

Isolation and identification of potential host probiotic bacteria from Malaysian mahseer, *Tor tambroides* for aquaculture practices

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Abstract. Hossain MK, Iehata S, Noordin NM, Kader MA, Emilia SN, Sung YY, Abol-Munafi AB. 2022. Isolation and identification of potential host probiotic bacteria from Malaysian mahseer, *Tor tambroides* for aquaculture practices. *Biodiversitas* 23: 5423-5430. The digestive tract has been revealed as a reservoir of potential probiotics derived from the host. The goal of this study was to isolate, identify, and characterize putative host-associated probiotic bacteria (HAPs) from the digestive tract of Malaysian mahseer *Tor tambroides*. To evaluate potential *T. tambroides* HAPs, in-vitro digestive enzyme activity (such as a cellulolytic, proteolytic, and lipolytic activity) and antibacterial activity against two fish pathogens (*Vibrio parahaemolyticus* and *Aeromonas hydrophila*) were utilized. Thirty-seven isolates with digestive enzyme activities were tested for their ability to inhibit pathogenic bacteria growth using an agar well-diffusion assay. Three isolates displayed in-vitro suppression of pathogenic bacteria, with two strains (KT03 and KM07) inhibiting the growth of *V. parahaemolyticus* and one strain (KT27) suppressing the proliferation of both harmful bacteria (*V. parahaemolyticus* and *A. hydrophila*). Strains KT03 and KM07 exhibited the most resemblance to *Enterococcus faecalis* (strains 2674 and FC11682, respectively) based on 16S rRNA sequences, whereas KT27 had a 97% similarity to *Aeromonas* sp. A8-29. The study's findings provide valuable data on the prospective use of these three isolates (KT03, KT27, and KM07) as potential HAPs for better understanding their physiological activities, such as growth and disease resistance on *T. tambroides*.

Keywords: *Aeromonas*, antibacterial activity, *Enterococcus*, probiotics, *Tor tambroides*

INTRODUCTION

Disease outbreaks reduce aquaculture production, leading in significant financial losses (Martínez et al. 2012; van Doan et al. 2018). Antimicrobial compounds like antibiotics and chemotherapeutants have been employed in this context to prevent diseases in aquatic species (Serrano 2005; Fekaninová et al. 2017). Antibiotics and chemotherapeutants are effective, however, they have a severe impact on the environment and promote the emergence of antibiotic-resistant bacteria, which might pose a health risk (Romero et al. 2012; Langdon et al. 2016; Al-Asif et al. 2021). As a result, many countries have enacted legislation prohibiting the use of antibiotics and chemotherapeutants in aquaculture (Dawood and Koshio 2016; Van et al. 2020). Alternatively, several biological control approaches, including probiotics and vaccination, have been developed as disease control strategies through research and clinical practice to replace antibiotics (Hossain et al. 2009; Hossain et al. 2011; Lazado et al. 2015).

Aeromonas hydrophila and *Vibrio parahaemolyticus* are common bacterial fish pathogens. Fish become infected when the host immune system become weak or compromised (Dawood et al. 2017; Soto Dávila et al.

2020). *Aeromonas hydrophila* has been identified as the causative pathogen for the epizootic ulcerative syndrome (EUS), fin rot disease, tail rot, and hemorrhagic septicemia in the Indian major carps, such as *Labeo rohita*, *Catla catla* and *Labeo calbasu*, and motile *Aeromonas* septicemia in tilapia fish (Koziońska et al. 2002; Pridgeon and Klesius 2012; Saikot et al. 2013; Ina-Salwany et al. 2019). *Vibrio parahaemolyticus*, along with *Vibrio harveyi* and *V. fluvialis*, causes vibriosis in aquatic organisms and is often found in marine and freshwater fish (Lee et al. 2018). Vibriosis can be found in a number of body parts, including the gastrointestinal (GI) tract (Mishra et al. 2009; Tey et al. 2015; Yan et al. 2019). The most prevalent clinical indications of vibriosis include lethargy, aberrant swimming patterns, skin ulcers, exophthalmia, and gill necrosis, which result in 30-80% mortality (Ina-Salwany et al. 2019). The economic consequences of this disease have been estimated to be approximately US\$9 billion per year (Novriadi 2016).

Many studies on aquaculture probiotics have documented the use of non-host associated probiotics (non-HAPs) originating from the terrestrial environment to suppress pathogenic bacteria in aquaculture (Lazado et al. 2015; van Doan et al. 2018). These non-HAPs were either added to feed as a nutritional supplement to promote

growth performance or used in culture water to improve water quality in aquaculture systems. Through food and the aquatic environment, they may colonize the digestive systems of fish and other aquaculture species. As a result, the use of host-associated probiotics (HAPs) in aquaculture has been promoted (van Doan et al. 2020), and they are thought to be safe for the host and the surrounding environment (Iehata et al. 2010; Interaminense et al. 2018; van Doan et al. 2018; Tarkhani et al. 2020). Due to the presence of digestive enzymes such as amylase, proteases, and lipases produced by probiotics during digestion and absorption, dietary supplementation with HAPs has been proven to improve growth performance (Ray et al. 2012; van Doan et al. 2020; Zaineldin et al. 2021). The host probiotics served to promote disease resistance through immune activation, as well as to maintain the interlinkage between immune responses and intestinal bacteria in the host gut (van Doan et al. 2020), and to improve the host's response to stressful conditions and to stabilize water quality parameters by removing nitrogen from wastes in water (Giraffa et al. 2010; Abdelkhalek et al. 2017). HAPs act as an effective growth promoter and antibiotic substitute to improve aquatic animal disease resistance (Nath et al. 2019). For example, in vitro and ex vivo studies demonstrated lactic acid bacteria (LAB) colonization in sturgeon, *Acipenser persicus* fish, and their adhesion capability varies depending on their isolation habitat (Lazado et al. 2015; van Doan et al. 2020), and their adhesion capability varies based on their isolation habitat (Askarian et al. 2011; Buntin et al. 2017). Potential probiotic bacteria in the host gut may offer health benefits (Adnan et al. 2017; Alshammari et al. 2019), however, the gut bacterial composition may be altered by genetic, dietary, and aquatic environmental factors (Abomughaid 2020; Mohammadi et al. 2022). Thus, screening of HAPs is focused primarily on their antibacterial inhibitory action against pathogens, as well as digesting enzyme activity, which plays an important role in the development of species and environment-specific probiotics (Hai 2015).

The Malaysian mahseer *Tor tambroides* is a valuable cyprinid fish species in Malaysia and other Asian countries, both as a food and ornamental fish in great demand among anglers and hobbyists (Azfar et al. 2019). Despite the fact that this piscine species' breeding is effective, slow growth in culture systems remains a major concern for commercial farming (Lee et al. 2014). *Tor tambroides* growth performance has been accelerated by supplying good nutrition, such as protein, fat, carbohydrate, and vitamins (Ng et al. 2008; Ng and Andin 2011; Kamarudin et al. 2012; Azfar-Ismail et al. 2020). Probiotic bacteria obtained from the ideal fish host are expected to perform better in their native habitat than those derived from terrestrial hosts. Thus, in recent years, studies focused on the application of host probiotic supplements for nutrition and health management of juvenile *T. tambroides* where feeds were supplemented with gut-derived probiotic bacteria (Asaduzzaman et al. 2018a; Asaduzzaman et al. 2018b). The effects on growth performance, muscle fiber, growth-related gene expressions, intestinal morphology, and formation of volatile short-chain fatty acids in the gut were

determined for *T. tambroides* (Asaduzzaman et al. 2018a; Asaduzzaman et al. 2018b). Therefore, the study's objective was to isolate, screen, and identify suitable host gut-derived probiotic bacteria from *T. tambroides*. In this study, the isolates were screened in vitro to determine their nutritional enzyme activity and disease resistance capability through antibacterial activity against *A. hydrophila* and *V. parahaemolyticus*.

MATERIALS AND METHODS

Ethical statement

Tor tambroides is frequently and openly marketed for human consumption in Malaysian markets. They were purchased from the farm with the intention of isolating a probiotic strain from their intestines. Throughout the course of this study, no live *T. tambroides* fish were harmed or utilized in any other experiments. All of the experiments in this study were carried out in line with Universiti Malaysia Terengganu and European regulations on laboratory animal welfare, as well as the guiding principles for laboratory animal use and care.

Fish collection

Three healthy *T. tambroides* (average weight 75.18 ± 6.00 g and age 24 weeks) were transported from a local aquaculture farm (Ikan Kelah Aquafarm Selangor, Malaysia) to the hatchery of the Institute of Tropical Aquaculture and Fisheries, Universiti Malaysia Terengganu, Malaysia. The fish were acclimatized for 3 hours, anesthetized using clove oil (50 mg/L), and their skin wiped with 70% alcohol to minimize surface contamination.

Isolation of candidate probiotic bacteria

For isolation of candidate probiotic bacteria, fish were dissected in aseptic conditions (Zhou et al. 2009), and the whole digestive tract was removed prior to washing three times with sterile 0.01M phosphate buffer saline (PBS; Sigma-Aldrich Cheme GmbH, Munich, Germany). Then, individual digestive tract samples were aseptically removed, homogenized, and suspended with a sterile 0.01M PBS solution. The homogenized samples were diluted using sterile PBS and plated on TSA agar or poured on de Man, Rogosa, and Sharpe (MRS) agar containing 1.0% CaCO₃. TSA plates were incubated at room temperature (28-30°C) for 24h and inoculated MRS plates were incubated at room temperature (28-30°C) for 48-72h. Bacterial colonies with different shapes, characteristics and colors were selected from TSA agar, while colonies with clear zones on MRS agar were selected as candidate probiotics bacteria (Garcés et al. 2020).

In-vitro digestive enzyme activity analysis

Isolated candidate probiotic bacteria were subcultured for 24-48h at room temperature and spotted on each selective media to observe the cellulolytic, lipolytic, and proteolytic activity. We used carboxymethyl cellulose agar (CMCA) with 1% congo red for cellulolytic activity, TSA

or MRS medium consisting of 1% Tween-80 and 0.001% CaCl₂·2H₂O for lipolytic activity, and TSA or MRS medium consisting of 1% skim milk for proteolytic activity. Each media was subsequently incubated for 72-90h at room temperature (28-30°C) (Asaduzzaman et al. 2018b; Selim et al. 2019). After incubation, clear zones surrounding colonies in the selective media were an indicator for the presence of cellulolytic, lipolytic, and proteolytic activity, whereas the presence of white particles surrounding the colonies were identified as positive of lipolytic activity.

In-vitro antibacterial analysis

Pathogenic bacteria *V. parahaemolyticus* (Deris et al. 2020) and *A. hydrophila* ATCC19570 were cultured at 35°C for 24 hours in agar plates containing tryptone soya agar (TSA) media. Isolates with positive nutritional enzyme activity were further selected to be analyzed for antibacterial activity analysis against two pathogens (*A. hydrophila* and *V. parahaemolyticus*) by the agar well diffusion method (Amin et al. 2017; Azahar et al. 2018) with some modification. Briefly, each pathogen was incubated in trypticase soya broth (TSB) broth for 24h and spread on TSA plate. After the spread of each pathogen on TSA plate, five (5) wells measuring 5mm in diameter were punched using sterile micropipette tips. After all candidate bacteria were incubated in broth media for 24 to 48 hours at room temperature (28-30°C), centrifuged at 3000 rpm for 10 minutes with 5 mL of broth culture and 50 uL of the supernatant put into the well of TSA plate. After incubation at 37°C 24h, the plates were observed and measured clear zone around the well. Positive results were evaluated when the clear zone exceeded 1 mm.

Identification of probiotic bacterial strains

Bacterial genomic DNA was extracted with a commercial genomic DNA purification kit, NucleoSpinR (Macherey-Nagel GmbH and Co.KG, Duren, Germany), following the manufacturer's protocol. The extracted DNA was subjected to polymerase chain reaction (PCR) amplification in PCR tubes that contained: 2.5uL of 10X PCR buffer with MgCl₂, 0.5uL of dNTP, 0.5 uL of each primer, 1uL of DNA extract supernatant, 19.5 uL sterile double distilled water with 0.5 uL master mix (MyTaq Mix; Bioline, London, UK), and 0.2mM of universal primers for bacterial PCR amplification (8F: 5'-AGAGTTTGATCATGGCTCAG-3' and 1492R: 5'-GGCTACCTT TTACGACTT-3') (Asaduzzaman et al. 2018b). PCR reaction samples were run for 30 cycles: 95°C for 30 seconds, 56°C for 30 seconds, and 72°C for 1.5 minutes, followed by an extension of 72°C for 7 minutes (SuperCycler Thermal Cycler; Kyratec, Queensland, Australia). After PCR amplification, the PCR products were analyzed on 1.5% agarose gel at 100 volts for 30 minutes (Mohd-Nosi et al. 2018). Thereafter, the PCR products were purified and sequenced at First BASE Laboratories Sdn. Bhd. in Selangor, Malaysia.

Data analysis

After sequencing, the results of chromatograms were examined using chromas version 2.6.2 (Technelysium, Queensland, Australia). Then, all sequences were checked with DECIPHER (<http://decipher.cee.wisc.edu/FindChimeras.html>) for chimeric sequences (Wright et al. 2012). Homology searches were performed for culturable bacterial isolates, and sequences of approximately ~600 nucleotides were used. The close relatives were assigned by the GenBank database of the National Centre for Biotechnology (NCBI) through the BLAST program (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>). Multiple alignments were performed by MEGA version7 software (Kumar et al. 2016).

RESULTS AND DISCUSSION

Isolation and selection of bacteria for nutritional enzyme activity analysis

In the present study, a total of 37 bacterial isolates were obtained (30 isolates marked as 'KT' from TSA media and 7 isolates from 'MRS' media) from the digestive tracts of *Tor tambroides* (Table 1). Nine of 37 isolates (6 isolates from TSA and 3 isolates from MRS media) exhibited all three nutritional enzyme activities (lipolytic, proteolytic, and cellulolytic activity) and were selected to use the next process.

Antibacterial activity analysis

Antibacterial activity of nine isolates with positive nutritional enzyme activities was tested against two pathogens (*A. hydrophila* and *V. parahaemolyticus*) by well diffusion method. Three isolates displayed inhibitory activity (Figure 1 and Table 2). Isolates KT03 and KM07 showed growth suppression against fish pathogen *V. parahaemolyticus*, whereas KT27 exhibited growth suppression against both pathogens, *A. hydrophila* and *V. parahaemolyticus*, in well diffusion assay.

Identification of the selected bacterial isolates

Three isolates with nutritional and antibacterial activities were identified. Strain KT03 had 100% similarity with *Enterococcus* sp. strain 2674, while strain KM07 showed 93% similarity with *Enterococcus* sp. strain FC11682. Strain KT27 was 97% similar with *Aeromonas* sp. strain A8-29. The phylogenetic analysis demonstrated that isolates KT03 and KM07 composed the same cluster with *Enterococcus* sp., whereas isolate KT27 was in the same branch as the genus *Aeromonas* (Figure 1).

Discussion

Applications of probiotic bacteria have drawn a lot of interest and offer an alternate strategy for managing diseases in aquaculture (Van Doan et al. 2018). Moreover, attention has been given to host-associated microorganisms for investigation of beneficial probiotic bacteria because such bacteria are assumed to play a key function in increasing resistance against pathogenic bacteria and being well-habituated to the targeted host gut environment (Mukherjee et al. 2016).

Table 1. Bacterial nutritional enzyme activity of isolates from *Tor tambroides* digestive tract ‘KT’ where letter ‘K’ for Kelah-local name of *T. tambroides* and letter ‘T’ from the word ‘TSA’ agar medium ‘KM’ where ‘K’ stands for Kelah and ‘M’ stand for MRS medium

Isolates number*	Cellulolytic**	Proteolytic**	Lipolytic**
KM01	+	+	+
KM02	-	-	+
KM03	-	-	+
KM04	-	-	+
KM05	-	-	+
KM06	+	+	+
KM07	+	+	+
KT01	-	-	+
KT02	-	+	-
KT03	+	+	+
KT04	-	+	+
KT05	-	+	+
KT06	+	-	-
KT07	+	-	+
KT08	-	-	-
KT09	+	+	+
KT10	-	-	+
KT11	-	-	-
KT12	+	+	+
KT13	+	-	-
KT14	-	+	+
KT15	-	-	-
KT16	+	-	+
KT17	+	+	+
KT18	-	-	-
KT19	+	-	+
KT20	-	-	-
KT21	+	+	+
KT22	+	+	+
KT23	+	+	+
KT24	-	+	-
KT25	+	+	+
KT26	+	-	-
KT27	+	+	+
KT28	+	+	-
KT29	+	+	-
KT30	-	-	+

Note: *KT represents isolation using TSA medium; *KM represents isolation using MRS medium; **+ represents presence of nutritional enzyme activity; **- represents absence of nutritional enzymes activity

Table 2 Antibacterial activities of isolates from *Tor tambroides* digestive tract

Strain	Growth inhibition of pathogen in well diffusion assay			
	<i>A. hydrophila</i>	Diameter of inhibition zones (mm)	<i>V. parahaemolyticus</i>	Diameter of inhibition zones (mm)
KM01	-	-	-	-
KM06	-	-	-	-
KM07	-	-	+	12
KT03	-	-	+	14
KT17	-	-	-	-
KT22	-	-	-	-
KT23	-	-	-	-
KT25	-	-	-	-
KT27	+	15	+	16

Note: “+” represents presence of clear zone and “-” represents absence of clear zone in antibacterial activity analysis

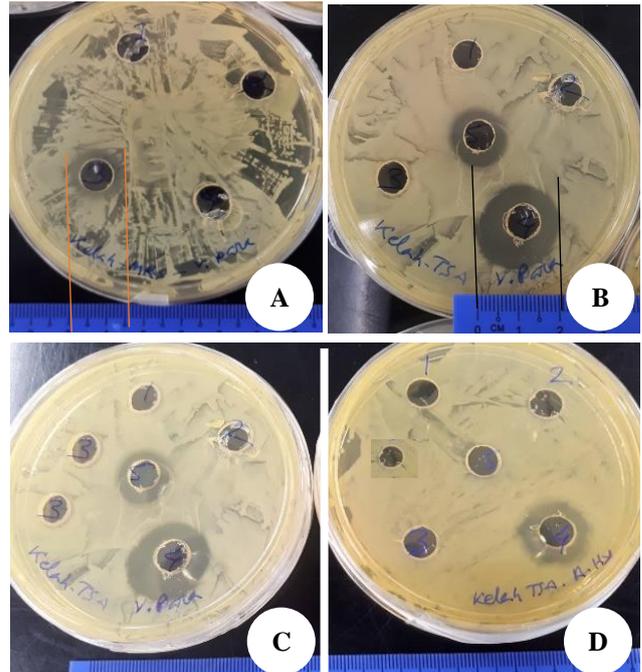


Figure 1. Antibacterial activity analysis of isolates against *Aeromonas hydrophila* and *Vibrio parahaemolyticus*; well diffusion method: A. Isolate KM01, KM06, KM07: against *A. hydrophila*; B. Against *V. parahaemolyticus*; C. For isolates KT03, KT17, KT22, KT23, KT25, KT27 against *A. hydrophila*; D. *V. parahaemolyticus*

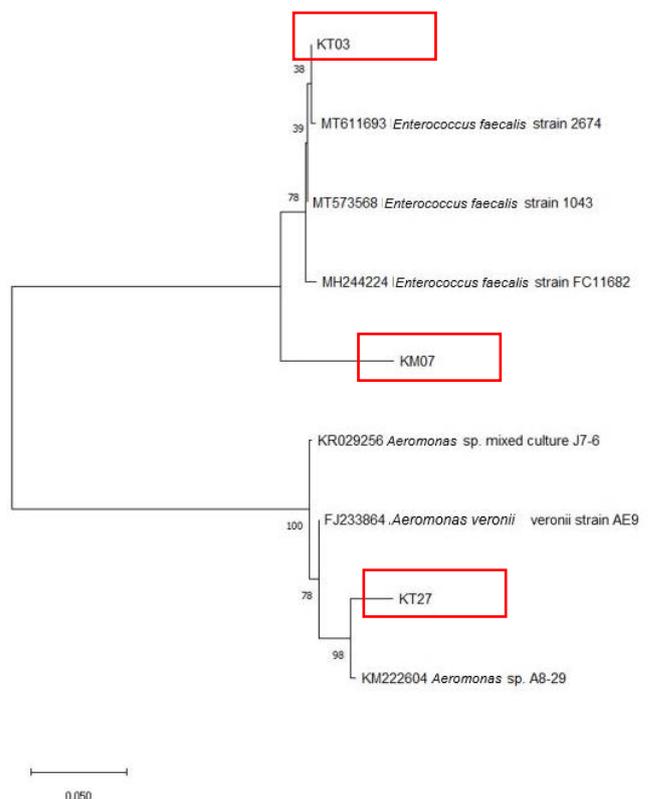


Figure 2. Phylogenetic relationship among the sequences of 16S rRNA gene of potential probiotics candidate (KT03, KM07 and KT27) derived from *Tor tambroides* digestive tract

A series of sequential screening processes for both biosafety and functional properties were required to find well-suited probiotics for use in aquaculture. The use of an in vitro screening process for selecting probiotic bacteria with the highest potential is essential as a means for reducing the number of potential strains. Thus, the screening methods play a vital role in reducing time and resources required for final selection of probiotics (Hai 2015). Digestive enzymatic activity and antibacterial activity are two important recommended methods for probiotic bacteria screening (Ray et al. 2010; Ray et al. 2012). Digestive enzymes enhance the efficiency of feed utilization and assimilation during the digestion process. Consequently, amino acids, fatty acids, and vitamins are produced, which improve general health condition of the host (Ray et al. 2012; Dawood et al. 2019; Ashraf et al. 2020; Patel et al. 2020). Digestive enzyme activity analysis was used to isolate and to prove the efficacy of probiotics (Kuebutornye et al. 2020). Similarly, antibacterial activity analysis was used in the probiotic screening process (Patel et al. 2020) for the selection of potential probiotics (Gomez-Gil et al. 2000; Messaoudi et al. 2013; Liu et al. 2014), which was considered for reduction, or removal of the abundance aquatic pathogens in the intestine of fish (Merrifield et al. 2010; Etyemez and Balcazar 2016; Kong et al. 2021). Probiotic bacteria candidates must be tested against pathogenic bacteria for the effectiveness of inhibitory function to demonstrate their abilities to protect host fish and to increase the survival rate. Furthermore, isolates with antibacterial properties can survive and colonize the digestive system of fish (Christensen 1989; Kavitha et al. 2018). Several studies reported the isolation of candidate probiotic bacteria based mainly on in vitro inhibitory activity against some common fish pathogens (Hai 2015; Nandi et al. 2017; Abomughaid 2020). Thus, this study was conducted in vitro on digestive enzyme activity and antibacterial activity analysis to isolate probiotics from Malaysian mahseer *T. tambroides*.

In the present study, all the selected isolates (KT03, KM07 and KT27) through nutritional and antibacterial activity were examined and their identity was determined; isolate KT03 was identified as *Enterococcus* sp. strain 1043 displaying the highest similarity (100%), isolate KM07 displayed 93% similarity with *Enterococcus* sp. strain FC11682, and isolate KT27 was identified as *Aeromonas* sp. strain A8-29 showing 97% match with the genus *Aeromonas*. It has been reported that *E. faecalis* is an intestinal bacterium capable of producing amylase, lipase, and protease (Kong et al. 2021), and displayed robust antagonistic activity against many pathogenic bacteria, such as *A. hydrophila*, *A. veronii*, *A. salmonicida*, and *A. caviae* (Kong et al. 2020). Despite the fact that studies on using bacteria from this species as probiotics have been conducted, such as *Enterococcus hirae* (Adnan et al. 2017), and *E. durans* F3 was isolated from freshwater fish *Catla catla* (Alshammari et al. 2019). Protease and lipase activity significantly increased when the probiotic *E. faecalis* was applied to the culture of Javanese carp, *Puntius gonionotus* (Allameh et al. 2017) reported and *Channa argus* (Kong et al. 2021). In our present study, isolates KT03 and KM07

demonstrated in vitro digestive enzyme activity for all three digestive enzymes, such as cellulolytic, proteolytic, and lipolytic activity.

The antibacterial activity of *E. faecalis* against common fish pathogens such as *Aeromonas* spp. *Flavobacterium* spp., *Pseudomonas* spp. infection in fish has also been investigated in several studies (Peçala-Safiński 2018; Zaheen et al 2022). Shahid et al. (2017) identified *E. faecalis* from Indian major carps, such as *Labeo rohita* and *Cirrhinus mrigala*, and investigated its antibacterial activity against some pathogenic bacteria, and found that they exhibited potential antibacterial activity against common fish pathogens, such as *Streptococcus agalactiae*, *Staphylococcus aureus* and *Escherichia coli*. Moreover, Touraki et al. (2012) observed the inhibitory activity of *E. faecalis* against pathogenic *Vibrio anguillarum* and *Photobacterium damsela*. Similar results were obtained in this work, where isolates KT03 and KM07 demonstrated in vitro inhibitory action against *V. parahaemolyticus*.

Aeromonas sp. strain A8-29 was identified in isolate KT27. It has been reported that the genus *Aeromonas* is a fish pathogen; nevertheless, it has also been stated that *Aeromonas* may be used as probiotic bacteria in both fin and shellfish aquaculture (Ringo 2020). In our study, *Aeromonas* sp. KT27 exhibited both nutritional enzyme activity and growth inhibition of pathogens (Table 1 and Table 2). Several studies revealed that the application of live *Aeromonas* spp. during culture decreased the mortality of rainbow trout *Oncorhynchus mykiss* against *Aeromonas salmonicida* infection (Irianto and Austin 2002), while formalin-inactivated cells improved disease resistance in goldfish, *Carassius auratus* (Irianto et al. 2003). In another study, *Aeromonas veronii* enhanced common carp, *Cyprinus carpio*, tolerance to *A. hydrophila* infection (Chi et al. 2014). The probiotic effects of live *A. hydrophila* on brine shrimp *Artemia* were also demonstrated, increasing total biomass output from nauplii through more effective digestive enzymes secretion (Gunasekara et al. 2010). The exact mechanism by which *Aeromonas* spp. contribute to pathogen defense is unknown, but they have been shown to aid in the production of cellulase, protease, and lipase, all of which are essential enzymes that help in digestion (Ray et al. 2012). In our study, the isolates KT03, KM07, and KT27 from the *T. tambroides* exhibited nutritional enzyme activity and suppressed the growth of two fish pathogens (*A. hydrophila* and *V. parahaemolyticus*).

The study identified three possible probiotic strains from *T. tambroides*, namely *E. faecalis* strains (KT03 and KM07) and *Aeromonas* sp. strain (KT27). These probiotics candidates produced digestive enzymes and displayed growth suppression of *A. hydrophila* and *V. parahaemolyticus*, suggesting the implementation their possible use in aquaculture, although further research is needed to investigate how these bacteria influence nutritional adsorption and immune status, which is the first step in developing strategies to promote the general health and well-being of fish during aquaculture.

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