* 2020; Sheng & Wang, 2021). This is also corroborated by prior research, which has found a link between the degree of bacterial contamination, pathogen identification, and characteristics such as hygiene standards, slaughter facilities, and labor habits in these marketplaces (Siddiky *et al.,* 2022).

In addition to industry, traditional marketplaces are one of the focal points for boosting the economics of small-scale fishermen who sell their catch (García-Lorenzo *et al.,* 2023; Penca *et al.,* 2021). Traditional markets in Indonesia are distributed throughout several regions, including Traditional markets on Bali Province's coast are used as fish market centers in each district/city (Wiradana *et al.*, 2023). Fishermen utilize traditional fish markets to sell their catches, which include yellowfin tuna, pelagic and demersal fish, and cephalopod items. Traditional markets in Bali province can be either either open or closed, and often have unclean sanitary conditions and lack storage facilities, leading to a particularly uncertain setting for the formation and transmission of foodborne infections. Interestingly, in addition to captures from the seas of Bali Island, marine fisheries goods sold in traditional markets are sourced from diverse places in Indonesia where the state of the aquatic environment is still poorly recorded.

Surveillance studies are one strategy for monitoring the presence of bacteria that have the potential to cause foodborne pathogens from fishery products, particularly in traditional markets, which are one of the sites for bacteria spread due to suboptimal post-harvest practices (Karanth *et al.,* 2023; Novoslavskij *et al.,* 2016). Based on this, the purpose of this study is to investigate the prevalence of contaminating bacteria in marine fishery goods sold at traditional fish markets across Bali Province. In addition to determining prevalence, this study will also inform the genotype of bacterial isolates that are positive for virulence genes using the PCR method. To our knowledge, there is no information on the prevalence of pathogenic bacteria in seafood from traditional markets in Bali Province.

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MATERIALS AND METHODS

Study Period and Location

This research was carried out from January to December 2023 in the several fish markets in Denpasar city, Badung Regency, Tabanan Regency, Klungkung Regency, Jembrana Regency and Buleleng Regency. Samples of fishery products collected include yellowfin tuna, pelagic fish, demersal fish, cephalopods, and sardines.

Sampling Procedures for Seafood Products

Samples of fish (yellowfin tuna, demersal fish, and pelagic fish) and squid (Figure 1) were obtained at each traditional market using composite random sampling. From January to December 2023, fish and squid samples will be gathered once a month or more frequently. Fish and squid sample (500 grams of each) was collected from fish dealers in each market. Fish and squid samples were gathered aseptically with sterile gloves and placed in a sterile plastic bag measuring 30×20 cm^2. The bag, labeled with the sample name and market, was placed in a cooler box filled with ice gel until the temperature reached 4˚C. Samples that have been labeled are then placed in a sterile cooler box filled with ice gel and transported to the Microbiology Laboratory, Center for Quality Control and Supervision of Marine and Fishery Products (BPPMHKP) Denpasar for further analysis.

Isolation and Identification of Contaminating Bacteria

Bacterial contamination analyzed in this study included: *Escherichia coli*, coliform, *Salmonella* sp., *Vibrio cholerae*, and *Vibrio parahaemolyticus*. The samples obtained were then examined based on the US FDA Bacteriological Analytical Manual (BAM) with several modifications. A total of 25 g of each seafood sample was weighed and transferred into a 250 mL Erlenmeyer which had been filled with 225 mL of alkaline peptone water (Merck, Germany). The samples were then mixed with a Stomacher Lab-Blender 400 (Seward Medical, UK) for 2 minutes. Dilution was carried out using a 10-fold serial dilution method up to 10^{-5} by transferring 1 mL of the mixture into 9 mL of alkaline peptone water. Each dilution reaction tube was incubated at 37°C for 24 hours. After the incubation period ends, 1 sample loop wastaken from each test tube, then streaked onto each bacterial selective medium. Petri dishes are labeled according to the fish sample observed and the type of bacterial contamination. The petri dishes used to observe the growth of *E. coli* were grown with Levine EMB Agar media (Merck, Germany), as were the petri dishes

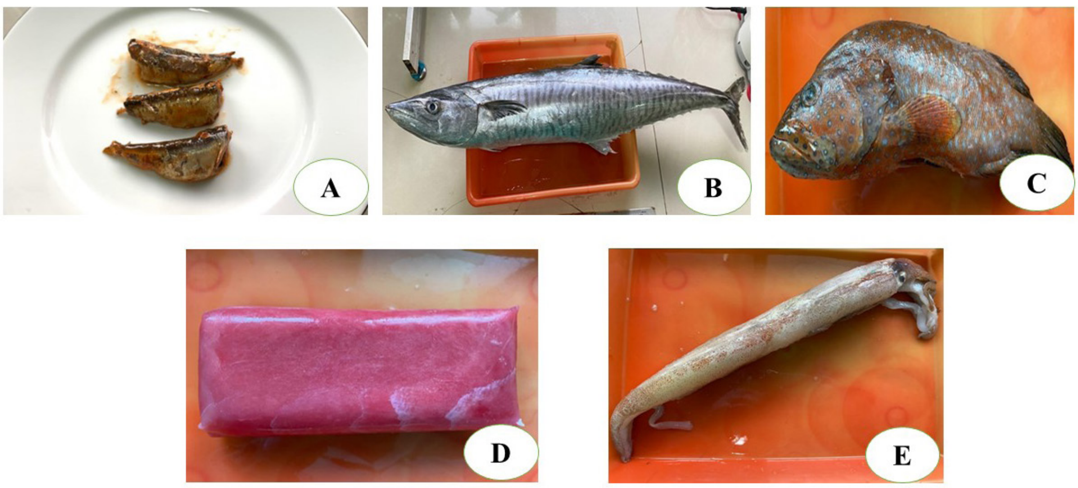

Figure 1 Samples of fisheries product collected in this study; (A) sardines, (B) pelagic fish; (C) demersal fish, (D) Yellow fin tuna meat, and (E) cephalopod

Gambar 1 Sampel produk perikanan yang dikumpulkan dalam penelitian ini; (A) ikan sarden, (B) ikan pelagis, (C) ikan demersal, (D) daging tuna sirip kuning; dan (E) sefalopoda for coliform growth using Brilliant Green Bile Lactose Broth (BGBLB, *Salmonella* sp. using Xylose Lysine Deoxycholate agar (XLD) media (Merck, Germany), and *Vibrio cholerae* and *Vibrio parahaemolyticus* using Thiosulfate–citrate–bile salts–sucrose (TCBS) agar media (Merck, Germany).

Molecular Identification

Molecular identification was carried out on samples that show positive results after being grown on each selective medium. Petri dishes showing the same bacterial growth in each sample were taken randomly from each fishery product and pooled in 1 microtube for subsequent DNA extraction, amplification and electrophoresis.

DNA Extraction

DNA extraction of bacterial cultures that have grown on selective media was carried out using the boiling method. The boiling method was carried out for 10 minutes and continued with centrifugation for 5 minutes at a speed of 6,000 rpm. The supernatant that was formed was then used for amplification and was shown in Table 1 below.

Amplification

Detection of genes encoding *E. coli* and *V. parahaemolyticus* was carried out using the Polymerase Chain Reaction (PCR) test. The reagents used in PCR amplification consisted of template DNA (2.5 μL), GoTaq DNA Polymerase (5 units), 1× GoTaq PCR reaction buffer containing 1.5 mm $MgCl_2$, PCR nucleotide mixture (0.2 mm), and Primary DNA. The PCR reagent mixture is then put into a thermocycler machine with details including initial incubation at a temperature of 94°C for 1 minute, followed by 35 cycles consisting of a temperature of 94°C for denaturation for 1 minute, annealing at a temperature of 58.3°C for 30 seconds, and 72°C. Extension for 30 seconds followed by final extension at 72°C for 7 minutes *(Yanestria et al.,* 2019). Each 3 μL of amplification product was mixed with 3 μL of loading solution until homogeneous.

Electrophoresis

The amplified PCR products were electrophoresed in a 1.5% agarose gel and stained with ethidium bromide. Markers were also placed into the wells of the agarose gel to determine the size of the DNA from the PCR results, and electrophoresis was carried out for 40 minutes at a constant voltage of 100 volts. Electrophoresis findings are viewed under ultraviolet light. The finding is a pattern of DNA bands, which vary in number and pattern. A 1,000-bp DNA ladder was used as a marker (Wiradana *et al.,* 2024; Yanestria *et al.,* 2019).

Data Analysis

Data on bacterial contamination found in each fishery product were tabulated periodically (January – December 2023) tabulated in Microsoft Excel (Microsoft, USA) and analyzed quantitatively to obtain the prevalence percentage. Molecular identification data were analyzed qualitatively. The analyzed data are displayed in the form of graphs, tables and figures.

Table 1 Specific primary nucleotide sequences used in this study
Tabel 1 Urutan nukleotida primer spesifik yang digunakan dalam penelitian ini

Bacterial detection	Gene target	Nucleotide sequences (5' – 3')	References
Escherichia coli	lacZB	Forward ATG AAA GCT GGC TAC AGG AAG GCC	(Molina *et al.*, 2015)
		Reverse CAC CAT GCC GTG GGT TTC AAT ATT	
Vibrio parahaemolyticus	vp	Forward CGA TAC ACA CCA CGA TCC AG	(Chimalapati *et al.*, 2020)
		Reverse ATA CGG CCG GGG TGA TGT TTCT	

RESULTS AND DISCUSSION

Traditional markets in Bali Province for marine fish sales activities include Kedonganan Market (Badung Regency), Kubutambahan Fish Market (Buleleng Regency), Gunung Agung Market (Denpasar City), Beringkit Fish Market (Badung Regency), Kusamba Fish Market (Klungkung Regency), Senggol Market (Gianyar Regency), and Perancak Market (Jembrana). This traditional market sells a broad range of freshly caught marine fish, raising worries about the health dangers involved with eating fresh seafood. The prevalences of bacterial contamination in fisheries products shows that tuna fish has an 87% prevalence of *E. coli* and Coliform, and 95% of *V. parahaemolyticus*. Pelagic fish species had the highest incidence of *E. coli* and Coliform, 93%, with *V. parahaemolyticus* at 1%. The sardine fish has a 70% frequency of *E. coli*, Coliform, and *V. parahaemolyticus*. *E. coli* and Coliform are prevalent in 88% of demersal and pelagic fish species, whereas *V. parahaemolyticus* is found in 100% (Table 2).

The prevalence of bacterial contaminants in seafood originating from seafood retailers in the United States is *Salmonella* sp. (0%-0.4%), *Aeromonas* sp. (19%-26%), *Vibrio* sp. (7%-43%), *Pseudomonas aeruginosa* (0.8%-2.3%), *Staphylococcus* sp. (23%-30%), and Enterococcus (39%-66%). Shrimp commodities have the highest prevalence of bacterial contamination of at least one species of bacteria (Tate *et al.,* 2022). A surveillance report on 335 seafood samples collected from all areas of Bangkok, Thailand showed that the prevalence of fecal coliform reached 100% and *E. coli* was 85%. Followed by the prevalence of *V. parahaemolyticus* at 59%, *V. cholerae* 49%, *V. alginolyticus* 19%, *V. vulnificus* 18%, and Salmonella 36%. The prevalence of fecal coliform and *E. coli* was seen in oyster samples, while *Salmonella* sp. was seen in shrimp samples (Atwill & Jeamsripong, 2021).

Another report stated that as many as 140 samples of seafood in the form of blood clams *(Anadara granosa),* shrimp (*Penaeus* spp.), surf clams (*Paphia undulata*), and squid (*Loligo* spp.) collected from a fish market in Selangor, Malaysia showed the total prevalence of *V. parahaemolyticus* was 85.71% (120/140), with 91.43% (32/35) in blood cockles, 88.57% (31/35) in shrimp, 82.86% (29/35) in surf clams, and 80% (28/35) in squid (Tan et al., 2020). Surveillance on the prevalence of MRSA has been carried out on fishery products collected in Gujarat State, India. A total of 498 fish samples in fresh, cold or worn conditions showed that 15.0% and 3.0% of the total samples were positive for *S. aureus* and methicillin-resistant *Staphylococcus aureus* (MRSA) (Sivaraman *et al.,* 2022)the prevalence of methicillin-resistant Staphylococcus aureus (MRSA.

Escherichia coli is a bacteria commonly found in the digestive tract of humans and animals (Jang *et al.,* 2017). In this study, samples that showed positive results for *E. coli* were continued with molecular identification using the PCR method. The results showed that the *E. coli* isolate was successfully amplified at 876 bp *(Figure 2*). The *lacZ* gene in *E. coli* is able to code for β-galactosidase (β-gal), which is a lactose metabolism enzyme from the lactose operon (Beal *et al.*, 2023).

Although *E. coli* is generally used as a bioindicator because it is able to detect fecal contamination in water and food, *E. coli* is also a major food-borne disease in humans (Wiradana *et al.*, 2019). Contamination of seafood due to *E. coli* is often caused by household waste and coastal air pollution often occurs in densely populated countries such as Indonesia (Wiradana *et al.*, 2020). In this study, traders often used ice to cool fish products sold in traditional markets. Melting ice can spread bacteria from one product to another to nearby retailers, making it easier to contaminate other seafood left in the contaminated melted ice (Atwill & Jeamsripong, 2021).

The high prevalence rates of *E. coli* and coliforms in fishery products found in this study could originate from the ice used to cool seafood. This ice can also harbor *E. coli*, *Aeromonas* spp., *S. enteritidis*, and fecal coliform which cause diarrhea. The high prevalence of coliforms and *E. coli* in this research sample indicates unhealthy

Table 2 Prevalence of bacterial contamination in seafood products traded at traditional fish markets in Bali Province
Tabel 2 Prevalensi kontaminasi bakteri pada produk hasil laut yang diperdagangkan di pasar ikan tradisional Provinsi Bali

Sample of seafood products	Number (n)	Prevalence (%)				
		E. coli	Coliform	*Salmonella*	*V. cholerae*	*V. parahaemoliticus*
Tuna	108	87	87	0	0	95
Pelagic fish	78	93	93	0	0	100
Cephalopods	37	91	91	0	0	83
Sardines	14	70	70	0	0	70
Demersal fish	53	88	88	0	0	100

sanitation conditions. Post-harvest methods, management, and waste contamination can increase the prevalence of *E.coli* in samples (Lenzi *et al.,* 2021). Pathogenic and spoilage bacteria can enter fish and fishery products at any point along the production and supply chain. The use of Next Generation Sequencing (NGS) technology has enabled a deeper understanding of the fish microbiome—the consortium of all microbial inhabitants of the fish and its surrounding environment—which has increased knowledge of the origins of pathogenic and spoilage bacteria in this study (Brugman *et al*., 2018).

The highest prevalence of *V. parahaemolyticus* was found in pelagic, demersal fish, tuna, cephalopod and sadines samples. *V. parahaemolyticus* is a halophilic gram-negative bacterium frequently associated with food-borne gastroenteritis. This disease is claimed to have caused an epidemic throughout the world (Jeamsripong *et al*., 2020; Letchumanan *et al*., 2019; Narayanan *et al.,* 2020). The high incidence of *V. parahaemolyticus* infection causes large medical costs worldwide. For example, the annual health costs of seafood infected with *V. parahaemolyticus* in the US is approximately $21 million (Tan *et al*., 2020). A total of 900 samples of ready-to-eat seafood from China were contaminated with *V. parahaemolyticus* at 3.67, 19.33 and 10.67% and the prevalence was highest in summer (Xie *et al.,* 2020).

The results of amplification of PCR products against *V. parahaemolyticus* showed positive results for each sample. Positive results were shown in the amplified band at 369 bp (Figure 3). Most *V. parahaemolyticus*

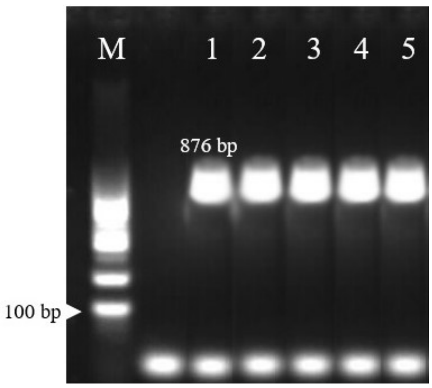

Figure 2 Results of amplification of PCR products of the *E. coli* with LacZB target gene (876 bp) in fishery products in this study. Note: M = marker; 1 = tuna meat; 2 = pelagic fish; 3 = cephalopod; 4 = sardines; and 5 = demersal fish
Gambar 2 Hasil amplifikasi produk PCR *E. coli* dengan target gen LacZB (876 bp) pada produk perikanan dalam penelitian ini. Keterangan: M = marker; 1 = daging tuna; 2 = ikan pelagis; 3 = cephalopoda; 4 = ikan sarden; dan 5 = ikan demersal

strains isolated from food or the environment do not have pathogenic potential, however clinical isolates generally have virulence factors such as thermostable direct hemolysin *(tdh)* and/or TDH-related hemolysin *(trh)* (Li *et al.,* 2023). The hemolysin gene is encoded by the tdh and trh genes which are the most important virulence factors related to hemolytic, enterotoxic and cytotoxic activities in host cells *(Letchumanan et al.,* 2014).

Based on these findings, it is emphasized that diseases transmitted through contaminated seafood can pose a significant public health risk worldwide (Elbashir *et al.,* 2018), including in Indonesia. The increase in seafood consumption worldwide also requires attention, considering that several cases of human gastroenteritis have been associated with consumption of seafood transmitted by norovirus, *Vibrio* spp., *E. coli*, and other bacteria (Fehrenbach *et al.,* 2024; Koutsoumanis *et al.,* 2024). Based on these findings, it is expected that stakeholders will continuously monitor fish sellers in traditional markets, including post-harvest handling methods, storage, and processing of fishery products. Traders and consumers must also be provided with counseling on environmental health promotion related to seafood-borne bacteria as in this study. Further research is still needed to study the resistance patterns of each bacterial isolate found in this study.

CONCLUSIONS

It can be concluded that there is *E. coli*, coliform and *V. parahaemolyticus* contamination in seafood samples taken from several traditional markets in Bali Province. Furthermore, *E. coli* and coliforms were found to be highest in samples of tuna, pelagic fish, demersal fish, cephalopods and sardines. Meanwhile, the prevalence of *V. parahemolyticus* was highest in pelagic, demersal fish, tuna, cephalopods and sardines. Handling and using ice as a coolant that is contaminated with bacteria is thought to be the cause of this seafood contamination. Isolates of *E. coli* and *V. parahaemolyticus* can be amplified accurately based on the PCR test. Implementing more hygienic handling of captured fishery products in terms of catching, storing, cutting and processing them as *ready-to-cook/eat* of fishery products is still needed to minimize the cause of foodborne diseases. In addition, research into the detection of antimicrobial resistance (AMR) in bacterial isolates in seafood needs to be carried out.

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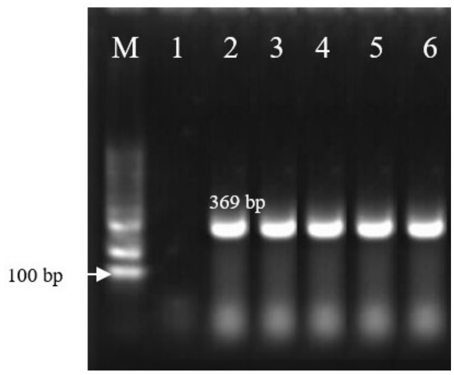

Figure 3 Results of amplification of PCR products of the *V. parahaemolyticus* with Vp target gene (369 bp) in fishery products in this study. Note: M = marker; 1 = blank well; 2= tuna meat;3 = pelagic fish; 4 = cephalopod; 5 = sardines; and 6 = demersal fish

Gambar 3 Hasil amplifikasi produk PCR *V. parahaemolyticus* dengan target gen Vp (369 bp) pada produk perikanan dalam penelitian ini. Catatan: M = marker; 1 = lubang kosong; 2 = daging tuna; 3 = ikan pelagis; 4 = sefalopoda; 5 = ikan sarden; dan 6 = ikan demersal

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