

ISOLATION OF POTENTIAL PROBIANTS FROM BRACKISHWATER ENRICHED WITH HIGH LEVELS OF CARBON SOURCE

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ABSTRACT

The majority of shrimp producers utilize probiotics derived from terrestrial sources as part of their aquaculture management. The beneficial effects of terrestrial probiotics on shrimp may be affected due to environmental differences between the cultivated species and the source of the probiotics. To ensure maximum effects on the host, it is essential to use probiotics derived from the host or the environment of the cultured organism. Consequently, the objective of this study was to isolate and characterize potential probiotics from brackishwater by enriching the water with organic sources containing a high ratio of carbon to nitrogen (C:N). Six 10-li containers were filled with brackishwater from an estuary for a mesocosm experiment. To stimulate bacterial growth, water was enriched with either molasses or brown sugar at a C:N ratio of 15. After twenty days, all heterotrophic bacteria in the enriched water were enumerated. The *in vitro* antagonistic activities of distinct bacterial colonies against *Vibrio harveyi*, a crustacean pathogen, were evaluated on fresh Nutrient Agar plates containing 1% sodium chloride. There were 10 bacterial isolates with *in vitro* antibacterial activity. These bacterial isolates are categorized as belonging to the putative genera *Acinetobacter*, *Pseudomonas*, *Sphingobium*, and *Rheinheimera*. The implications of this study suggest that enriching brackishwater with organic carbon sources at high C:N ratios may increase the likelihood of isolating and developing potential probiotics for shrimp aquaculture.

Keywords: aquaculture, biofloc, disease control, organic matter, shrimp

INTRODUCTION

Biofloc technology (BFT) is a cutting-edge technology anchored on zero water exchange and recycling of wastes generated within a cultured system. BFT is a promising technology for ensuring the sustainability of marine shrimp aquaculture in shrimp culture (Krummenauer *et al.*, 2011; Ferreira *et al.*, 2015). The bacterial community that maintains stable levels of nutrients in the water is crucial to BFT-based shrimp aquaculture systems (Wasielesky *et al.*, 2006). This bacterial community associated with bioflocs in the culture system can inhibit the growth and proliferation of pathogens through competitive exclusion (Crab *et al.*, 2010), as well as supplement the nutrition of the cultured stock (McIntosh *et al.*, 2000). However, this microbial community may also harbor pathogenic and opportunistic bacteria that are harmful to farm animals (Schulze *et al.*, 2006).

Vibrios stand out among the opportunistic bacteria in the marine environment (Song & Lee, 1983). *Vibrio harveyi* and *V. parahaemolyticus* are members of the Vibrionaceae family, which is linked to a number of bacterial diseases in crustaceans, including luminous vibriosis, early mortality syndrome (EMS), and acute hepatopancreatopancreatic necrosis syndrome (AHPNS) (Leaño & Mohan, 2012). Vibrios are opportunistic bacteria that influence the growth and survival of farmed shrimp at various life stages (Costa *et al.*, 2008). Consequently, the threat posed by Vibrios during shrimp culture is evident. It is essential to manipulate the rearing water to promote the dominance of beneficial bacteria, which in turn reduces the population of these opportunistic bacterial pathogens that threaten the growth and health of cultured shrimp.

Though recently used in aquaculture, most of the probiotics that fish and shrimp farmers utilize are of terrestrial origins (Lazado & Caipang, 2014). There are differences in the environment of the shrimp and the source of the probiotics; thus, the beneficial effects of terrestrial probiotics may be affected when applied during the culture of shrimp. In view of these limitations, there is a need to explore the possibility of identifying and characterizing host-derived probiotics or from the environment of the cultured organism to ensure higher efficiency of the probiotics (Lazado & Caipang, 2014; Zorriehzakra *et al.*, 2016). Hence, this study aimed to isolate and characterize potential probiotics from brackishwater that is used in shrimp culture by enriching the water with organic sources with high carbon to nitrogen (C:N) ratio. These organic carbon sources include the use of brown sugar

and molasses in stimulating biofloc production in brackishwater for the isolation of bacterial isolates that can be further developed as probiotics in shrimp aquaculture.

MATERIAL AND METHODS

Collection of water samples and screening of bacterial isolates

This research was conducted in the Biology laboratory of the University of San Agustin College of Liberal Arts, Sciences, and Education in Iloilo City, Philippines. Brackishwater samples from Iloilo River were transported to the laboratory and poured in six 10-li plastic containers with a capacity of 80%. At the time of sampling, the salinity was 28 ppt and the pH of the water was 7.8. The production of biofloc was accomplished by adding either brown sugar or molasses in triplicate containers at a carbon-to-nitrogen (C: N) ratio of 15 in accordance with the procedures of Caipang *et al.* (2022), with minor modifications for small tank systems. Biofloc was maintained in all containers for a duration of 25 days with minimal water exchange.

The biofloc culture water from treatments containing either brown sugar or molasses was serially diluted and plated onto nutrient agar (NA) containing 1% sodium chloride (NaCl). The agar plates were incubated between 27 and 30 degrees Celsius for twenty-four hours. Individual bacterial colonies with diverse morphological characteristics were restreaked onto fresh NA-1% NaCl plates, incubated at 27-30°C for 24 hours, and stored at 8°C until further characterization. *Vibrio harveyi*, a known crustacean pathogen, was isolated in a previous study (Pakingking *et al.*, 2018). A single colony of this bacterium was inoculated into 10 ml of nutrient broth (NB) supplemented with 1% NaCl and cultivated overnight at 27-30 degrees Celsius with gentle shaking. The overnight culture of the bacterium was diluted with normal saline solution (NSS) to a concentration of 10³ colony forming units (CFU) ml⁻¹, and 100 µl of the bacterial suspension was plated onto a NA-1% NaCl plate and allowed to adhere for 1 hour. Following this was the spot on-lawn assay (Pilet *et al.*, 1995) with individual bacterial colonies obtained from the biofloc water. The agar plates were incubated at 27-30 °C for 24 hours and then the zones of inhibition were observed.

Characterization of bacterial isolates

The bacterial isolates that exhibited inhibition zones on NA plates seeded with *V. harveyi* were subjected to standard morphological, physiological, and biochemical assays. The phenotypic characters and biochemical properties of the different bacterial isolates were determined based on the descriptions provided in the Bergey's Manual of Systematic Bacteriology (Holt et al., 2000).

Molecular identification of the isolates was accomplished by extracting bacterial genomic DNA from an overnight culture of the isolates in 5 ml Trypticase Soy Broth (TSB) using a commercial kit (Purelink Genomic DNA Mini, Thermo Fisher Scientific, California, USA) according to the manufacturer's instructions. Polymerase chain reaction (PCR) amplification of the 16S rRNA was done using the eubacterial universal primers (Forward: GAGAGTTTGATCCTGGCTCAG; Reverse: CTACGGCTACCTTGTTACGA) of Bianciotto et al. (2003) in a 25 µL PCR reaction. This consisted of: 2 µL (10-15 ng) of DNA as the template, 2 µL of each primer (5 pmol), 2.5 µL of 10 PCR buffer, 1.5 µL of 2 mM dNTP, 1µL of 50 mM MgCl₂ and scaled up to the desired volume using distilled water. The PCR conditions described by Caipang et al. (2010) were utilized for the amplification. The PCR products were cleaned and sent for sequencing (Macrogen, Korea). Using publicly available data from NCBI GenBank (blast.ncbi.nlm.nih.gov), sequenced data were aligned and analyzed to determine the closest homolog of bacterial isolates.

Co-incubation assay

The anti-*Vibrio harveyi* activity of the bacterial isolates was determined utilizing a modified co-incubation assay (Caipang et al., 2008). Using normal saline solution (NSS) as a diluent, an overnight culture of *V. harveyi* and the putative probiotics were diluted to a concentration of 10³ CFU ml⁻¹. In a 1.5 ml microfuge tube, 100 µl of each probiotic isolate and *V. harveyi* were transferred and thoroughly mixed. The control consisted of *V. harveyi* added to an equal volume of nutrient broth containing 1% NaCl. All mixtures were placed on a rotary agitator and incubated between 27 and 30 degrees Celsius for 24 hours.

Following a 24-hour incubation, a 10-fold serial dilution of each mixture was prepared, and 100 µl aliquots of each dilution were plated onto Thiosulfate–citrate–bile salts–sucrose (TCBS) agar plates for the counting of *V. harveyi*. The probiotic candidates did not grow on TCBS plates, as determined by a preliminary assay; therefore, only *V. harveyi* grew on TCBS plates. The agar plates were placed in an incubator at 27 to 30 degrees Celsius for 24 hours. Colonies of bacteria were enumerated, and the results were expressed as log₁₀ CFU ml⁻¹. Following the procedures outlined by Caipang et al. (2008), the reduction in *V. harveyi* counts in the co-incubation groups was expressed as a percentage reduction relative to the *V. harveyi* count in the control group. Each experiment was performed three times. Bactericidal activity was defined as a decrease in bacterial counts of at least 1.5 log₁₀ units.

Data analyses

Co-incubated samples and the control were compared using one-way ANOVA (Systat version 8; Systat Software Inc., San Francisco, CA, U.S.A.). Bacterial counts were expressed as log₁₀ CFU ml⁻¹. If the differences were significant, the

Tukey test was further used for the analysis. All statistical calculations were performed at a significance level of 0.05.

RESULTS AND DISCUSSION

Bacterial isolates from brackishwater enriched with high carbon source

A total of 200 bacterial isolates were obtained from brackishwater with biofloc using either molasses or brown sugar as sources of carbon. From these isolates, there were 10 bacterial strains that possessed *in vitro* antagonistic activity against *V. harveyi* as shown by the zones of inhibition on the NA plates. Molecular identification showed that five isolates, namely, *Acinetobacter* (2 isolates), *Rheinheimera*, and *Pseudomonas* (2 isolates) were obtained from biofloc water with molasses as carbon source, while *Sphingobium*, *Pseudomonas* and three isolates of *Acinetobacter* were identified from biofloc water with brown sugar as carbon source (Table 1).

Bioflocs are composed of flocculated organic matter colonized by heterotrophic bacteria, filamentous cyanobacteria, dinoflagellates, ciliates, flagellates and rotifers (Ballester et al., 2007; Avnimelech, 2009). This diverse microbial community includes pathogenic and opportunistic bacteria, as well as neutral and beneficial bacteria (Schulze et al., 2006; Ferreira et al., 2015). A previous study by Anand et al. (2014) used wheat flour as carbon source in the production of biofloc at a C:N ratio of 10:1. Their results showed that microbial succession in the shrimp ponds occurred and the main microorganisms were *Vibrio*, *Lactobacillus*, *Bacillus* and some fungal species. This indicates that dominant bacterial isolates can be identified in biofloc water during enrichment with carbon sources at higher C:N ratio.

Table 1 Bacterial isolates obtained from biofloc water enriched with either molasses or brown sugar as carbon source

Isolate Number	Source	Closest match
SB-C1-2021	Biofloc with molasses	<i>Acinetobacter indicus</i>
SB-C2-2021	Biofloc with molasses	<i>Acinetobacter indicus</i>
SB-C3-2021	Biofloc with molasses	<i>Rheinheimera</i> sp.
SB-C4-2021	Biofloc with molasses	<i>Pseudomonas aeruginosa</i>
SB-C5-2021	Biofloc with molasses	<i>Pseudomonas plecoglossicida</i>
SB-C6-2021	Biofloc with brown sugar	<i>Sphingobium</i> sp.
SB-C7-2021	Biofloc with brown sugar	<i>Acinetobacter</i> sp.
SB-C8-2021	Biofloc with brown sugar	<i>Pseudomonas stutzeri</i>
SB-C9-2021	Biofloc with brown sugar	<i>Acinetobacter</i> sp.
SB-C10-2021	Biofloc with brown sugar	<i>Acinetobacter</i> sp.

Table 2 Morphological characteristics of the bacterial isolates obtained from biofloc water enriched with either molasses or brown sugar as carbon source

Characteristics	Isolate Number									
	1	2	3	4	5	6	7	8	9	10
Gram stain	-	-	-	-	-	-	-	-	-	-
Cell Shape ^{1/}	CB	CB	CB	B	B	CB	CB	B	CB	CB
Colony description										
1. Margin										
Entire (smooth)	+	+	+	+	+	+	+	+	+	+
Undulate (wavy)										
2. Colour										
Orange			+						+	+
Opaque or white	+	+					+			
Milky (yellowish)				+	+	+		+		
3. Elevation										
Flat										
Convex	+	+	+	+	+	+	+	+	+	+
4. Texture										
Slimy,Moist										
Matte	+	+	+				+		+	+
Mucoid				+	+	+		+		
5. Shape										
Round	+	+	+		+		+			
Punctiform				+		+		+	+	+
6. Motility	-	-	-	+	+	-	-	+	-	-
7. Endospore	-	-	-	-	-	-	-	-	-	-
8. Acid fast	-	-	-	-	-	-	-	-	-	-

Legend: ^{1/}CB- coccobacillus; B – bacillus

Characterization of bacterial isolates

All of the identified bacterial isolates were either rod-shaped or coccobacilli and Gram-negative (Table 2). The biochemical characterization of these isolates revealed that they contained catalase (Table 3). In addition, all isolates, with the exception of isolates 9 and 10 (*Acinetobacter*), can ferment carbohydrates. The addition of higher quantities of carbon sources to the rearing water could be responsible for the isolation of sugar-fermenting bacteria, as these bacteria catabolize the complex carbon molecules present in the water as their population increases. Acetoin was only found in isolates 9 and 10. *Bacillus* species, lactic acid-producing bacteria, and members of the Enterobacteriaceae family are well-known acetoin-producing microorganisms (Xiao & Lu, 2014). *Bacillus* is the most well-known acetoin producer among these families due to its high production efficiency and safety. Isolates 9 and 10 are putative *Acinetobacter* in this study. Though this bacterial group is not known for its ability to produce acetoin, Lee et al. (2009) isolated *Acinetobacter* capable of acetoin production from tobacco plant roots during the screening of antiviral substances that possessed inhibitory effects against Tobacco mosaic virus (TMV).

Table 3 Biochemical characteristics of the bacterial isolates obtained from biofloc water enriched with either molasses or brown sugar as carbon source

Biochemical Characteristics	Isolate Number									
	1	2	3	4	5	6	7	8	9	10
β-galactosidase						+			+	+
Arginine dihydrolase					+					
Citrate utilization				+	+			+		
Detection of acetoin									+	+
Gelatinase			+	+				+		
Fermentation of glucose				+	+	+		+		
Fermentation of melibiose				+	+			+		
Fermentation of arabinose	+	+	+	+			+	+		
Oxidase				+	+			+		
Catalase	+	+	+	+	+	+	+	+	+	+

Reduction of *Vibrio harveyi* in a co-incubation assay

Table 4 shows the counts of *V. harveyi* on NA plates when co-incubated with various bacterial isolates. Using a co-incubation assay, all 10 isolates significantly

Table 4 *Vibrio harveyi* counts* and their reduction^a, expressed as Mean ± SD, during a co-incubation assay with the different bacterial isolates

	Isolate										Control
	1	2	3	4	5	6	7	8	9	10	
<i>Vibrio harveyi</i> counts (Log ₁₀ CFU/ml)	6.26 ± 0.05	6.23 ± 0.21	6.24 ± 0.06	6.30 ± 0.02	6.37 ± 0.32	6.46 ± 0.41	6.43 ± 0.31	6.74 ± 0.23	6.63 ± 0.25	6.71 ± 0.02	8.19 ± 0.31
Reduction in <i>V. harveyi</i> counts (%) relative to Control	23.6 ± 0.05	23.9 ± 0.21	23.8 ± 0.06	23.1 ± 0.02	22.2 ± 0.32	21.2 ± 0.41	21.5 ± 0.31	17.7 ± 0.23	19.0 ± 0.25	18.1 ± 0.02	

Legend: *Co-incubation of the bacterial isolates with *V. harveyi* (pathogen) had significantly lower counts of the pathogen than the control at p < 0.05. N=3.

^aReduction of *V. harveyi* co-incubated with the different bacterial isolates was computed relative to the population of *V. harveyi* grown in Nutrient Broth supplemented with 1% NaCl.

CONCLUSION

In conclusion, the addition of high carbon sources to brackish water facilitated the isolation of bacterial isolates with potential probiotic applications in shrimp aquaculture. The isolation of *Acinetobacter* and *Pseudomonas* from brackishwaters enriched with brown sugar and molasses suggests that these bacteria could be the dominant isolates in a biofloc system. The ability of the various bacterial isolates to inhibit *in vitro* the proliferation of *V. harveyi*, a known crustacean bacterial pathogen, demonstrates their probiotic potential. If these isolates are to be used as probiotics in shrimp culture, it is necessary to conduct additional research into their probiotic mechanisms.

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reduced the population of *V. harveyi in vitro*. Except for isolates 8 and 10, co-incubation with the bacterial isolates resulted in at least a 1.5 log₁₀ reduction of *V. harveyi*. Similarly, the population of *V. harveyi* was reduced by 17.7% to 23.9% relative to the control in the co-incubation assay. With the exception of isolates 8, 9, and 10, all other isolates reduced *V. harveyi* by more than 20%.

Sphingobium is a recently described genus (Takeuchi et al., 2001) that is thought to be a component of the crustacean intestinal microbiota (Hu et al., 2019). This bacterium has been previously isolated from both untreated and treated water (Sheu et al., 2013; Corre et al., 2019) as well as the gut of Pacific white shrimp fed a yeast cell wall-based feed additive (Servin Arce et al., 2021). This group of bacteria can degrade polycyclic aromatic hydrocarbons; therefore, it is utilized in soil bioremediation (Chen et al., 2016). It was also isolated from an aquaponics system and linked to antibiotic resistance in an aquaculture facility (Colombo et al., 2016). In contrast, Brisou & Prévot (1954) were the first to describe *Acinetobacter*, a genus of non-motile, aerobic, Gram-negative bacteria. Some species of *Acinetobacter*, specifically *A. baumannii*, are regarded as human and marine pathogens (Bergogne-Berezin & Towner, 1996; Xia et al., 2008). Recent studies, however, have shown its denitrifying activity in the elimination of nitrite in wastewaters (Cao et al., 2012) and its probiotic activities for juvenile catfish by enhancing lysozyme and respiratory activities (Bunnoy et al., 2019). While the present investigation demonstrated *in vitro* anti-*V. harveyi* activity of *Acinetobacter* sp., Verschuere et al. (2000) recommend evaluating this bacterial isolate for pathogenicity if it is to be used as probiotics in shrimp aquaculture in the future.

The presence of *Pseudomonas*, *Acinetobacter*, *Sphingobium*, and *Rheinheimera* in brackishwater that had been supplemented with high carbon sources may indicate the significance of these substances in promoting the growth and dominance of beneficial bacterial species that possess anti-*V. harveyi* activities. Particularly, *Pseudomonas* and *Acinetobacter* were isolated from brackish water enriched with brown sugar and molasses. These bacterial isolates are capable of producing substances with antagonistic activity against *V. harveyi*, or they can directly compete with the bacterial pathogen via mechanisms such as competition, exclusion, and displacement (Lazado et al., 2011; El-Saadony et al., 2020). Since the bacterial pathogen and probiotic candidates were introduced at comparable concentrations at the same time, the reduction in *V. harveyi* counts is likely due to competition, according to Lazado et al. (2011). However, a previous study in fish demonstrated that displacement is also one of the mechanisms that inhibited the proliferation of bacterial pathogens in the gut (Lazado et al., 2011). Future research will investigate what specific mechanism is responsible for inhibiting shrimp bacterial pathogens in water.

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Data Availability: The data used to support the findings of this study are available from the corresponding author upon request.

Conflict of Interest: No conflict of interest declared.

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