



Molluscan shellfish: a potential source of pathogenic and multidrug-resistant *Vibrio* spp.

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Abstract

Vibrio spp. are ubiquitous bacteria that are frequently discovered in aquatic environments. Globally, they are recognized as the primary cause of seafood-related illnesses. Over decades, vibrios have been a major health concern, and the number of cases is on the rise due to unhygienic eating habits and increasing demand for raw seafood. Among the 2 groups of *Vibrio* bacteria, the non-cholera *Vibrio* bacteria group mainly associate with seafood-borne illness. Though ~12 species have been recognized as causative agents of diseases in humans, horizontal gene transfer has attributed to an increase in emerging human pathogenic *Vibrio* spp. The assortment of virulence determinants contributes to the pathogenicity of vibrios. They carry specific genes to produce toxins and hemolysin, which are correlated with pathogenicity. In addition, the expanding antimicrobial use in humans and aquaculture resulted in a surge of resistant *Vibrio* strains found in shellfish. This has adversely affected the therapeutic results in the case of *Vibrio* infection. Thus, this article provides insight into the potential public health threat that may pose to seafood consumers as a consequence of the presence of virulence factors and antimicrobial resistance determinants in molluscan shellfish-borne vibrios.

Keywords Oysters · Food-borne illnesses · Virulence and antibiotic resistance genes · *Vibrio* spp.

1 Introduction

The aquaculture industry consists of various species, including aquatic plants and animals, with total production estimated over US\$ 406 billion (FAO 2022). Over 65 different mollusk species are worth US\$ 30.4 billion to the industry (FAO 2019). Mollusks represent the second largest group by weight, estimated at 17.7 million tonnes and valued at US\$ 29.8 billion (FAO 2022). Oysters constitute the largest species group, accounting for 32.8% of the total mollusk, followed by clams, cockles and ark shells (FAO 2019). Mollusks are filter feeders that can filter out a great quantity of water while feeding on suspended materials in the water, due

to this process they may bioaccumulate a high number of microorganisms in their tissues (Baker-Austin et al. 2017).

Vibrio spp. are naturally occurring Gram-negative bacteria characterized by their curved or comma-shaped morphology; originated from aquatic and marine ecosystems (Baker-Austin et al. 2017; Farmer et al. 2015). These bacteria can be found in warm and slightly salty water, and they actively mirror environmental temperatures. Vibrios are accountable for most human infections concerning the microbiota associated with seafood and aquatic environments (Baker-Austin et al. 2018). Ingestion of raw or undercooked contaminated seafood with *Vibrio* spp. may result in a variety of infections in humans. The number of *Vibrio* spp. infections vary with seasonal distribution, where most incidents take place during warmer months (Altekruse et al. 2000). Vibrios are widely recognized for their ability to cause a wide range of clinical symptoms and diseases, including digestive, ophthalmological, dermatological and otorhinolaryngological infections (Oliver 2005). The 2 major groups of human pathogenic vibrios are cholera and non-cholera *Vibrio* spp. *Vibrio cholerae* causes a severe diarrhoeal illness known as Cholera which is frequently caused by the intake of contaminated food or water (Howard-Jones 1984). Non-cholera vibrios like *Vibrio parahaemolyticus* and *Vibrio vulnificus* are the

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etiological agents of vibriosis and cause infections that can result in diverse clinical manifestations which vary depending on the specific pathogen involved, the route of infection, and the susceptibility of the host. (Baker-Austin et al. 2018). Generally, non-cholera vibrios dominate in moderate or high salinity aquatic habitats and thus can originate with seafood more frequently. *V. parahaemolyticus* has been widely acknowledged as the primary cause of food-borne illnesses in various Asian countries including Japan, Korea, and China (Wong et al. 2000; Lee et al. 2001; Alam et al. 2002; Liu et al. 2004). In addition, *V. cholerae* and *V. vulnificus* are also recognized as significant pathogens responsible for causing food-borne illnesses (Sawabe et al. 2007, 2013). Furthermore, *V. alginolyticus* and *V. fluvialis* have also been categorized as food-borne infectious agents as they have caused food poisoning in humans (Liang et al. 2013).

A complex group of genes is associated with the virulence of vibrios, and expression of these virulence factors is crucial for the host infection process (Lida et al. 1998; McCarthy et al. 1999). In addition, antimicrobial resistance plays a major role during infection and has become a public and animal health threat. These resistances are often carried on bacteria plasmids encoded by respective resistance genes (Balsalobre et al. 2010). The overuse or mishandling of antimicrobials can be a cause of the emergence of multidrug-resistant bacteria in different environments. Considering these factors, studies have suggested an association between resistance and virulence factors, where traits that confer a particular benefit will be chosen and become fixed with time (Beceiro et al. 2013). Therefore, the purpose of this review is to present comprehensive evidence regarding the virulence factors and antimicrobial resistance determinants found in *Vibrio* spp. associated with mollusks for consumer awareness and public health safety.

2 Vibriosis

Vibrio spp. are common bacteria found in different varieties of aquatic and marine habitats that cause human infections. Although over 100 *Vibrio* spp. have been described, ~12 *Vibrio* spp. have been identified as a source of human infections (Baker-Austin et al. 2018). Vibriosis affects a considerable number of people in the United States annually. Specifically, according to Centers for Disease Control and Prevention (CDC), roughly 80,000 individuals contract this bacterial infection, which results in the death of around 100 individuals each year (CDC 2023). A severe diarrheal disease caused by *V. cholerae* can be fatal if untreated, and it usually spreads rapidly through polluted water and personal contact. Vibriosis is caused by non-cholerae vibrios (for example, *V. parahaemolyticus*, *V. alginolyticus* and *V. vulnificus*) when exposed to seawater or eating raw or

undercooked contaminated seafood (Di et al. 2017). Several symptoms of non-cholerae bacteria lead to the most common mild self-limiting gastroenteritis. Particularly, *V. vulnificus* infection can be a reason for fatal wound infections that may induce septicemia (Coerd and Khachemoune 2021; Torres et al. 2002).

2.1 *Vibrio parahaemolyticus*

V. parahaemolyticus has a wide distribution in temperate and tropical coastal regions across the globe (Shen et al. 2009). *V. parahaemolyticus* infection was limited to the areas of Japan until late 1960. Afterward, it was reported in other parts of the countries, comprising the Atlantic, Pacific, Gulf states and Hawaii in the USA (Barker et al. 1974). During 2007–2012, *V. parahaemolyticus*, serotype O3: K6 strains turn out to be the main reason to cause bacterial infectious diarrhea in the region of southern China (Li et al. 2014). *V. parahaemolyticus* can cause gastroenteritis in humans eating raw or undercooked contaminated seafood, particularly bivalve shellfish, such as oysters and ready-to-eat food (Park et al. 2018; Pang et al. 2019). Other symptoms of *V. parahaemolyticus* comprise abdominal cramps, diarrhea, vomiting, and nausea (Daniels et al. 2000). Moreover, *V. parahaemolyticus* infections are accountable for a significant number of food-borne infections in the USA (Iwamoto et al. 2010). In 2018, a seafood-related outbreak of *V. parahaemolyticus* infections resulted in 26 cases of illness and 9 individuals requiring hospitalization (Seelman et al. 2023). In Korea, 9 outbreaks occurred in 2017 with 354 patients that were infected with *V. parahaemolyticus* (KCDC 2016; KMFDS 2017).

2.2 *Vibrio vulnificus*

This pathogen is commonly found in estuarine waters and various environmental sources, such as seawater, sediment, and seafood products (DePaola et al. 1994; Baker-Austin et al. 2010). *V. vulnificus* infections are caused by two main sources; intake of contaminated seafood, specifically oysters, leading to gastroenteritis or bacterial infections; or exposure of wounds to seawater or contaminated seafood products, resulting in the development of wound infections and secondary septicemia (Jones and Oliver 2009). *V. vulnificus* infections are reported to have the highest fatality rate (50%) among food-borne microorganisms. Compared to *V. parahaemolyticus*, *V. vulnificus* is a lethal human pathogen evidenced to be responsible for more than 95% of seafood-related deaths in the USA (Oliver and Bockian 1995). Furthermore, about 20% of individuals with a *V. vulnificus* infection will not survive, and death can occur within a short period of 24–48 h after the onset of illness (CDC 2023). *V. vulnificus* can cause severe wound

infections. The infection can progress rapidly, requiring intensive care and sometimes even limb amputations (CDC 2023). In South Korea, a total of 257 cases were reported as a result of *V. vulnificus* infection from 2017 to 2022 (KCDC 2022).

2.3 *Vibrio alginolyticus*

This bacterium can be found in seawater worldwide and is known to cause various infections, including wound and ear infections such as otitis media and otitis externa. These infections can be effectively treated using appropriate antimicrobial agents. Occasionally, these infections can be aggravated to cause septicemia and necrotizing fasciitis, especially in people with a compromised immune system (Baker-Austin et al. 2016). The incidence of these infections significantly increases during the warmer months. A French study revealed that *V. alginolyticus* is accountable for nearly 34% of all vibriosis infections for the last 19 years (Hoeffler et al. 2022). In Spain, the occurrence of *V. alginolyticus* infected wounds of 2 patients exposed to contaminated seawater in 2019 (Fernández-Bravo et al. 2019). In many reports, *V. alginolyticus* wound infections happened in patients that had cuts and abrasions exposed to contaminated seawater (Reilly et al. 2011). In the US, 20% of all vibriosis infections were caused by *V. alginolyticus*, including 131 cases in Florida (Weis et al. 2011). Another study has reported that 96% of *V. alginolyticus* infections happen in coastal states (Slifka et al. 2017). *V. alginolyticus* was found in a stool sample of a patient with gastroenteritis due to the ingestion of diseased abalone (Liu et al. 2001). In Europe, several studies have reported

the incidence of *V. alginolyticus* (Suñén et al. 1995; Barbieri et al. 1999; Hervio-Heath et al. 2002).

2.4 Other *Vibrio* spp.

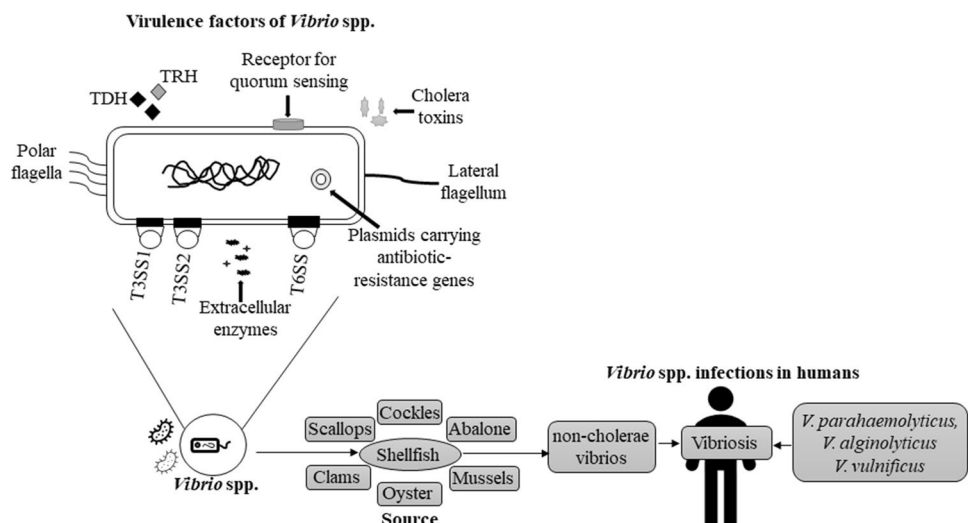
Human infections due to other *Vibrio* spp. including *V. mimicus*, *V. cincinnatiensis*, *V. hollisae*, *V. furnissii*, *V. fluvialis* and *V. metschnikovii* have also been documented. These infections are relatively rare, although these pathogens are important for clinical treatment decisions and to distinguish the exact causative agents. However, *V. fluvialis* is widely recognized as an emerging food-borne pathogen that poses a public health concern (Igbinsosa et al. 2010; Ramamurthy et al. 2014). An infection with *V. fluvialis* was reported in a 75-year old man with diarrhea and abdominal rash after consumption of uncooked clams (Arora and McHargue 2021). Another case report dealt with a wound infection caused by *V. fluvialis*, acquired through an impalement injury in shallow waters of the Baltic Sea (Hecht et al. 2022). In Korea, mollusk seafood has been found to harbor *V. diabolicalus*, *V. harveyi*, *V. antiquarius*, *V. anguillarum* and *V. aestuarianus* strains with virulent determinants and multidrug-resistant characteristics (Dahanayake et al. 2020b; De Silva et al. 2019; Hossain et al. 2020). Figure 1 summarizes the virulence factors and infections caused by the *Vibrio* spp.

3 Virulence factors of *Vibrio* spp.

3.1 TDH (thermostable direct hemolysin), TRH (TDH-related hemolysin) and *toxR* gene

Generally, *V. parahaemolyticus* strains are well-known to produce various virulence factors during pathogenesis

Fig. 1 Virulence factors and infections of *Vibrio* spp. isolated from shellfish



(Letchumanan et al. 2014). Among those virulence factors, the toxins TDH (thermostable direct hemolysin) and TRH (TDH-related hemolysin) are encoded by *tdh* and *trh* genes, respectively. The *tdh* gene is responsible for kanagawa, with produces β hemolysis on Wagatsuma agar (Honda et al. 1988; Nishibuchi and Kaper 1995). These 2 virulence factors cause similar biological activities such as enterotoxicity, cytotoxicity and hemolytic activity (Park et al. 2004). The presence of both TDH and TRH toxins plays a major role during infections, however, irregularity among cases are reported. In most common scenarios, the *tdh* gene has been found in only 1–2% of environmental strains (Honda and Iida 1993). *Vibrio parahaemolyticus* isolated from different marine products showed the presence of *tdh* and *trh* genes (Ryu et al. 2019; Ashrafudoulla et al. 2021; Zhong et al. 2022). In Korea, a study reported 2 (2.4%) and 8 (9.5%) of 84 strains with *tdh* and *trh* genes positive samples isolated from shellfish (Oh et al. 2011). Previously, the presence of *tdh* and *trh* genes in other *Vibrio* spp, including *V. cholerae* non-O1/non-O139, *V. diabolicus* and *V. alginolyticus* had been studied by Raghunath (2015). Dahanayake et al. (2020a) found *tdh* in *V. diabolicus* isolates from cockles and *V. alginolyticus* isolates from abalone in Korean seafood. And *V. parahaemolyticus* isolated from oysters and clams harbored *tdh* and *trh* genes (Robert-Pillot et al. 2004; Vongxay et al. 2008). *Tdh* and *trh* genes in *V. parahaemolyticus* and *V. vulnificus* were isolated from retail raw oysters in Thailand (Changchai and Saunjit 2014). Ahmed et al. (2018) found *tdh* and *trh* genes in *V. parahaemolyticus* isolated from crustaceans in Egypt. *V. parahaemolyticus* strains isolated from mussels, clams and cockles expressed *trh* and *tdh* genes (Jingjit et al. 2021). According to Jang et al. (2020), the incidence of the *trh* gene was identified in *V. parahaemolyticus* strains isolated from shellfish and shrimp samples collected from the West Coast of Korea.

The *toxR* virulence gene is known to regulate the expression of virulence genes in *Vibrio* species and also produces chemotaxis proteins that aid in colonization in the intestine (Mey et al. 2015). This gene was found prevalent among *V. alginolyticus* isolates in mollusk seafood in Korea (Dahanayake et al. 2018, 2020b). *V. parahaemolyticus* isolated from clams, oysters and scallops in Poland expressed *toxR* genes (Lopatek et al. 2015). *V. cholerae* isolates from mussels were positive for *toxR* and *hlyA* genes (Ottaviani et al. 2009). Tan et al. (2020) identified the *toxR* gene in *V. parahaemolyticus* isolated from surf clams and blood clams in Malaysia. *V. parahaemolyticus* isolated from oysters and mussels express *toxR* gene (Stratev et al. 2023). *Vibrio parahaemolyticus* isolates from shellfish in India expressed *tdh*, *trh* and *toxR* genes (Narayanan et al. 2020). *Vibrio* species carrying the *tdh* and *trh* genes are acknowledged as pathogenic, capable of

inducing acute infections in humans (Robert-Pillot et al. 2004). Table 1 summarizes the virulence factors of *Vibrio* spp. isolated from shellfish.

3.2 Extracellular enzymes

The extracellular enzymes of *Vibrio* spp. actively participate in potential virulence as secretions (Soto-Rodriguez et al. 2003; Elavarashi et al. 2017). These enzymes are health risk indicators of *Vibrio* spp. and present in clinical, environmental and food sources (Lafisca et al. 2008). All mussel-borne *Vibrio* isolates showed DNase and gelatinase activities while most of the isolates showed caseinase, phospholipase and lipase activities (Hossain et al. 2020). Furthermore, *Vibrio* isolates from oysters, manila clams, scallops, cockles and abalones were positive for most of the enzyme activities (Dahanayake et al. 2018, 2020a). The extracellular DNase enzymes facilitate DNA hydrolysis and reproduction of the bacterial strains (Vergis et al. 2002). *V. parahaemolyticus* isolated from fresh oysters were positive for lipase, phospholipase, protease, gelatinase, caseinase and Dnase activities (Costa et al. 2013). In another study, *V. parahaemolyticus* isolated from clams, sea mussels and oyster showed hemolytic, lipase, protease, gelatinase, and Dnase activities (Ashrafudoulla et al. 2021). Narayanan et al. (2020) and Silvester et al. (2022) studied β -hemolytic activity (KP) of *V. parahaemolyticus* isolated from shellfish, shrimps and crabs in India. Jingjit et al. (2021) also observed the hemolytic activity of *V. parahaemolyticus* strains isolated from mussels, clams and cockles. Cytotoxic, proteolytic, DNase, mucinase, lecithinase and lipase activities of *V. vulnificus* isolated from oyster was reported by Quiñones-Ramírez et al. (2010). Gelatinase and caseinase enzymes are related to gelatin and protein deterioration, respectively. Lipase helps to obtain nutrients by deteriorating the lipid membrane of host cells, while phospholipase involves in hemolysis and lecithinase activity (Fiore et al. 1997; Cocchiario et al. 2008). *V. parahaemolyticus*, *V. cholerae*, *V. parahaemolyticu*, *V. ponticus*, *V. littoralis*, *V. metschnikovii* and *V. crassostreae* isolated from fresh and processed mollusk showed positive activities for lipase, phospholipase, gelatinase, caseinase, DNase, amylase and β -hemolysin (Silva et al. 2018). Shellfish can be vehicles of *Vibrio* spp. that can express extracellular enzymes associated with bacterial pathogenesis. Cooking is recommended in case of human consumption.

3.3 Other virulence factors and virulence genes

V. parahaemolyticus binds to the host cell during infection with the use of adhesion factors such as fibronectin and phosphatidic acid (Wang et al. 2015). Vongxay et al. (2008) observed the adherence activity of *V. parahaemolyticus* isolated from clams and mussels to Caco-2 cells. The

Table 1 Prevalence of virulence factors of *Vibrio* spp. in shellfish

Country	Sample type	<i>Vibrio</i> spp. (number of isolates)	Virulence factors	Virulence genes	Origin of Virulence genes	References
Brazil	Oyster (<i>C. rhizophorae</i>)	<i>V. parahaemolyticus</i> (70)	Gelatinase, caseinase, elastase, phospholipase, lipase, amylase, DNase			Costa et al. (2013)
China	Oyster, mussels	<i>V. parahaemolyticus</i> (23)		<i>tdh</i> , <i>tlh</i> , <i>trh</i>	Intrinsically harbored	Rojas et al. (2011)
	Shellfish, shrimps, crab	<i>V. parahaemolyticus</i> (152)		<i>tdh</i> , <i>trh</i> , <i>toxR</i>	Intrinsically harbored	Zhong et al. (2022)
	Oysters, clams	<i>V. parahaemolyticus</i> (150)		<i>tdh</i> , <i>trh</i> , <i>vscP</i> , <i>vopS</i> , <i>vscK</i> , <i>vscF</i> , <i>vopB2</i> , <i>vscC2</i> , <i>vscS2</i> , <i>vopT</i>	Intrinsically harbored+ horizontal gene transfer	Chen et al. (2018)
	Shellfish, shrimp, sea cucumber	<i>V. Parahaemolyticus</i> (60)		<i>tdh</i> , <i>trh</i>	Intrinsically harbored	Jiang et al. (2019)
India	Shellfish (<i>B.camalicutals.H. discusshanna</i> , <i>M. iridescens</i> , <i>S. subrenata</i> , <i>T. granosa</i>)	<i>V. parahaemolyticus</i> (208)		<i>tdh</i> , <i>trt</i>	Intrinsically harbored	Hu and Chen (2016)
	Razor clams (<i>Sinonovacula constricta canarck</i>), short-necked clams (<i>Cyclina sinensis</i>), mussels, shrimps	<i>V. parahaemolyticus</i> (191)	Enteropathogenicity, hemolysin, urease, adherence to Caco-2	<i>tdh</i> , <i>trh</i>	Intrinsically harbored	Vongxay et al. (2008)
	Shrimps, crabs	<i>V. parahaemolyticus</i> (34), <i>V. cholerae</i> (02)	Thermostable direct hemolysin, biofilm formation	<i>tdh</i> , <i>trh</i> , <i>ctx</i> , <i>hlyA</i>	Intrinsically harbored	Ahmed et al. (2018)
India	Oyster	<i>V. parahaemolyticus</i> (80)		<i>tdh</i> , <i>trh</i> , <i>toxR</i>	Intrinsically harbored	Parthasarathy et al. (2021)
Italy	Mussels, prawns	Non-O1 non-O139 <i>V. cholerae</i> (12)	Cytotoxic, protease, hemolysin	<i>hlyA</i> , <i>toxR</i>	Intrinsically harbored	Ottaviani et al. (2009)
Korea	Oyster, short-necked clam, ark shell, sea mussel	<i>V. parahaemolyticus</i> (30)	Biofilm formation			Ashrafudoulla et al. (2021)
Pacific abalone (<i>Haliotis discus hannai</i> Ino, 1953)		<i>V. alginolyticus</i> (15), <i>V. diabolitus</i> (14), <i>V. anti-quarius</i> (02), <i>V. parahaemolyticus</i> (01)	Lipase, phospholipase, DNase, amylase hemolysin, slime production	<i>tdh</i> , <i>tlh</i> , <i>trh</i> , <i>toxR</i> , <i>vac</i> , <i>vfh</i> , <i>hupO</i> , <i>VPI</i> , <i>ctxAB</i>	N/A	Wickramanayake et al. (2020)
	Hard-shelled mussel (<i>M. coruscus</i>)	<i>V. diabolitus</i> (16), <i>V. alginolyticus</i> (13), <i>V. parahaemolyticus</i> (02), <i>V. harveyi</i> (01)	Lipase, phospholipase, gelatinase, caseinase, DNase, hemolysin, slime production	<i>tlh</i> , <i>trh</i> , <i>toxR</i> , <i>vac</i> , <i>vfh</i> , <i>hupO</i> , <i>VPI</i> , <i>ctxAB</i>	N/A	Hossain et al. (2020)
Cockles (<i>Tegillarca granosa</i>)		<i>V. parahaemolyticus</i> (04), <i>V. alginolyticus</i> (11), <i>V. diabolitus</i> (14), <i>V. harveyi</i> (03)	Lipase, phospholipase, gelatinase, caseinase, DNase, hemolysin, amylase	<i>tdh</i> , <i>tlh</i> , <i>trh</i> , <i>toxR</i> , <i>vac</i> , <i>ctxAB</i>	N/A	Dahanayake et al. (2020a)
	Manila clam (<i>R. philippinarum</i>)	<i>V. alginolyticus</i> (01), <i>V. diabolitus</i> (27), <i>V. anti-quarius</i> (01), <i>V. fluvialis</i> (02)	Slime production, gelatinase, hemolysin, collagenase	<i>F-toxR</i> , <i>hupO</i> , <i>VPI</i> , <i>tlh</i> , <i>vac</i>	N/A	Dahanayake et al. (2020b)
Yesso scallop (<i>Patinopecten yessoensis</i>)		<i>V. parahaemolyticus</i> (02), <i>V. alginolyticus</i> (09), <i>V. diabolitus</i> (07), <i>V. anguillarum</i> (04), <i>V. fluvialis</i> (07), <i>V. aesturianus</i> (01)	Lipase, phospholipase, gelatinase, caseinase, DNase, hemolysin, amylase, protease, slime production	<i>tdh</i> , <i>tlh</i> , <i>trh</i> , <i>toxR</i> , <i>vac</i> , <i>vfh</i> , <i>hupO</i> , <i>VPI</i>	Intrinsically harbored+ horizontal gene transfer	De Silva et al. (2019)
	Oyster, mussels, ark shell, short-necked clam, chinese cyclina, spiny top shell	<i>V. parahaemolyticus</i> (31), <i>V. vulnificus</i> (5), <i>V. cholerae</i> (5)		<i>tdh</i> , <i>trh</i>	Intrinsically harbored in <i>V. parahaemolyticus</i>	Mok et al. (2019a)
Oysters, mussels, short-necked clams, ark shells		<i>V. parahaemolyticus</i> (160)		<i>tdh</i> , <i>trh</i>	Intrinsically harbored	Ryu et al. (2019)
	Oyster, Mussels, ark shell	<i>V. parahaemolyticus</i> (50), <i>V. cholerae</i> (01)		<i>tdh</i> , <i>trh</i>	Intrinsically harbored	Mok et al. (2019b)

Table 1 (continued)

Country	Sample type	<i>Vibrio</i> spp. (number of isolates)	Virulence factors	Virulence genes	Origin of Virulence genes	References
	Oyster (<i>C. gigas</i>)	<i>V. alginolyticus</i> (23), <i>V. amiquarius</i> (07), <i>V. fluvialis</i> (11)	Lipase, phospholipase, gelatinase, caseinase, DNase, hemolysin, amylase, protease, slime production	<i>tdh</i> , <i>tlh</i> , <i>trh</i> , <i>toxR</i> , <i>vac</i> , <i>vfh</i> , <i>hupO</i> , <i>VPI</i> , <i>ctxAB</i>	N/A	Dahanayake et al. (2018)
	Bivalve shellfish	<i>V. parahaemolyticus</i> (257)		<i>tdh</i> , <i>trh</i>	Intrinsically harbored	Park et al. (2018)
	Oyster	<i>V. parahaemolyticus</i> (59)		<i>tdh</i> , <i>trh</i>	Intrinsically harbored	Kang et al. (2018)
	Shellfish	<i>V. parahaemolyticus</i> (44)		<i>tdh</i> , <i>trh</i>	Intrinsically harbored	Kang et al. (2017)
	Oyster (<i>C. gigas</i>)	<i>V. parahaemolyticus</i> (80)		<i>tdh</i> , <i>trh</i>	Intrinsically harbored	Kang et al. (2016)
	Corb shell (<i>Cyclina sinensis</i>), razor clam (<i>Solen stricus</i>), short neck clam (<i>V. philippinarum</i>), sea cucumber (<i>Stichopus japonicus</i>), sea mussel (<i>M. coruscus</i>), pacific oyster (<i>C. gigas</i>), charm abalone (<i>Haliotis discus hannai</i>)	<i>V. parahaemolyticus</i> (19)		<i>toxR</i> , <i>tlh</i>	N/A	Jun et al. (2012)
Malaysia	Cockle, shrimps	<i>V. parahaemolyticus</i> (65)		<i>toxR</i> , <i>trh</i> , <i>tdh</i> , <i>tlh</i>	Intrinsically harbored	My Alothrubi (2014)
	Short-neck clam, blood clam	<i>V. parahaemolyticus</i> (75)		<i>toxR</i> , <i>trh</i> , <i>tdh</i>	Intrinsically harbored	Letchumanan et al. (2019)
Mexico	Oysters, clams, mussels, shrimps	<i>V. mimicus</i> (66), <i>V. parahaemolyticus</i> (82), <i>V. vulnificus</i> (60), <i>V. alginolyticus</i> (77)		<i>pvuA</i> , <i>pvsA</i> , <i>wza</i> , <i>lafA</i> , <i>gmbD</i> , <i>motA</i> , <i>iutA</i> , <i>toxR</i> , <i>wcrA</i>	Intrinsically harbored + horizontal gene transfer	Álvarez-Contreras et al. (2021)
	Oyster	<i>V. alginolyticus</i> (30)	Hemolysin, protease, siderophore production	<i>proA</i> , <i>wza</i> , <i>vopD</i> , <i>vopB</i> , <i>hcp</i> , <i>vash</i> , <i>vgrG</i> , <i>tdh</i> , <i>lafA</i> , <i>pvsA</i> , <i>pvuA</i>	Intrinsically harbored + horizontal gene transfer	Hernández-Robles et al. (2016)
	Oyster	<i>V. vulnificus</i> (143)	Haemolysin protease, adherence, DNase, mucinase, lecithinase, lipase			Quiñones-Ramírez et al. (2010)
Poland	Clams (Manila clams, razor clams, hard clams), cockles, mussels, oysters, scallops	<i>V. Parahaemolyticus</i> (92)		<i>tlh</i> , <i>trh</i>	Intrinsically harbored	Lopatek et al. (2018)
	Clams (<i>Tapes semidecussatus</i> , <i>Ruditapes philippinarum</i>), oysters (<i>C. gigas</i>), scallops (<i>Pecten maximus</i>), mussels (<i>M. edulis</i>)	<i>V. parahaemolyticus</i> (400)		<i>toxR</i>	Horizontal gene transfer	Lopatek et al. (2015)
Thailand	Oyster (<i>Saccostrea cucullata</i>)	<i>V. Parahaemolyticus</i> (219), <i>V. vulnificus</i> (53)		<i>tdh</i> , <i>trh</i> , <i>vvh</i>	Intrinsically harbored	Changechai and Saunjit (2014)

adherence ability of *V. vulnificus* strains from oysters was reported by Quiñones-Ramírez et al. (2010). *Vibrio* spp. can form biofilm and can survive in stressful conditions resulting in increased infectivity and transmission (Song et al. 2017). Sadat et al. (2021) reported the biofilm-forming ability of *V. parahaemolyticus* and *V. alginolyticus* isolated from seafood. *V. cholerae* strains isolated from crustaceans also displayed biofilm formation (Ahmed et al. 2018). The biofilm-forming ability of *V. parahaemolyticus* isolated from mussels was shown by Ashrafudoulla et al. (2019).

V. vulnificus consists of various virulence factors that facilitate invasion and growth in the host environment. The *V. vulnificus* hemolysin gene (*vvh*) is one of the multiple virulence factors of *V. vulnificus*. Ingestion of contaminated seafood can also cause *V. vulnificus* human infection, which results in 1% of food-related deaths around the globe (Miyoshi 2006; Giltner et al. 2012). *V. vulnificus* strains from oysters in Thailand showed the presence of *vvh* gene (Changchai and Saunjit 2014). Castello et al. (2022) also studied the *vvh* gene in *V. vulnificus* strains isolated from oysters, clams and mussels.

According to the results obtained from whole-genome sequencing studies, the pathogenic isolates of *V. parahaemolyticus* encode 2 types of type III secretion systems (T3SS) known as T3SS1 and T3SS2 (Makino et al. 2003; Ritchie et al. 2012). The *vopB*, *vscP*, *vopS*, *vscK*, *vscF*, *vopB2*, *vscC2*, *vscS2*, *vopT*, and *vopD* genes are involved in translocating effector proteins and are essential for the performance of T3SS (Dietsche et al. 2016). *V. parahaemolyticus* isolated from mussels expressed biofilm genes *VP950* (encoding a lipoprotein-related protein), type VI secretion T6SS (*VP1409*), *VP952*, and *VP962* (encoding a hypothetical protein), Type I pilus (*VP1510*), pathogenicity Island-2 (*VPaI-2*), and *VPaI-6* (*VP1253*) genes (Ashrafudoulla et al. 2019). Cytotoxicity and serious diseases are caused by transporting distinct effectors and toxins into the cytoplasm via T3SS1 and T3SS2 systems (Wang et al. 2015). *Hcp*, *vasH*, *vgrG* and PAAR genes encode proteins that are a key component of type VI secretion system (T6SS) (Church et al. 2016). *Hcp*, *vasH*, *vgrG*, *vopB*, *vopD*, *proA*, *pvsA* (ferric Vibrioferrin receptor), *pvuA*, *wza* (capsular polysaccharide) and *lafA* (lateral flagella's flagellin) genes were reported in *V. alginolyticus* isolated from oysters in Mexico City (Hernández-Robles et al. 2016). *V. parahaemolyticus* isolated from fresh oysters, clams and shrimps expressed *vscP*, *vopS*, *vscK*, *vscF*, *vopB2*, *vscC2*, *vscS2* and *vopT* genes (Chen et al. 2018). The *pirABvp* genes, which are the Photorhabdus insect-related toxin genes, are located on a plasmid in *Vibrio parahaemolyticus*. These genes have been recognized as virulence factors implicated in the development of acute hepatopancreatic necrosis disease (AHPND) in shrimp. Hong et al. (2020) reported the presence of these genes in *Vibrio parahaemolyticus* isolated from molluscan

shellfish and shrimps in Vietnam. The *pirABvp* genes identified in *Vibrio parahaemolyticus* strains that were isolated from shellfish and shrimp collected from the West Coast of Korea (Jang et al. 2020).

Álvarez-Contreras et al. (2021) reported the presence of different virulence genes. *vppC* (collagenase), *tlh* (thermolabile hemolysin), *vvhA* (hemolytic cytolysin) and *vmh* (hemolysin), *pvsA*, *wza* and *lafA* genes were displayed in *V. parahaemolyticus*, *V. mimicus*, *V. vulnificus* and *V. alginolyticus* isolated from oysters, mussels and clams. The *pvsA* and *pvsD* genes that play role in the siderophore formation have been reported in *V. alginolyticus* (Sha et al. 2013). *V. cholerae* pathogenicity island (VPI) is known to harbor several virulence genes at the same location, mainly in epidemic strains was prevalent in molluscan seafood in Korea (Hosain et al. 2020; Wickramanayake et al. 2020). Ahmed et al. (2018) studied *ctx* (cholera toxin) and *hlyA* (*hlyA*-Class) genes of *V. cholerae* strains isolated from crustaceans. *V. cholerae* strains isolated from oysters, mussels and clams expressed *ctx* and *hlyAET* genes (Castello et al. 2022). Presence of several virulence genes in *Vibrio* spp. isolated from shellfish indicate that these strains possess potential virulence characteristics and can act as reservoirs of pathogenic *Vibrio* in humans.

4 Use of antimicrobials and disinfectants in the fish industry

Fish farms contribute to the pollution of the environment through the release of antimicrobials and other therapeutic agents, leading to environmental contamination. Most of the administrated antimicrobials are released into the surrounding aquatic environments as effluents such as untreated seawater, pollutants such as excessive feed and fish excretions (Jang et al. 2018). The excessive use of antimicrobials as therapeutic agents has resulted in the emergence of multidrug-resistant bacterial strains and has facilitated the transfer of antimicrobial resistance genes through horizontal gene transfer mechanisms. This has contributed to the proliferation of antimicrobial-resistant bacteria in various environments (Son et al. 1997; Levy 2001; Manjusha et al. 2005).

4.1 Occurrence of multidrug-resistant *Vibrio* spp. in molluscan shellfish

Among the list of extensively used antimicrobials, cefotaxime, amikacin, gentamicin, tetracycline and trimethoprim-sulfamethoxazole are being used to treat *Vibrio* infections (Daniels et al. 2000; Shaw et al. 2014). In a previous study, all Manila clam-borne vibrios showed resistance to at least two antimicrobials. Of the resisted antimicrobials, high resistance rates among isolates were observed particularly

for ampicillin, piperacillin, rifampicin, colistin sulfate and cephalothin (Dahanayake et al. 2018; De Silva et al. 2019). *V. alginolyticus*, *V. parahaemolyticus*, *V. harveyi*, *V. vulnificus* and *V. cholerae* harbored from oysters, Japanese carpet shells, cockles, clams (*Venus gallina/Chamelea gallina*) and mussels (*Mytilus galloprovincialis* and *Modiolus barbatus*) were resistant to tetracycline, ceftazidime, piperacillin, amoxicillin/clavulanic acid, azithromycin, cefoxitin, and streptomycin (Mancini et al. 2023).

Previous studies have reported high ampicillin resistance among *Vibrio* spp. isolated from coastal areas, estuaries, fish, and shellfish farms (Kim et al. 2005; Lee et al. 2009; Oh et al. 2009). *Vibrio* spp. isolated from clams and oysters in Nigeria showed resistance to Trimethoprim-Sulfamethoxazole (Udoekong et al. 2021). Particularly, *V. parahaemolyticus* isolates were found resistant to ampicillin in most of the mollusk's *Vibrio* isolates (Jun et al. 2012). *V. parahaemolyticus* isolated from short-necked clams (*Venerupis philippinarum*) and oysters (*Crassostrea gigas*) showed resistance to ampicillin, cefotaxime, cefepime, cephalothin, kanamycin, streptomycin and vancomycin (Jo et al. 2020). Resistance for ampicillin, cephalothin, carbenicillin, trimethoprim-sulfamethoxazole and gentamicin was reported in *V. parahaemolyticus*, *V. mimicus*, *V. vulnificus* and *V. alginolyticus* isolated from oysters, mussels and clams (Álvarez-Contreras et al. 2021). Castello et al. (2022) found ampicillin, cephalothin, ceftriaxone, ceftazidime, gentamicin, tetracycline, kanamycin, cefazolin and streptomycin-resistant *V. parahaemolyticus*, *V. vulnificus*, *V. cholerae* NCV and *V. alginolyticus* isolated from clams, mussels and oysters in Sicily. *V. parahaemolyticus* isolated from bivalve shellfish were found resistant to ampicillin, cefixime, streptomycin, trimethoprim and amikacin (Hu and Chen 2016; Ryu et al. 2019). In a study by Lopatek et al. (2015), *V. parahaemolyticus* from shellfish; which were sold in Polish markets and originated from France, Norway, Italy and Netherlands, were found resistant to ampicillin, streptomycin and gentamicin. Resistant for ampicillin, streptomycin and colistin was observed in molluscan shellfish and shrimps borne *Vibrio parahaemolyticus* in Vietnam (Hong et al. 2020). Mok et al. (2019a) reported ampicillin, cefazolin, aztreonam, amikacin, streptomycin, trimethoprim, kanamycin, gentamicin, aztreonam resistant strains of *V. parahaemolyticus* and *V. cholerae* isolated from oyster, ark shell and mussel from Korea. *V. parahaemolyticus* and *V. alginolyticus* strains collected from common cockle (*Cerastoderma edule*) and white leg shrimp in Egypt were resistant to ampicillin, trimethoprim-sulfamethoxazole, erythromycin, tetracycline, penicillin, gentamicin, ciprofloxacin and nalidixic acid (Sadat et al. 2021). Stratev et al. (2023) observed ampicillin, cefepime, and ceftazidime resistance in *V. parahaemolyticus* isolated from oysters and mussels. The multiple antimicrobial resistance (MAR) index > 0.2 is considered a high-risk source

of contamination where antimicrobials are frequently used (Krumperman 1983). Over 50% of the *Vibrio* isolates from oysters, Manila clams, scallops and cockles showed > 0.2 (MAR) index (Sadat et al. 2021; Stratev et al. 2023). Table 2 summarizes the resistant antibiotic of *Vibrio* spp. isolated from shellfish.

The production of extended-spectrum β -lactamases (ESBL) facilitates the isolates to be resistant against β -lactam antimicrobials. Among beta-lactamase enzyme groups, ESBLs are associated with hydrolyzing penicillins, extended-spectrum cephalosporins and carbapenems. ESBLs are most frequently reported in vibrios isolated from a variety of sources such as clinical, environmental and food sources (Jun et al. 2012). A study reported 88.9% of the vibrios carrying beta-lactam resistance among marine or coastal environmental isolates (Zanetti et al. 2001). In previous studies, ESBL gene *bla_{CTX}* was reported as the most prevalent among the *Vibrio* spp. from molluscan seafood. The *bla_{CTX-M}* gene was identified in *Vibrio* spp. isolated from Manila clams (87%), cockles (78%), mussels (87.5%), and abalone (85%). The *bla_{TEM}* gene was present in Manila clams (55%), cockles (40%), mussels (40.6%), and abalone (10%) *Vibrio* isolates. In addition, few molluscan *Vibrio* isolates carrying *aphA-IAB*, *strA-strB* (regulate the kanamycin and streptomycin resistance mechanism, respectively), *bla_{SHV}*, *tetA*, *tetB* (responsible for tetracycline resistance) and Class 1 integron-related Integrase 1 (*intI1*) resistance genes were also detected (Dahanayake et al. 2020a; Wickramanayake et al. 2020). Silvester et al. (2019) studied the presence of *bla_{CTX-M}* and *bla_{NDM-1}* genes in *Vibrio* spp. isolated from seafood. The *intI1* gene acts as an exhibitor which helps to identify different environmental pressures and is mostly engaged in the dissemination of antimicrobial resistance genes (Gillings et al. 2015). Rojas et al. (2011) reported *bla_{TEM}* gene in *V. parahaemolyticus* isolated from oysters and mussels. *V. parahaemolyticus* isolated from oysters in Thailand demonstrated the presence of *qnr* (quinolones), *strB* (streptomycin), *sul2* (sulfamethoxazole), *tetA* (tetracycline), *ermB* (erythromycin) and *bla_{TEM}* genes (Jeamsripong et al. 2020). Nsikan et al. (2021) studied the *qnrB*, *VIM* (Vimentin) and *SHV* (sulfhydryl reagent variable) genes in *Vibrio* spp. isolated from shellfish in Nigeria. *V. splendidus*, *V. kanaloae*, *V. hemicentroti*, *V. neocaledonicus* and *V. jasicida* strains isolated from razor shells and clams expressed *cat* (C acetyltransferase genes) and *tet* genes (Dubert et al. 2016). *Vibrio* resistance to antibiotics is not only mediated by chromosomal gene transfer but also by plasmids transfer. Manjusha and Sarita (2013) reported the plasmid-mediated transfer of amoxicillin, ampicillin, amikacin, carbenicillin, cefuroxime, furazolidone, streptomycin, chloramphenicol, trimethoprim and tetracycline in *Vibrio* spp. isolated from molluscan and shrimp. In aquaculture farming, judicious exploitation of antibiotics should be followed to prevent antibiotic resistance in pathogenic bacteria. Resistance of shellfish-associated pathogenic *Vibrio* spp.

Table 2 Prevalence of antibiotics resistance of *Vibrio* spp. in shellfish

Country	Sample type	<i>Vibrio</i> spp. (number of isolates)	Antimicrobial resistance phenotypes	ARGs	References
Brazil	Oyster (<i>C. rhizophorae</i>), mussel (<i>Mytella guyanensis</i>)	<i>V. parahaemolyticus</i> (08), <i>V. cholerae</i> (03), <i>V. parahaemolyticus</i> (05), <i>V. parahaemolyticus</i> (01), <i>V. metschnikovii</i> (01), <i>V. crassostreae</i> (01)	AMP, KF, CAZ, C		Silva et al. (2018)
China	Oyster, mussels	<i>V. parahaemolyticus</i> (23)	AMP, GEN, CIP, CTX	<i>bla</i> _{TEM}	Rojas et al. (2011)
	Shellfish, shrimp, sea cucumber	<i>V. Parahaemolyticus</i> (60)	AMP, AMK, TET, SXT, STR, CEZ, CEX		Jiang et al. (2019)
Egypt	Shellfish (<i>B. canaliculata</i> , <i>H. discusshanna</i> , <i>M. tirdescens</i> , <i>S. suberentata</i> , <i>T. granosa</i>)	<i>V. parahaemolyticus</i> (208)	AMP, RD, STR	<i>SulII</i> , <i>StrA</i> , <i>StrB</i> , <i>adaA</i>	Hu and Chen (2016)
	Shrimps, crabs	<i>V. parahaemolyticus</i> (34), <i>V. cholerae</i> (02)	AMP, CTX, CAZ, AMK, GEN, K, TET, NAL, CIP, SXT		Ahmed et al. (2018)
India	Oyster	<i>V. parahaemolyticus</i> (80)	AMP, CTX, TET, CEF, C, CIP, NAL		Parthasarathy et al. (2021)
Italy	Shellfish	<i>V. parahaemolyticus</i> (30), <i>V. alginolyticus</i> (44)	AMP, SXT, TET		Ferrini et al. (2008)
Kerala	Molluscan (<i>Perma viridis</i> , Sepia), Crustacean (Shrimp)	<i>V. parahaemolyticus</i> (01), <i>V. costicola</i> (01), <i>V. alginolyticus</i> (01), <i>V. mimicus</i> (02), <i>V. proteolyticus</i> (02), <i>V. splendidus</i> (04), <i>V. Martinus</i> (02), <i>V. nereis</i> (01), <i>V. orientalis</i> (01), <i>V. carchariae</i> (01), <i>V. mediterranei</i> (01), <i>V. hollisae</i> (01), <i>V. Pelagius</i> (01), <i>V. carchariae</i> (01), <i>V. cholera</i> (05), <i>V. cincinnatiensis</i> (01), <i>V. vulnificus</i> (02), <i>V. costicola</i> (01)	AMOX, AMP, AMK, C, CIP, TET, GEN, NAL, RD, STR, SXT, TMR, TET, MPR, CARB, DO, CO, FUR, NET, NOR		Manjusha and Surtia (2013)
Korea	Oysters, short-necked clams, ark shells, sea mussel	<i>V. parahaemolyticus</i> (63)	VA, TET, NAL, AMP, K, AMK, CIP, CAZ, CEF, C, E, PRL, PENG, DA, LEV, DO		Ashrafudoulla et al. (2021)
	Pacific abalone (<i>Haliotis discus hannai</i> Ito, 1953)	<i>V. alginolyticus</i> (15), <i>V. diabolis</i> (14), <i>V. antiquarius</i> (02), <i>V. parahaemolyticus</i> (01)	AMP, PRL, COL, STR, K, IMI, CEF, TET, RD	<i>IntI1</i> , <i>bla</i> _{CTX} , <i>bla</i> _{TEM} , <i>bla</i> _{SHV} , <i>strAB</i> , <i>aphAI-IAB</i>	Wickramanayake et al. (2020)
shellfish	Hard-shelled mussel (<i>M. cornucopis</i>)	<i>V. diabolis</i> (16), <i>V. alginolyticus</i> (13), <i>V. parahaemolyticus</i> (02), <i>V. harveyi</i> (01)	AMOX, AMP, CEF, COL, E, IMI, K, KF, OT, PRL, STR, ESBL	<i>bla</i> _{CTX} , <i>bla</i> _{TEM} , <i>bla</i> _{SHV} , <i>strAB</i> , <i>aphAI-IAB</i> , <i>tetE</i> , <i>bla</i> _{OXA}	Hossain et al. (2020)
	Oysters, mussels, short-necked clams, ark shells	<i>V. parahaemolyticus</i> (38)	AMP, CTX, KF, GEN, K, STR, VA, RD		Jo et al. (2020)
Cockles (<i>Tegillarca granosa</i>)	<i>V. parahaemolyticus</i> (160)	AMP, STR, TMR, AMK, Cefixime		Ryu et al. (2019)	
Manila clam (<i>R. philippinarum</i>)	Oysters, mussels, short-necked clams, ark shells	<i>V. parahaemolyticus</i> (04), <i>V. alginolyticus</i> (11), <i>V. diabolis</i> (14), <i>V. harveyi</i> (03)	AMP, PRL, COL, STR, K, AMK, E, RD, CEF, KF	<i>bla</i> _{CTX} , <i>bla</i> _{TEM} , <i>bla</i> _{SHV} , <i>aac(6)-Ib</i> , <i>tetB</i> , <i>strAB</i> , <i>aphAI-IAB</i>	Dahanayake et al. (2020a)
	Yesso scallop (<i>Patinopecten yessoensis</i>)	<i>V. alginolyticus</i> (01), <i>V. diabolis</i> (27), <i>V. antiquarius</i> (01), <i>V. fluvialis</i> (02)	AMP, PRL, TET, COL, DA, STR, K, AMK, E, CIP, IMI, MPR, RD, CEF, KF	<i>Bla</i> _{CTX} , <i>bla</i> _{TEM} , <i>tetA</i> , <i>strAB</i>	Dahanayake et al. (2020b)
Oysters, mussels, ark shell, short-necked clam, chinese cyclina, spiny top shell	<i>V. parahaemolyticus</i> (02), <i>V. alginolyticus</i> (09), <i>V. diabolis</i> (07), <i>V. anguillarum</i> (04), <i>V. fluvialis</i> (07), <i>V. aestuarius</i> (01)	AMP, PRL, COL, VA, STR, G, KAN, AMK, E, NAL, CIP, IMI, MPR, SXT, CPL, KF, CRO, CEF, CTX, DA, OFX		De Silva et al. (2019)	
Oysters, Mussels, ark shell	<i>V. parahaemolyticus</i> (5)	AMP, PRL, CZ, ATM, AMK		Mok et al. (2019a)	
Oyster	<i>V. parahaemolyticus</i> (50), <i>V. cholerae</i> (01)	AMP, AMK, STR, TMR, K, GEN, CZ, ATM		Mok et al. (2019b)	
Oyster (<i>C. gigas</i>)	<i>V. parahaemolyticus</i> (23), <i>V. antiquarius</i> (07), <i>V. fluvialis</i> (11)	AMP, CTX, KF, GEN, K, STR, VA, RD, CIP, TET, E		Kang et al. (2018)	
		AMP, KF, NAL, GEN, STR, SXT, VA, FOX, OFX		Dahanayake et al. (2018)	

Table 2 (continued)

Country	Sample type	<i>Vibrio</i> spp. (number of isolates)	Antimicrobial resistance phenotypes	ARGs	References
	Oysters (<i>C. gigas</i>), short-necked clams (<i>Ruditapes philippinarum</i>), corb shells (<i>Cyclina sinensis</i>)	<i>V. parahaemolyticus</i> (194)	AMP, NA, AMOX, TMR		Ryu et al. (2017)
	Shellfish	<i>V. parahaemolyticus</i> (44)	AMP, STR, TMR, K, GEN, CIP, NAL, E, RD ATM, KF		Kang et al. (2017)
	Oyster (<i>C. gigas</i>)	<i>V. parahaemolyticus</i> (80)	AMP, VA, KF, RD, STR		Kang et al. (2016)
	Oyster, short-neck clams	<i>V. parahaemolyticus</i> (436)	AMP, STR, TMR, RD		Yu et al. (2014)
	Corb shell (<i>Cyclina sinensis</i>), razor clam (<i>Solen strictus</i>), short neck clam (<i>V. philippinarum</i>), sea cucumber (<i>Stichopus japonicus</i>), sea mussel (<i>M. coruscus</i>), pacific oyster (<i>C. gigas</i>), charm abalone (<i>Haliotis discus hannai</i>)	<i>V. parahaemolyticus</i> (19)	AMP, PRL, AMOX, AMK, GEN, LEV, TET, CIP, SXT, TMR, CZ, CTX, CAZ, IMI, TAZ, CEP, CAB, CEF	<i>tetA</i> , <i>strB</i>	Jun et al. (2012)
Malaysia	Cockle, shrimps	<i>V. parahaemolyticus</i> (65)	AMP, CIP		My Alohrubi (2014)
Mexico	Oysters, clams, mussels	<i>V. mimicus</i> (66), <i>V. parahaemolyticus</i> (82), <i>V. vulnificus</i> (60), <i>V. alginolyticus</i> (77)	AMP, SXT, C, GEN, KF, CARB, CEF, NIF		Álvarez-Contreras et al. (2021)
	Oyster	<i>V. alginolyticus</i> (30)	CEL, CET, PER		Hernández-Robles et al. (2016)
Poland	Clams (Manila clams, razor clams, hard clams), cockles, mussels, oyster, scallops	<i>V. Parahaemolyticus</i> (92)	AMP, STR, GEN		Lopatek et al. (2018)
	Clams (<i>Tapes semidecussatus</i> , <i>Ruditapes philippinarum</i>), Oysters (<i>Crassostrea gigas</i>), Scallops (<i>Pecten maximus</i>), Mussels (<i>Mytilus edulis</i>), scallops	<i>V. parahaemolyticus</i> (400)	AMP, STR, GEN		Lopatek et al. (2015)
Spain	Pod razor shell (<i>Ensis siliqua</i>), grooved razor shell (<i>Solen marginatus</i>), wedge clam (<i>Donax trunculus</i>), manila clam (<i>Ruditapes philippinarum</i>), carpet shell clam (<i>R. decussatus</i>)	<i>V. splendidus</i> (24), <i>V. kanaloae</i> (02), <i>V. hemiцентроти</i> (05), <i>V. neocaledoni-</i> <i>cus</i> (01), <i>V. jasicida</i> n = (03)	CHL, TET, AMX, STR	<i>cat</i> , <i>tet</i>	Dubert et al. (2016)
Thailand	Oyster (<i>Crassostrea lugubris</i> , <i>C. belcheri</i>)	<i>V. parahaemolyticus</i> (361)	E, SXT, TMR, AMP, STR, TET	<i>qnr</i> , <i>strB</i> , <i>sul2</i> , <i>tetA</i> , <i>ermB</i> , <i>sul2</i> , <i>bla</i> _{TEM}	Jeamsrirong et al. (2020)

AMP ampicillin, COL colistin sulfate, STR streptomycin, GEN gentamycin, K kanamycin, AMK amikacin, NAL nalidixic acid, CIP ciprofloxacin, SXT trimethoprim-sulfamethoxazole, TET Tetracycline, RD Rifampin, VA Vancomycin, E Erythromycin, C chloramphenicol, TMP trimethoprim, PRL piperacillin, ATM Aztreonam, KF Cephalothin, CTX Cefotaxime, CARB carbenicillin, CEF ceftriaxone, MRP meropenem, IMI imipenem, DA clindamycin, CZ: cefazolin, FOX cefoxitin, OFX ofloxacin, ESBL extended-spectrum b-lactamas, PENG penicillin, LEV levofloxacin, Do Doxycycline, TAZ tazobactam, CEP cepheims, CAB carbapenems, CEF cefoxitin, COT Cotrimaxazole, FUR Furazolidone, NET Netilmycin, NOR Norfloxacin, CEL Cephalotin, CET cepho-taxime, CEZ cephalozin, CEX cefuroxime sodium

to antibiotics and expression of antibiotic resistance genes indicate a potential risk to treat vibrios infection in humans. Consuming raw or undercooked seafood, especially shellfish, poses a significant threat to consumers.

5 Control measures to minimize *Vibrio* spp. in molluscan shellfish

Shellfish offer a nutritious and valuable source of high-quality proteins, beneficial polyunsaturated fatty acids, essential vitamins, and minerals contributing to a balanced and healthful diet (Prester 2011). But the prevalence of different multidrug resistance pathogens including *Vibrio* spp. increases the incidence of infection by seafood for consumers (Dubert et al. 2016; Mancini et al. 2023). Several measures should be taken to avoid or minimize the potential threat of multidrug resistance, pathogenic *Vibrio* spp. in molluscan shellfish. Implementation of good aquaculture practices including the maintenance of proper water quality, minimizing pollution or contamination and ensuring appropriate nutrition and feeding practices can help reduce the risk of *Vibrio* spp. contamination (Vaiyapuri et al. 2021). Application of proper harvesting and handling techniques, use of clean equipment and ensuring proper temperature control during storage and transportation can minimize contamination risks (Tan et al. 2020). High-temperature processing of molluscan shellfish can effectively reduce the level of pathogenic bacteria (CDC 2023). Raising awareness among consumers, food handlers, and producers about the risks associated with multidrug-resistant *Vibrio* can promote safe handling and consumption practices (Serwecińska 2020). Implementing and enforcing regulatory controls, such as regular monitoring and testing of shellfish for *Vibrio* contamination, can help ensure compliance with safety standards (Tan et al. 2020). Conducting regular surveillance of *Vibrio* strains present in shellfish can help identify potential multidrug-resistant strains. This information can guide appropriate interventions and preventive measures (Bayliss et al. 2017). Furthermore, the utilization of probiotics and prebiotics, immunostimulants, quorum quenching bacteria, phytochemicals (essential oils) and antimicrobial peptides against *Vibrio* spp. as viable alternatives to antibiotics have demonstrated promising potential in the field. By incorporating them into various treatment approaches, the risk of *Vibrio* infections and the emergence of multidrug-resistant strains can be significantly reduced (Vaiyapuri et al. 2021).

6 Conclusions

This review emphasizes the significance of molluscan shellfish as potential reservoirs of *Vibrio* spp., which can spread to seafood, humans, and the surrounding environment. Vibriosis, caused by various *Vibrio* species, is a significant

public health concern associated with the consumption of contaminated seafood, particularly mollusks. *V. parahaemolyticus*, *V. vulnificus* and *V. alginolyticus* are among the most common *Vibrio* species implicated in human infections. The presence of virulence genes and antimicrobial resistance among *Vibrio* spp. isolates from shellfish indicate that pathogenic and resistant strains of *Vibrio* spp. are already distributed in seafood and are a matter of concern for public health. It is recommended that enhanced monitoring for examining the occurrence patterns of potentially pathogenic seafood production, improved sanitation practices, and the development of rapid diagnostic methods to detect virulence markers more efficiently can aid in the early detection and control of *Vibrio* contamination. In addition, new strategies involving effective and safer antimicrobials or alternative non-antimicrobial compounds should be developed to overcome this issue. It emphasizes the need for continued research, surveillance, and education to ensure the safety of seafood consumers and mitigate the impact of vibriosis on public health. By implementing comprehensive strategies, we can strive towards reducing the incidence of *Vibrio* infections and safeguarding the well-being of individuals who consume mollusks and other seafood products.

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Data availability Data sharing does not apply to this article as no new data were created or analysed in this study.

Declarations

Conflict of interest The authors have no conflict of interest to disclose.

References

- Ahmed HA, El Bayomi RM, Hussein MA, Khedr MH, Remela EM, El-Ashram AM (2018) Molecular characterization, antibiotic resistance pattern and biofilm formation of *Vibrio parahaemolyticus* and *V. cholerae* isolated from crustaceans and humans. *Int J Food Microbiol* 274:31–37. <https://doi.org/10.1016/j.jfoodmicro.2018.03.013>
- Alam MJ, Tomochika KI, Miyoshi SI, Shinoda S (2002) Environmental investigation of potentially pathogenic *Vibrio parahaemolyticus* in the Seto-Inland Sea, Japan. *FEMS Microbiol Lett* 208:83–87. <https://doi.org/10.1111/j.1574-6968.2002.tb11064.x>
- Altekruse SF, Bishop RD, Baldy LM, Thompson SG, Wilson SA, Ray BJ, Griffin PM (2000) *Vibrio* gastroenteritis in the US Gulf of Mexico region: the role of raw oysters. *Epidemiol Infect* 124:489–495. <https://doi.org/10.1017/S0950268899003714>

- Álvarez-Contreras AK, Quiñones-Ramírez EI, Vázquez-Salinas C (2021) Prevalence, detection of virulence genes and antimicrobial susceptibility of pathogen *Vibrio* species isolated from different types of seafood samples at “La Nueva Vega” market in Mexico City. *Antonie van Leeuwenhoek. Int J Gen Mol Microbiol* 114:1417–1429. <https://doi.org/10.1007/s10482-021-01591-x>
- Arora H, McHargue C (2021) 28353 hemorrhagic cellulitis secondary to *vibrio fluvialis* infection. *J Am Acad Dermatol* 85:AB184. <https://doi.org/10.1016/j.jaad.2021.06.750>
- Ashrafudoulla M, Mizan MF, Park H, Byun KH, Lee N, Park SH, Ha SD (2019) Genetic relationship, virulence factors, drug resistance profile and biofilm formation ability of *Vibrio parahaemolyticus* isolated from mussel. *Front microbiol* 10:513. <https://doi.org/10.3389/fmicb.2019.00513>
- Ashrafudoulla Md, Na KW, Hossain MI, Mizan MF, Nahar S, Toushik SH, Roy PK, Park SH, Ha SD (2021) Molecular and pathogenic characterization of *Vibrio parahaemolyticus* isolated from seafood. *Mar Pollut Bull* 172:112927. <https://doi.org/10.1016/j.marpolbul.2021.112927>
- Baker-Austin C, Stockley L, Rangdale R, Martinez-Urtaza J (2010) Environmental occurrence and clinical impact of *Vibrio vulnificus* and *Vibrio parahaemolyticus*: a European perspective. *Environ Microbiol Rep* 2:7–18. <https://doi.org/10.1111/j.1758-2229.2009.00096.x>
- Baker-Austin C, Trinanes JA, Salmenlinna S, Löfdahl M, Siitonen A, Taylor NG, Martinez-Urtaza (2016) Heat wave-associated vibriosis, Sweden and Finland, 2014. *Emerg Infect Dis* 22:1216. <https://doi.org/10.3201/eid2207.151996>
- Baker-Austin C, Trinanes J, Gonzalez-Escalona N, Martinez-Urtaza J (2017) Non-cholera vibrios: the microbial barometer of climate change. *Trends Microbiol* 25:76–84. <https://doi.org/10.1016/j.tim.2016.09.008>
- Baker-Austin C, Oliver JD, Alam M, Ali A, Waldor MK, Qadri F, Martinez-Urtaza J (2018) *Vibrio* spp. infections. *Nat Rev Dis Primers* 4:1–9
- Balsalobre LC, Dropa M, de Oliveira DE, Lincopan N, Mamizuka EM, Matté GR, Matté MH (2010) Presence of blaTEM-116 gene in environmental isolates of *Aeromonas hydrophila* and *Aeromonas jandaei* from Brazil. *Braz J Microbiol* 41:718–719. <https://doi.org/10.1590/S1517-83822010000300023>
- Barbieri E, Falzano L, Fiorentini C, Pianetti A, Baffone W, Fabbri A, Matarrese P, Casiere A, Katouli M, Kühn I, Möllby R (1999) Occurrence, diversity, and pathogenicity of halophilic *Vibrio* spp. and non-O1 *Vibrio cholerae* from estuarine waters along the Italian Adriatic coast. *Appl Environ Microbiol* 65:2748–2753. <https://doi.org/10.1128/AEM.65.6.2748-2753.1999>
- Barker WHJ (1974) International symposium on *Vibrio parahaemolyticus*. Saikon Publishing Co., Ltd, Tokyo, pp 47–52
- Bayliss SC, Verner-Jeffreys DW, Bartie KL, Aanensen DM, Sheppard SK, Adams A, Feil EJ (2017) The promise of whole genome pathogen sequencing for the molecular epidemiology of emerging aquaculture pathogens. *Front microbiol* 8:121. <https://doi.org/10.3389/fmicb.2017.00121>
- Beceiro A, Tomás M, Bou G (2013) Antimicrobial resistance and virulence: a successful or deleterious association in the bacterial world? *Clin Microbiol Rev* 26:185–230. <https://doi.org/10.1128/CMR.00059-12>
- Castello A, Alio V, Sciortino S, Oliveri G, Cardamone C, Butera G, Costa A (2022) Occurrence and molecular characterization of potentially pathogenic *Vibrio* spp. in seafood collected in Sicily. *Microorganisms* 11:53. <https://doi.org/10.3390/microorganisms11010053>
- CDC Centers for Disease Control and Prevention (2023) Available at: <https://www.cdc.gov/foodsafety/communication/oysters-and-vibriosis.html>
- Changchai N, Saunjit S (2014) Occurrence of *Vibrio parahaemolyticus* and *Vibrio vulnificus* in retail raw oysters from the eastern coast of Thailand. *Southeast Asian J Trop Med Public Health* 45:662
- Chen X, Zhu Q, Yu F, Zhang W, Wang R, Ye X, Jin L, Liu Y, Li S, Chen Y (2018) Serology, virulence and molecular characteristics of *Vibrio parahaemolyticus* isolated from seafood in Zhejiang province. *PLOS One* 13:e0204892. <https://doi.org/10.1371/journal.pone.0204892>
- Church SR, Lux T, Baker-Austin C, Buddington SP, Michell SL (2016) *Vibrio vulnificus* type 6 secretion system 1 contains anti-bacterial properties. *PLOS One* 11:e0165500. <https://doi.org/10.1371/journal.pone.0165500>
- Cocchiari JL, Kumar Y, Fischer ER, Hackstadt T, Valdivia RH (2008) Cytoplasmic lipid droplets are translocated into the lumen of the *Chlamydia trachomatis* parasitophorous vacuole. *Proc Natl Acad Sci* 105:9379–9384. <https://doi.org/10.1073/pnas.0712241105>
- Coerdts KM, Khachemoune A (2021) *Vibrio vulnificus*: review of mild to life-threatening skin infections. *Cutis* 107:E12–E17
- Costa RA, Amorim LM, Araújo RL, Vieira RH (2013) Múltiples perfiles enzimáticos de cepas de *Vibrio parahaemolyticus* aisladas de ostras. *Rev Argent Microbiol* 45:267–270
- Dahanayake PS, De Silva BC, Hossain S, Shin GW, Heo GJ (2018) Occurrence, virulence factors, and antimicrobial susceptibility patterns of *Vibrio* spp. isolated from live oyster (*Crassostrea gigas*) in Korea. *J Food Saf* 38:e12490. <https://doi.org/10.1111/jfs.12490>
- Dahanayake PS, Hossain S, Wickramanayake MV, Heo GJ (2020a) Prevalence of virulence and extended-spectrum β -lactamase (*ESBL*) genes harbouring *Vibrio* spp. isolated from cockles (*Tegillarca granosa*) marketed in Korea. *Lett Appl Microbiol* 71:61–69. <https://doi.org/10.1111/lam.13232>
- Dahanayake PS, Hossain S, Wickramanayake MV, Wimalasena SH, Heo GJ (2020b) Manila clam (*Ruditapes philippinarum*) marketed in Korea as a source of vibrios harbouring virulence and β -lactam resistance genes. *Lett Appl Microbiol* 71:46–53. <https://doi.org/10.1111/lam.13229>
- Daniels NA, MacKinnon L, Bishop R, Altekruse S, Ray B, Hammond RM, Thompson S, Wilson S, Bean NH, Griffin PM, Slutsker L (2000) *Vibrio parahaemolyticus* infections in the United States, 1973–1998. *J Infect Dis* 181:1661–1666. <https://doi.org/10.1086/315459>
- De Silva BC, Hossain S, Dahanayake PS, Kang TM, Heo GJ (2019) *Vibrio* spp. from Yesso scallop (*Patinopecten yessoensis*) demonstrating virulence properties and antimicrobial resistance. *J Food Saf* 39:e12634. <https://doi.org/10.1111/jfs.12634>
- DePaola AN, Capers GM, Alexander D (1994) Densities of *Vibrio vulnificus* in the intestines of fish from the US Gulf Coast. *Appl Environ Microbiol* 60:984–988. <https://doi.org/10.1128/aem.60.3.984-988.1994>
- Department FAOF, Information F, Data and Statistics Unit (2019) FishStatJ, a tool for fishery statistics analysis. Release: 3.5.0, Universal Software for Fishery Statistical Time Series. Global aquaculture production: quantity 1950–2017; Value 1950–2017; global capture production. FAO, Rome, Italy, pp 1950–2017
- Di DY, Lee A, Jang J, Han D, Hur HG (2017) Season-specific occurrence of potentially pathogenic *Vibrio* spp. on the southern coast of South Korea. *Appl Environ Microbiol* 83:e02680–e02616. <https://doi.org/10.1128/AEM.02680-16>
- Dietsche T, Tesfazgi Mebrhatu M, Brunner MJ, Abrusci P, Yan J, Franz-Wachtel M, Schärfe C, Zilkenat S, Grin I, Galan JE, Kohlbacher O (2016) Structural and functional characterization of the bacterial type III secretion export apparatus. *PLOS Pathog* 12:e1006071. <https://doi.org/10.1371/journal.ppat.1006071>
- Dubert J, Osorio CR, Prado S, Barja JL (2016) Persistence of antibiotic resistant *Vibrio* spp. in shellfish hatchery environment. *Microb Ecol* 72:851–860. <https://doi.org/10.1007/s00248-015-0705-5>

- Elavarashi E, Kindo AJ, Rangarajan S (2017) Enzymatic and non-enzymatic virulence activities of dermatophytes on solid media. *J Clin Diagn Res* 11:DC23. <https://doi.org/10.7860/JCDR/2017/23147.9410>
- FAO. Food and agriculture organization (2022) Retrieved from <https://www.fao.org/3/cc0461en/online/sofia/2022/world-fisheries-aquaculture-production.html>. Accessed on 2 February 2023
- Farmer Iii JJ, Michael Janda J, Brenner FW, Cameron DN, Birkhead KM (2015) *Vibrio*. Bergey's manual of systematics of archaea and bacteria. Wiley, Hoboken
- Fernández-Bravo A, Ballester F, Pujol I, Gomez-Bertomeu F, Martí C, Rezusta A, Ferrer-Cerón I, Aspiroz C, Puyod MJ, Figueras MJ (2019) *Vibrio alginolyticus* infections: report of two cases from Spain with literature review. *J Med Microb Diagn* 8:2161–0703
- Ferrini AM, Mannoni V, Suffredini E, Cozzi L, Croci L (2008) Evaluation of antibacterial resistance in *Vibrio* strains isolated from imported seafood and Italian aquaculture settings. *Food Anal Methods* 1:164–170. <https://doi.org/10.1007/s12161-007-9011-2>
- Fiore AE, Michalski JM, Russell RG, Sears CL, Kaper JB (1997) Cloning, characterization, and chromosomal mapping of a phospholipase (lecithinase) produced by *Vibrio cholerae*. *Infect Immun* 65:3112–3117. <https://doi.org/10.1128/iai.65.8.3112-3117.1997>
- Gillings MR, Gaze WH, Pruden A, Smalla K, Tiedje JM, Zhu YG (2015) Using the class 1 integron-integrase gene as a proxy for anthropogenic pollution. *ISME J* 9:1269–1279. <https://doi.org/10.1038/ismej.2014.226>
- Giltner CL, Nguyen Y, Burrows LL (2012) Type IV pilin proteins: versatile molecular modules. *Microbiol Mol Biol R* 76:740–772. <https://doi.org/10.1128/MMBR.00035-12>
- Hecht J, Borowiak M, Fortmeier B, Dikou S, Gierer W, Klempien I, Nekat J, Schaefer S, Strauch E (2022) Case report: *Vibrio fluvialis* isolated from a wound infection after a piercing trauma in the Baltic Sea. *Access Microbiol*. <https://doi.org/10.1099/acmi.0.000312>
- Hernández-Robles MF, Álvarez-Contreras AK, Juárez-García P, Natividad-Bonifacio I, Curiel-Quesada E, Vázquez-Salinas C, Quiñones-Ramírez EI (2016) Virulence factors and antimicrobial resistance in environmental strains of *Vibrio alginolyticus*. *Int Microbiol* 19:191–198. <https://doi.org/10.2436/20.1501.01.277>
- Hervio-Heath D, Colwell RR, Derrien A, Robert-Pillot A, Fournier JM, Pommepuy M (2002) Occurrence of pathogenic vibrios in coastal areas of France. *J Appl Microbiol* 92:1123–1135. <https://doi.org/10.1046/j.1365-2672.2002.01663.x>
- Hoeffler F, Pouget-Abadie X, Roncato-Saberan M, Lemarié R, Takoudju EM, Raffi F, Corvec S, Le Bras M, Cazanave C, Lehours P, Guimard T (2022) Clinical and Epidemiologic Characteristics and Therapeutic Management of Patients with *Vibrio* Infections, Bay of Biscay, France, 2001–2019. *Emerg Infect Dis* 28:2367–2373
- Honda T, Iida T (1993) The pathogenicity of *Vibrio parahaemolyticus* and the role of the thermostable direct haemolysin and related haemolysins. *Rev Med Microbiol* 4:106–113
- Honda TA, Ni YX, Miwatani TO (1988) Purification and characterization of a hemolysin produced by a clinical isolate of Kanagawa phenomenon-negative *Vibrio parahaemolyticus* and related to the thermostable direct hemolysin. *Infect Immun* 56:961–965. <https://doi.org/10.1128/iai.56.4.961-965.1988>
- Hong To TT, Yanagawa H, Khanh Thuan N, Hiep DM, Cuong DV, Khai LT, Taniguchi T, Kubo R, Hayashidani H (2020) Prevalence of *Vibrio parahaemolyticus* causing acute hepatopancreatic necrosis disease of shrimp in shrimp, molluscan shellfish and water samples in the Mekong Delta. *Vietnam Biol* 9:312. <https://doi.org/10.3390/biology9100312>
- Hossain S, Wickramanayake MV, Dahanayake PS, Heo GJ (2020) Occurrence of virulence and extended-spectrum β -lactamase determinants in *Vibrio* spp. isolated from marketed hard-shelled mussel (*Mytilus coruscus*). *Microb Drug Resist* 26:391–401. <https://doi.org/10.1089/mdr.2019.0131>
- Howard-Jones N (1984) Robert Koch and the cholera *Vibrio*: a century - *Br Med J. (Clinical research ed.)* 288:379. <https://doi.org/10.1136/bmj.288.6414.379>
- Hu Q, Chen L (2016) Virulence and antibiotic and heavy metal resistance of *Vibrio parahaemolyticus* isolated from crustaceans and shellfish in Shanghai, China. *J Food Prot* 79:1371–1377. <https://doi.org/10.4315/0362-028X.JFP-16-031>
- Igbinoso EO, Okoh AI (2010) *Vibrio fluvialis*: an unusual enteric pathogen of increasing public health concern. *Int J Environ Res Publ Health* 7:3628–3643. <https://doi.org/10.3390/ijerph7103628>
- Iwamoto M, Ayers T, Mahon BE, Swerdlow DL (2010) Epidemiology of seafood-associated infections in the United States. *Clin Microbiol Rev* 23:399–411. <https://doi.org/10.1128/CMR.00059-09>
- Jang HM, Kim YB, Choi S, Lee Y, Shin SG, Unno T, Kim YM (2018) Prevalence of antibiotic resistance genes from effluent of coastal aquaculture, South Korea. *Environ Pollut* 233:1049–1057. <https://doi.org/10.1016/j.envpol.2017.10.006>
- Jang GI, Park JI, Oh EG, Kim S (2020) The relationship between Acute Hepatopancreatic Necrosis Disease (AHPND) in shrimp *Litopenaeus vannamei* and *Vibrio parahaemolyticus* strains isolated from shellfish and shrimp of the West Coast of Korea in 2019. *Korean J Fish Aquat Sci* 53:752–760. <https://doi.org/10.5657/KFAS.2020.0752>
- Jeamsripong S, Khant W, Chuanchuen R (2020) Distribution of phenotypic and genotypic antimicrobial resistance and virulence genes in *Vibrio parahaemolyticus* isolated from cultivated oysters and estuarine water. *FEMS Microbiol Ecol* 96:fiia081. <https://doi.org/10.1093/femsec/fiaa081>
- Jiang Y, Chu Y, Xie G, Li F, Wang L, Huang J, Zhai Y, Yao L (2019) Antimicrobial resistance, virulence and genetic relationship of *Vibrio parahaemolyticus* in seafood from coasts of Bohai Sea and Yellow Sea, China. *Int J Food Microbiol* 290:116–124. <https://doi.org/10.1016/j.ijfoodmicro.2018.10.005>
- Jingjit N, Preeprem S, Surachat K, Mittrarp-arthorn P (2021) Characterization and analysis of clustered regularly interspaced short palindromic repeats (CRISPRs) in pandemic and non-pandemic *Vibrio parahaemolyticus* isolates from seafood sources. *Microorganisms* 9:1220. <https://doi.org/10.3390/microorganisms9061220>
- Jo S, Shin C, Shin Y, Kim PH, il Park J, Kim M, Park B, So JS (2020) Heavy metal and antibiotic co-resistance in *Vibrio parahaemolyticus* isolated from shellfish. *Mar Pollut Bull* 156:111246. <https://doi.org/10.1016/j.marpolbul.2020.111246>
- Jones MK, Oliver JD (2009) *Vibrio vulnificus*: disease and pathogenesis. *Infect Immun* 77:1723–1733. <https://doi.org/10.1128/IAI.01046-08>
- Jun JW, Kim JH, Choresca CH Jr, Shin SP, Han JE, Han SY, Chai JY, Park SC (2012) Isolation, molecular characterization, and antibiotic susceptibility of *Vibrio parahaemolyticus* in Korean seafood. *Foodborne Pathog Dis* 9:224–231. <https://doi.org/10.1089/fpd.2011.1018>
- Kang CH, Shin Y, Jang S, Jung Y, So JS (2016) Antimicrobial susceptibility of *Vibrio alginolyticus* isolated from oyster in Korea. *Environ Sci Pollut Res* 23:21106–21112. <https://doi.org/10.1007/s11356-016-7426-2>
- Kang CH, Shin Y, Jang S, Yu H, Kim S, An S, Park K, So JS (2017) Characterization of *Vibrio parahaemolyticus* isolated from oysters in Korea: resistance to various antibiotics and prevalence of virulence genes. *Mar Pollut Bull* 118:261–266. <https://doi.org/10.1016/j.marpolbul.2017.02.070>
- Kang CH, Shin Y, Yu H, Kim S, So JS (2018) Antibiotic and heavy-metal resistance of *Vibrio parahaemolyticus* isolated from oysters in Korea. *Mar Pollut Bull* 135:69–74. <https://doi.org/10.1016/j.marpolbul.2018.07.007>

- KCDC. Korea Center for Disease Control (2022) Available at: <http://www.cdc.go.kr>
- KCDC. Korea Center for Disease Control (2016) Available at: <http://www.cdc.go.kr>
- KIM SH, Sin YM, Lee MJ, Shin PK, Kim MC, Cho JS, Lee CH, Lee YJ, Chae KR (2005) Isolation of major foodborne pathogenic bacteria from ready-to-eat seafoods and its reduction strategy. *J Life Sci* 15:941–947
- Krumperman PH (1983) Multiple antibiotic resistance indexing of *Escherichia coli* to identify high-risk sources of fecal contamination of foods. *Appl Environ Microbiol* 46:165–170. <https://doi.org/10.1128/aem.46.1.165-170.1983>
- Lafisca A, Pereira CS, Giaccone V, Rodrigues DD (2008) Enzymatic characterization of *Vibrio alginolyticus* strains isolated from bivalves harvested at Venice lagoon (Italy) and Guanabara Bay (Brazil). *Rev Inst Med Trop Sao Paulo* 50:199–202. <https://doi.org/10.1590/S0036-46652008000400002>
- Lee WC, Lee MJ, Kim JS, Park SY (2001) Foodborne illness outbreaks in Korea and Japan studied retrospectively. *J Food Prot* 64:899–902
- Lee HW, Lim SK, Kim MN (2009) Characteristics of ampicillin-resistant *Vibrio* spp. isolated from a west coastal area of Korean Peninsula. *Korean J Fish Aquat Sci* 42:20–25. <https://doi.org/10.5657/kfas.2009.42.1.020>
- Letchumanan V, Chan KG, Lee LH (2014) *Vibrio parahaemolyticus*: a review on the pathogenesis, prevalence, and advance molecular identification techniques. *Front Microbiol* 5:705. <https://doi.org/10.3389/fmicb.2014.00705>
- Letchumanan V, Ab Mutalib NS, Wong SH, Chan KG, Lee LH (2019) Determination of antibiotic resistance patterns of *Vibrio parahaemolyticus* from shrimp and shellfish in Selangor, Malaysia. *Prog Microbes Mol Biol*. <https://doi.org/10.36877/pmmmb.a000019>
- Levy SB (2001) Antibiotic resistance: consequences of inaction. *Clin Infect Dis* 33:124–129. <https://doi.org/10.1086/321837>
- Li Y, Xie X, Shi X, Lin Y, Mou J, Chen Q, Lu Y, Zhou L, Jiang M, Sun H, Ma H (2014) *Vibrio parahaemolyticus*, southern coastal region of China, 2007–2012. *Emerg Infect Dis* 20:685. <https://doi.org/10.3201/eid2004.130744>
- Liang P, Cui X, Du X, Kan B, Liang W (2013) The virulence phenotypes and molecular epidemiological characteristics of *Vibrio fluvialis* in China. *Gut Pathog* 5:1–1. <https://doi.org/10.1186/1757-4749-5-6>
- Lida T, Park KS, Suthienkul O, Kozawa J, Yamaichi Y, Yamamoto K, Honda T (1998) Close proximity of the *tdh*, *trh* and *ure* genes on the chromosome of *Vibrio parahaemolyticus*. *Microbiology*. <https://doi.org/10.1099/00221287-144-9-2517>
- Liu PC, Chen YC, Lee KK (2001) Pathogenicity of *Vibrio alginolyticus* isolated from diseased small abalone *Haliotis diversicolor supertexta*. *Microbios* 104:71–77
- Liu X, Chen Y, Wang X, Ji R (2004) Foodborne disease outbreaks in China from 1992 to 2001 national foodborne disease surveillance system. *Wei sheng yan jiu* 33:725–727
- Lopatek M, Wiczorek K, Osek J (2015) Prevalence and antimicrobial resistance of *Vibrio parahaemolyticus* isolated from raw shellfish in Poland. *J Food Prot* 78:1029–1033. <https://doi.org/10.4315/0362-028X.JFP-14-437>
- Lopatek M, Wiczorek K, Osek J (2018) Antimicrobial resistance, virulence factors, and genetic profiles of *Vibrio parahaemolyticus* from seafood. *Appl Environ Microbiol* 84:e00537–e00518. <https://doi.org/10.1128/AEM.00537>
- Makino K, Oshima K, Kurokawa K, Yokoyama K, Uda T, Tagomori K, Iijima Y, Najima M, Nakano M, Yamashita A, Kubota Y (2003) Genome sequence of *Vibrio parahaemolyticus*: a pathogenic mechanism distinct from that of *V. cholerae*. *The Lancet* 361:743–749. [https://doi.org/10.1016/S0140-6736\(03\)12659-1](https://doi.org/10.1016/S0140-6736(03)12659-1)
- Mancini ME, Alessiani A, Donatiello A, Didonna A, D'Attoli L, Faleo S, Occhiochiuso G, Carella F, Di Taranto P, Pace L, Rondinone V (2023) Systematic survey of *Vibrio* spp. and *Salmonella* spp. in Bivalve Shellfish in Apulia Region (Italy): prevalence and Antimicrobial resistance. *Microorganisms* 11:450. <https://doi.org/10.3390/microorganisms11020450>
- Manjusha S, Sarita GB (2013) Characterization of plasmids from multiple antibiotic resistant *Vibrios* isolated from molluscan and crustacean of Kerala. *Int Food Res J* 20:77–86
- Manjusha S, Sarita GB, Elyas KK, Chandrasekaran M (2005) Multiple antibiotic resistances of *Vibrio* isolates from coastal and brackish water areas. *Am J Biochem Biotechnol* 1:201–206
- McCarthy SA, DePaola A, Cook DW, Kaysner CA, Hill WE (1999) Evaluation of alkaline phosphatase- and digoxigenin-labelled probes for detection of the thermolabile hemolysin (*tlh*) gene of *Vibrio parahaemolyticus*. *Lett Appl Microbiol* 28:66–70. <https://doi.org/10.1046/j.1365-2672.1999.00467.x>
- Mey AR, Butz HA, Payne SM (2015) *Vibrio cholerae* CsrA regulates ToxR levels in response to amino acids and is essential for virulence. *MBio* 6:e01064–e01015. <https://doi.org/10.1128/mBio.01064-15>
- Miyoshi S (2006) *Vibrio vulnificus* infection and metalloprotease. *Int J Dermatol* 33:589–595. <https://doi.org/10.1111/j.1346-8138.2006.00139.x>
- Mok JS, Ryu A, Kwon JY, Park K, Shim KB (2019a) Abundance, antimicrobial resistance, and virulence of pathogenic *Vibrio* strains from molluscan shellfish farms along the Korean coast. *Mar Pollut Bull* 149:110559. <https://doi.org/10.1016/j.marpolbul.2019.110559>
- Mok JS, Ryu A, Kwon JY, Kim B, Park K (2019b) Distribution of *Vibrio* species isolated from bivalves and bivalve culture environments along the Gyeongnam coast in Korea: virulence and antimicrobial resistance of *Vibrio parahaemolyticus* isolates. *Food Control* 106:106697
- My Alothrubi S (2014) Antibiotic resistance of *Vibrio parahaemolyticus* isolated from cockles and shrimp sea food marketed in Selangor, Malaysia. *Clin Microbiol* 3:148. <https://doi.org/10.4172/2327-5073.1000148>
- Narayanan SV, Joseph TC, Peeralil S, Mothadaka MP, Lalitha KV (2020) Prevalence, virulence characterization, AMR pattern and genetic relatedness of *Vibrio parahaemolyticus* isolates from retail seafood of Kerala, India. *Front Microbiol* 11:592. <https://doi.org/10.3389/fmicb.2020.00592>
- Nishibuchi M, Kaper JB (1995) Thermostable direct hemolysin gene of *Vibrio parahaemolyticus*: a virulence gene acquired by a marine bacterium. *Infect Immun* 63:2093–2099
- Nsikan SU, Bassey EB, Anne EA, Ootobong DA, Casmir ICI (2021) Multi-Drug Resistance genes associated with some Gram-Negative Bacterial isolated from Shellfish in Iko and Douglas River Estuaries, in Nigeria. *Int J Res Stud Med Health Sci* 6:11–23. <https://doi.org/10.22259/ijrsmhs.0604004>
- Oh EG, Son KT, Ha KS, Yoo HD, Yu HS, Shin SB, Lee HJ, Kim JH (2009) Antimicrobial resistance of *Vibrio* strains from brackish water on the coast of Gyeongsangnamdo. *Korean J Fish Aquat Sci* 42:335–343. <https://doi.org/10.5657/kfas.2009.42.4.335>
- Oh EG, Son KT, Yu H, Lee TS, Lee HJ, Shin S, Kwon JY, Park K, Kim J (2011) Antimicrobial resistance of *Vibrio parahaemolyticus* and *Vibrio alginolyticus* strains isolated from farmed fish in Korea from 2005 through 2007. *J Food Prot* 74:380–386. <https://doi.org/10.4315/0362-028X.JFP-10-307>
- Oliver JD (2005) Wound infections caused by *Vibrio vulnificus* and other marine bacteria. *Epidemiol Infect* 133:383–391. <https://doi.org/10.1017/S0950268805003894>
- Oliver JD, Bockian R (1995) In vivo resuscitation, and virulence towards mice, of viable but nonculturable cells of *Vibrio*

- vulnificus*. Appl Environ Microbiol 61:2620–2623. <https://doi.org/10.1128/aem.61.7.2620-2623.1995>
- Ottaviani D, Leoni F, Rocchegiani E, Santarelli S, Masini L, Di Trani V, Canonico C, Pianetti A, Tega L, Carraturo A (2009) Prevalence and virulence properties of non-O1 non-O139 *Vibrio cholerae* strains from seafood and clinical samples collected in Italy. Int J Food Microbiol 132:47–53. <https://doi.org/10.1016/j.ijfoodmicro.2009.03.014>
- Pang R, Xie T, Wu Q, Li Y, Lei T, Zhang J, Ding Y, Wang J, Xue L, Chen M, Wei X (2019) Comparative genomic analysis reveals the potential risk of *Vibrio parahaemolyticus* isolated from ready-to-eat foods in China. Front Microbiol 10:186. <https://doi.org/10.3389/fmicb.2019.00186>
- Park KS, Ono T, Rokuda M, Jang MH, Okada K, Iida T, Honda T (2004) Functional characterization of two type III secretion systems of *Vibrio parahaemolyticus*. Infect Immun 72:6659–6665. <https://doi.org/10.1128/IAI.72.11.6659-6665.2004>
- Park K, Mok JS, Ryu AR, Kwon JY, Ham IT, Shim KB (2018) Occurrence and virulence of *Vibrio parahaemolyticus* isolated from seawater and bivalve shellfish of the Gyeongnam coast, Korea, in 2004–2016. Mar Pollut Bull 137:382–387. <https://doi.org/10.1016/j.marpolbul.2018.10.033>
- Parthasarathy S, Das SC, Kumar A, Chowdhury G, Miyoshi SI, Dutta S, Mukhopadhyay AK (2021) Molecular characterization and antibiotic resistance of *Vibrio parahaemolyticus* from indian oyster and their probable implication in food chain. World J Microbiol Biotechnol 37:145. <https://doi.org/10.1007/s11274-021-03113-3>
- Prester L (2011) Biogenic amines in fish, fish products and shellfish: a review. Food Addit Contam: Part A 28:1547–1560. <https://doi.org/10.1080/19440049.2011.600728>
- Quiñones-Ramírez EI, Bonifacio IN, Betancourt-Rule M, Ramirez-Vives F, Vázquez-Salinas C (2010) Putative virulence factors identified in *Vibrio vulnificus* strains isolated from oysters and seawater in Mexico. Int J Environ Health Res 20:395–405. <https://doi.org/10.1080/09603123.2010.491856>
- Raghunath P (2015) Roles of thermostable direct hemolysin (TDH) and TDH-related hemolysin (TRH) in *Vibrio parahaemolyticus*. Front Microbiol 5:805. <https://doi.org/10.3389/fmicb.2014.00805>
- Ramamurthy T, Chowdhury G, Pazhani GP, Shinoda S (2014) *Vibrio fluvialis*: an emerging human pathogen. Front Microbiol 5:91. <https://doi.org/10.3389/fmicb.2014.00091>
- Reilly GD, Reilly CA, Smith EG, Baker-Austin C (2011) *Vibrio alginolyticus*-associated wound infection acquired in british waters, Guernsey, July 2011. Eurosurveillance 16:19994. <https://doi.org/10.2807/ese.16.42.19994-en>
- Ritchie JM, Rui H, Zhou X, Iida T, Kodoma T, Ito S, Davis BM, Bronson RT, Waldor MK (2012) Inflammation and disintegration of intestinal villi in an experimental model for *Vibrio parahaemolyticus*-induced diarrhea. PLOS Pathog 8:e1002593. <https://doi.org/10.1371/journal.ppat.1002593>
- Robert-Pillot A, Guérolé A, Lesne J, Delesmont R, Fournier JM, Quilici ML (2004) Occurrence of the *tdh* and *trh* genes in *Vibrio parahaemolyticus* isolates from waters and raw shellfish collected in two French coastal areas and from seafood imported into France. Int J Food Microbiol 91:319–325
- Rojas MV, Matté MH, Dropa M, Da Silva ML, Matté GR (2011) Caracterização de *Vibrio parahaemolyticus* isolados de ostras e mexilhões em São Paulo, Brasil. Rev Inst Med Trop Sao Paulo 53:201–205. <https://www.revistas.usp.br/rimtsp/article/view/31406>
- Ryu AR, Park K, Kim SH, Ham IT, Kwon JY, Kim JH, Yu HS, Lee HJ, Mok JS (2017) Antimicrobial resistance patterns of *Escherichia coli* and *Vibrio parahaemolyticus* isolated from shellfish from the west coast of Korea. Korean J Fish Aquat Sci 50:662–668. <https://doi.org/10.5657/KFAS.2017.0662>
- Ryu AR, Mok JS, Lee DE, Kwon JY, Park K (2019) Occurrence, virulence, and antimicrobial resistance of *Vibrio parahaemolyticus* isolated from bivalve shellfish farms along the southern coast of Korea. Environ Sci Pollut Res 26:21034–21043. <https://doi.org/10.1007/s11356-019-05426-1>
- Sadat A, El-Sherbiny H, Zakaria A, Ramadan H, Awad A (2021) Prevalence, antibiogram and virulence characterization of *Vibrio* isolates from fish and shellfish in Egypt: a possible zoonotic hazard to humans. J Appl Microbiol 131:485–498. <https://doi.org/10.1111/jam.14929>
- Sawabe T, Fujimura Y, Niwa K, Aono H (2007) *Vibrio comitans* sp. nov., *Vibrio rarus* sp. nov. and *Vibrio inusitatus* sp. nov., from the gut of the abalones *Haliotis discus discus*, *H. gigantea*, *H. madaka* and *H. rufescens*. Int J Syst Evol Micr 57:916–922. <https://doi.org/10.1099/ijs.0.64789-0>
- Sawabe T, Ogura Y, Matsumura Y, Feng G, Amin AR, Mino S, Nakagawa S, Sawabe T, Kumar R, Fukui Y, Satomi M (2013) Updating the *Vibrio* clades defined by multilocus sequence phylogeny: proposal of eight new clades, and the description of *Vibrio tritonius* sp. nov. Front Microbiol 4:414. <https://doi.org/10.3389/fmicb.2013.00414>
- Seelman SL, Whitney BM, Stokes EK, Elliot EL, Griswold T, Patel K, Bloodgood S, Jones JL, Cripe J, Cornell J, Luo Y (2023) An outbreak investigation of *Vibrio parahaemolyticus* Infections in the United States linked to crabmeat imported from Venezuela: 2018. Foodborne Pathog Dis 20:123–131. <https://doi.org/10.1089/fpd.2022.0078>
- Serwecińska L (2020) Antimicrobials and antibiotic-resistant bacteria: a risk to the environment and to public health. Water 12:3313. <https://doi.org/10.3390/w12123313>
- Sha J, Rosenzweig JA, Kozlova EV, Wang S, Erova TE, Kirtley ML, van Lier CJ, Chopra AK (2013) Evaluation of the roles played by Hcp and VgrG type 6 secretion system effectors in *Aeromonas hydrophila* SSU pathogenesis. Microbiology 159:1120–1135. <https://doi.org/10.1099/mic.0.063495-0>
- Shaw KS, Rosenberg Goldstein RE, He X, Jacobs JM, Crump BC, Sapkota AR (2014) Antimicrobial susceptibility of *Vibrio vulnificus* and *Vibrio parahaemolyticus* recovered from recreational and commercial areas of Chesapeake Bay and Maryland Coastal Bays. PLOS One 9
- Shen X, Cai Y, Liu C, Liu W, Hui Y, Su YC (2009) Effect of temperature on uptake and survival of *Vibrio parahaemolyticus* in oysters (*Crassostrea plicatula*). Int J Food Microbiol 136:129–132. <https://doi.org/10.1016/j.ijfoodmicro.2009.09.012>
- Silva IP, de Souza Carneiro C, Saraiva MA, de Oliveira TA, de Sousa OV, Evangelista-Barreto NS (2018) Antimicrobial resistance and potential virulence of *Vibrio parahaemolyticus* isolated from water and bivalve mollusks from Bahia, Brazil. Mar Pollut Bull 131:757–762. <https://doi.org/10.1016/j.marpolbul.2018.05.007>
- Silvester R, Pires J, Van Boeckel TP, Madhavan A, Balakrishnan Meenakshikutti A, Hatha (2019) Occurrence of β -lactam resistance genes and plasmid-mediated resistance among *Vibrios* isolated from Southwest Coast of India. Microb Drug Resist 25:1306–1315. <https://doi.org/10.1089/mdr.2019.0031>
- Silvester R, Saji A, Divakaran AR, Dilshana PM, Nair R, Hatha M, Harikrishnan M (2022) Increased incidence and antimicrobial resistance among *Vibrio parahaemolyticus* in shellfishes from major fish markets in Cochin, South India: Seafood risk assessment. Ann Anim Sci 22:1105–1114. <https://doi.org/10.2478/aos-2021-0077>
- Slifka KJ, Newton AE, Mahon BE (2017) *Vibrio alginolyticus* infections in the USA, 1988–2012. Epidemiol Infect 145:1491–1499
- Son R, Rusul G, Sahilah AM, Zainuri A, Raha AR, Salmah I (1997) Antibiotic resistance and plasmid profile of *Aeromonas*

- hydrophila* isolates from cultured fish, *Telapia (Telapia mossambica)*. Lett Appl Microbiol 24:479–482. <https://doi.org/10.1046/j.1472-765X.1997.00156.x>
- Song X, Ma Y, Fu J, Zhao A, Guo Z, Malakar PK, Pan Y, Zhao Y (2017) Effect of temperature on pathogenic and non-pathogenic *Vibrio parahaemolyticus* biofilm formation. Food Control 73:485–491. <https://doi.org/10.1016/j.foodcont.2016.08.041>
- Soto-Rodriguez SA, Roque A, Lizarraga-Partida ML, Guerra-Flores AL, Gomez-Gil B (2003) Virulence of luminous vibrios to *Artemia franciscana nauplii*. Dis Aquat Organ 53:231–240. <https://doi.org/10.3354/dao053231>
- Stratev D, Fasulkova R, Krumova-Valcheva G (2023) Incidence, virulence genes and antimicrobial resistance of *Vibrio parahaemolyticus* isolated from seafood. Microb Pathog 177:106050. <https://doi.org/10.1016/j.micpath.2023.106050>
- Suñén E, Acebes M, Fernández-Astorga A (1995) Occurrence of potentially pathogenic vibrios in bivalve molluscs (mussels and clams) from retail outlets in the north of Spain. J Food Saf 15:275–281. <https://doi.org/10.1111/j.1745-4565.1995.tb00139.x>
- Tan CW, Rukayadi Y, Hasan H, Thung TY, Lee E, Rollon WD, Hara H, Kayali AY, Nishibuchi M, Radu S (2020) Prevalence and antibiotic resistance patterns of *Vibrio parahaemolyticus* isolated from different types of seafood in Selangor, Malaysia. Saudi J Biol Sci 27:1602–1608. <https://doi.org/10.1016/j.sjbs.2020.01.002>
- Torres L, Escobar S, López A, Marco M, Pobo V (2002) Wound infection due to *Vibrio vulnificus* in Spain. Eur J Clin Microbiol 21:537–538. <https://doi.org/10.1007/s10096-002-0767-4>
- Udoekong NS, Basse BE, Asuquo AE, Akan OD, Ifeanyi CI (2021) Multi-Drug Resistance genes associated with some Gram-Negative Bacteria isolates from Shellfish in Iko and Douglas River Estuaries, in Nigeria. Eur J Biol Biotechnol 2:19–27
- Vaiyapuri M, Pailla S, Rao Badireddy M, Pillai D, Chandragiri Nagarajarao R, Prasad Mothadaka M (2021) Antimicrobial resistance in Vibrios of shrimp aquaculture: incidence, identification schemes, drivers and mitigation measures. Aquac Res 52:2923–2941. <https://doi.org/10.1111/are.15142>
- Vergis EN, Shankar N, Chow JW, Hayden MK, Snyderman DR, Zervos MJ, Linden PK, Wagener MM, Muder RR (2002) Association between the presence of enterococcal virulence factors gelatinase, hemolysin, and enterococcal surface protein and mortality among patients with bacteremia due to *Enterococcus faecalis*. Clin Infect Dis 35:570–575. <https://doi.org/10.1086/341977>
- Vongxay K, Wang S, Zhang X, Wu B, Hu H, Pan Z, Chen S, Fang W (2008) Pathogenetic characterization of *Vibrio parahaemolyticus* isolates from clinical and seafood sources. J Food Microbiol 126:71–75. <https://doi.org/10.1016/j.jfoodmicro.2008.04.032>
- Wang R, Zhong Y, Gu X, Yuan J, Saeed AF, Wang S (2015) The pathogenesis, detection, and prevention of *Vibrio parahaemolyticus*. Front Microbiol 6:144. <https://doi.org/10.3389/fmicb.2015.00144>
- Weis KE, Hammond RM, Hutchinson R, Blackmore CG (2011) *Vibrio* illness in Florida, 1998–2007. Epidemiol Infect 139:591–598. <https://doi.org/10.1017/S0950268810001354>
- Wickramanayake MV, Dahanayake PS, Hossain S, De Silva BC, Heo GJ (2020) Characterisation of pathogenic *Vibrio* spp. isolated from live Pacific abalone (*Haliotis discus hannai Ino*, 1953) marketed in South Korea. Indian J Fish 67:105–113. <https://doi.org/10.21077/ijf.2019.67.1.96348-14>
- Wong HC, Liu SH, Ku LW, Lee IY, Wang TK, Lee YS, Lee CL, Kuo LP, Shih DY (2000) Characterization of *Vibrio parahaemolyticus* isolates obtained from foodborne illness outbreaks during 1992 through 1995 in Taiwan. J Food Prot 63:900–906. <https://doi.org/10.4315/0362-028x-63.7.900>
- Yu H, Oh EG, Shin SB, Park YS, Lee HJ, Kim JH, Song KC (2014) Distribution and antimicrobial resistance of *Vibrio parahaemolyticus* isolated from Korean shellfish. Korean J Fish Aquat Sci 47:508–515
- Zanetti S, Spanu T, Deriu A, Romano L, Sechi LA, Fadda G (2001) In vitro susceptibility of *Vibrio* spp. isolated from the environment. Int J Antimicrob Agents 17:407–409
- Zhong X, Pan Z, Mu Y, Zhu Y, Zhang Y, Ma J, Yang M, Yao H (2022) Characterization and epidemiological analysis of *Vibrio parahaemolyticus* isolated from different marine products in East China. Int J Food Microbiol 380:109867

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