

Research Article

Amelioration of hemato-serological parameters, antioxidant capacity, and resistance against *Aeromonas hydrophila* in common carp (*Cyprinus carpio*) fed with quorum quenching probiotics

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Keywords

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Abstract

In this study, two probiotics (*Citrobacter freundii* and *Bacillus foraminis*) with indigenous quorum quenching (QQ) were isolated from the intestine of *Cyprinus carpio* and their effects on hemato-serological parameters and innate immune responses, antioxidant capacity and disease resistance in *C. carpio* were determined. The juveniles ($n=450$, 50.26 ± 10.47 g mean weight) were randomly divided into 6 groups (with 3 replications) and fed with diets containing 1×10^9 cfu g⁻¹ of *C. freundii* (QQ1, G1), *B. foraminis* (QQ2, G2), *Lactobacillus plantarum* (without characteristics QQ, WQQ, G3), QQ1+QQ2 (G4), QQ1+QQ2+WQQ (combine, G5), and a control diet (without probiotic) for 60 days. The hematocrit level was increased in the fish fed with QQ1 and WQQ supplemented diets compared to the control group. At 30 days, the combined probiotic treatments (QQ1+QQ2+WQQ) significantly increased hemoglobin and total leukocyte count compared to QQ1 and control, though these differences were not observed at 60 days. QQ2 notably improved complement activity and lysozyme levels after 30 days, while QQ1+QQ2 showed a higher antitrypsin activity at 30 days. The myeloperoxidase levels were elevated in the combined treatments at 60 days. The hepatic catalase activity was higher in QQ probiotic groups at 30 days but it was decreased by 60 days with significant differences noted between WQQ and other groups. The highest superoxide dismutase activity was obtained in QQ2 at 30 and 60 days. The liver glutathione level was decreased in the mixed probiotic groups but it was increased in the combined group at 60 days. A lower content of malondialdehyde was in QQ1 and QQ2 groups at 60 days. The probiotic-treated groups showed significantly lower mortality rates compared to the control against *A. hydrophila* infection, with the highest mortality occurring 30 hours post-infection [G1 (30.6%), G2 (30.6%), G3 (40.63%), G4 (30.6%), G5 (40.63%), and the control group (60.3%)]. Overall, the indigenous probiotics cause an improvement in various health parameters and could reduce mortality rates in infected fish.

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Introduction

Aquaculture has been defined in many ways to denote all forms of culturing aquatic animals and plants in fresh and brackish water and the marine environment. The most current accepted definition has been given by the Food and Agriculture Organization as the farming of aquatic organisms including fish, crustaceans, molluscs and aquatic plants (Palma and Viegas, 2022). The global production of fish via aquaculture and capture fisheries is estimated to have reached about 179 million tonnes in 2018. Of the 82.1 million tonnes of aquatic animals produced by aquaculture sectors, about 4.19 million tonnes belong to common carp (*Cyprinus carpio*) and about 0.21 million tonnes belong to production of Iran (FAO, 2020). Common carp is one of the economically important freshwater fish that is usually reared in earthen ponds. Carp species can be produced even in lower-quality waters, which is an especially valuable characteristic in the Asian and Middle east regions. From the aspect of sustainability achieved in carp pond, it is essential to perform fish meal-independent and cereal-based fish meat production which provides increasing production of this fish species in the long run. One of the problems of carp culture in the world is the high mortality due to various diseases. FAO has shown that the use of probiotics is one of the best ways to increase the resistance and safety of fish and reduce losses due to stressors (Mohammadian *et al.*, 2019). In this context, it has been reported that the highest cost paid for carp production in Iran is related to feed. Moreover, probiotics have beneficial impacts on the host due to the

inhibition of the growth of pathogens (Gatesoupe, 1999), alteration of antioxidant capacity and stimulation of immune responses (Shefat, 2018). Likewise, use of probiotics is an eco-friendly and sustainable approach that reduces the use of harmful chemical compounds particularly antibiotics in aquaculture (Gatesoupe, 1999). The *Aeromonas hydrophila* is one of the most important gram-negative pathogenic bacteria in fish that causes hemorrhagic septicemia, ascites and mortality at different ages and in different species of fish (Mzula *et al.* 2019). This bacterium is considered one of the most important health problems in fish farming in different countries. On the other hand, the increasing growth of aquaculture has caused the spread of more and more diseases, including infection with this bacterium (Alishahi *et al.*, 2022). Antibiotic resistance has been increasingly reported for a wide variety of bacteria of clinical significance. This widespread problem constitutes one of the greatest challenges of the twenty-first century. Faced with this issue, clinicians and researchers have been persuaded to design novel strategies in order to try to control pathogenic bacteria. Therefore, the discovery and elucidation of the mechanisms underlying bacterial pathogenesis and intercellular communication have opened new perspectives for the development of alternative approaches. Antipathogenic and/or antivirulence therapies based on the interruption of quorum sensing pathways are one of several such promising strategies aimed at disarming rather than at eradicating bacterial pathogens during the course of colonization and infection

(Ghanei-Motlagh *et al.*, 2019). Quorum sensing (QS) is a process by which bacteria monitor their population in a cell-density dependent manner through the synthesis, exchange, and the detection of small intracellular signals (autoinducers) (Xavier and Bassler, 2005). Among the various types of signals that are produced in bacteria (Autoinducer-1, Autoinducer-2, and Autoinducer-3) probably the best studied. Bacteria produce the QS molecules, and when the intensity of these signals reaches a threshold, they diffuse back into the bacterial cell and regulate the expression of QS-related genes such as those involved in biofilm formation and production of virulence determinants (Galloway *et al.*, 2011). Indeed, QS allows bacteria to operate as multicellular organisms. Since AHL-based QS is common among freshwater *Aeromonas*, improving our understanding of the procedures related to QS generation by *Aeromonas* and techniques to disrupt these mechanisms will provide new eco-friendly methods for the prevention and treatment of *Aeromonas* infections (Case *et al.*, 2008). Quorum quenching (QQ) is a phenomenon opposite to QS and refers to the inactivation of the chemical signals via a mechanism mediated by a number of enzymes, including AHL lactonase, AHL acylase, and AHL oxidoreductase (Nain *et al.*, 2020). As an anti-infective strategy, QQ may also compel less selective pressure on pathogens, and in turn, delay the development of resistance mechanisms (Shastry *et al.*, 2018). Application of AHL degrading bacteria able to utilize AHL molecules of marine and freshwater pathogens as a food source is a developing

idea due to their previously successful outcomes, however, the majority of the strains that have been tested in the past are allochthonous QQ bacteria (Ghanei-Motlagh *et al.*, 2019). Moreover, the isolation of autochthonous bacteria with QQ potential has frequently been reported from freshwater fish. On the other hand, despite the high mortalities caused by freshwater *Aeromonas*, QQ strategy has not been adopted against commonly occurring *Aeromonas* pathogens in fish, particularly, *C. carpio*, an adaptive freshwater fish with high economic importance that has gained much attention from researchers and farmers in the last decade. In contrast with some probiotics that are able to out-compete pathogens through the production of antimicrobials, QQ probiotics are neither bactericidal nor bacteriostatic against the targeted pathogens. Instead, they disrupt QS signals and affect the pathogenicity of their target. On the contrary, one of the main criteria for screening potential probiotic candidates is the inhibitory activity against different pathogens (van Kessel *et al.*, 2016). However, there is no comprehensive investigation of the real probiotic characterization of QQ bacteria prior to their administration to fish farm culture and their application on a commercial scale. In the present study, QQ bacteria with a potential to degrade the dominant range of AHL molecules produced by several significant and prevalent pathogenic *Aeromonas* spp. in fish, were isolated from the intestine of common carp and characterized and their efficacy as autochthonous probiotics was tested for the first time. The present investigation was undertaken to evaluate

the changes in various immune parameters of common carp after feeding them with QQ bacteria isolated from their intestine and also their resistance to a virulent strain of *A. hydrophila*.

Materials and methods

Bacteria

Bacterial isolates were recovered using a previously described method (Irianto and Austin, 2002). Briefly, the entire digestive tracts of *C. Carpio* captured from natural water resources of Khuzestan province (Abzi Company from Dezful) in Iran were removed and their contents were discarded. The quorum quenching potential of *C. freundii* QQ1 and *B. foraminis* QQ2 was confirmed in our previous study using the agar well diffusion and thin layer chromatography methods. In this study, their QQ activity was also tested against *Yersinia ruckerrie* by the degradation assay on Luria-Bertani agar as suggested by Chu *et al.* (2011). The tested *Y. ruckerrie* was able to induce *Chromobacterium violaceum* CV026. This biosensor responds to exogenous AHLs with *N*-acyl side chains from C₄ to C₈ in length with production of purple pigment violacein. *Pseudomonas fluorescence* P3/pME6863 and *Pseudomonas fluorescence* P3/pME6000 were respectively used as positive and negative controls in AHL degradation assay. The strains CV026, P3/pME6863 and P3/pME6000 were kindly provided by Dr. Torabi Delshad. The *L. plantarum* strains used in this study as none QQ character were primarily identified based on colony and cell morphology, Gram staining, biochemical characteristics, and 16S rRNA gene sequencing (GenBank

accession number EU520326 and EU520327) (Mohammadian *et al.*, 2016). These strains were grown for 30 h at 37°C in MRS broth (BD Difco, Sparks, MD, USA).

Diet preparation

The control diet was formulated using the ingredients as subsequently described. The proximate analysis of the basal diet according to the AOAC method was: 37.1% for crude protein, 8.8% for crude lipid, 9.6% ash and 390 Kcal per 100 g for gross energy. Probiotic bacterial suspensions were prepared by centrifuging (15min., 4000 rpm) the 72h TSB cultured bacteria and resuspending them in PBS at the concentration of Macfarland grade 3 (1.2×10^9 cfu mL⁻¹), The probiotic-enriched diets were prepared by gently spraying of the prepared bacterial suspension on the control and mixing that part by part in a drum mixer to obtain a final probiotic concentration of 1×10^9 cfug⁻¹. They were packed in sterile propylene containers and stored at 4°C for viability studies for a week. This dose was chosen based on a previously recommended dose (Takafoyan *et al.*, 2024). The final concentrations of probiotic bacteria in the diet were confirmed by suspending one gram of food in sterile PBS and culturing the serial diluted food suspension in TSA media. Counted bacteria in the food were almost the same as added probiotic bacteria in all batches of probiotic-enriched diets.

Experimental design

Juveniles of *C. carpio* (50±10 g) were transferred from a private cyprinid farm in Khuzestan Province, Iran, to the Lab of

Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz. The fish were acclimated for 2 weeks in indoor 300 L fiberglass tanks and were fed with a standard diet (37.1% crude protein, 8.8% crude lipid, 9.6% ash, and 390 Kcal 100g⁻¹ gross energy). Then, after verifying the health status of the fish, they were distributed randomly into 12 tanks at an initial density of 25 fish per tank and divided into 6 treatment groups, including control (n=25), QQ1 (G1, n=25), QQ2 (G2, n=25), *L. plantarum* (G3, n=25 as a without characteristics QQ), QQ1+QQ2 (G4,

n=25), QQ1+QQ2+W QQ (G5, n=25). Final concentration of each probiotic was about 1×10⁹cfu g⁻¹ of the diet (Table 1) (Nikoskelainen *et al.*, 2001). The aquaria were supplied with water from external Biofilteres (Athmann, China), at a temperature of 25.9±1.2°C. The fish were fed with probiotic-contained diets for 60 days (twice a day). During the experimental period, the temperature ranged from 24.5 to 28.5°C, salinity was from 0.6±0.11 % and the dissolved oxygen was 5.9±1.3mgL⁻¹.

Table 1: The experimental design and treatment setting up, applied in this study.

| Treatment | G1 | G2 | G3 | G4 | G5 | Control |
|--------------------------|-------------------|-------------------|-------------------------------|-------------------|-------------------|---------------|
| Probiotics category | QQ1 | QQ2 | <i>L. plantarum</i> (W QQ) | QQ1 + QQ2 | QQ1 + QQ2+W QQ | Normal saline |
| Additive quantity (g/kg) | 1×10 ⁹ | 1×10 ⁹ | 1×10 ⁹ | 1×10 ⁹ | 1×10 ⁹ | 0.0 |

Sample collection

Samples were collected at 30 and 60 days from the beginning of experiment. At these times, the fish were anesthetized with 2-phenoxyethanol (0.3 mL/L). Blood samples were withdrawn from the caudal vein of four fish per aquarium using a 2.5-mL syringe. One part of the collected blood was dropped in a heparinized microtube and the residue was subjected to centrifugation (30009g, 10 min, 4°C) to separate serum. The sera were then frozen at -80°C until use (Ghanei-Motlagh *et al.*, 2021).

Hemato-immunological parameters

Heparinized blood was used to measure the hematological indices. To estimate Hematocrit (Hct), blood was transferred from the eppendorf tubes to plain microcapillary tubes, up to about 75% of the tubes' capacity and the lower opening

of the tubes was plugged by capillary clay. They were centrifugated in a capillary microcentrifuge at 12,000 ×g for 5 min (Hematocrit centrifuge, Hettich, Germany) and the percentage of Hct was reported using a hematocrit reader. The hemoglobin (Hb) concentration was measured using the cyanomethemoglobin method (Drabkin, 1950).

Total erythrocyte count (TEC) and total leucocyte count (TLC) were simultaneously carried out using an improved Neubauer hemocytometer (Kerr, 2008). To address that, 5 µL of each blood sample were removed using a tip pre-attached to a micropipette. The outside of the pipette tip was wiped from any excess blood with a lint-free cloth, and then blood was diluted in 995 µL (dilution factor = 200) of Natt-Herrick's staining solution at room temperature for 5 min (Natt and

Herrick, 1952). Natt-Herrick's solution (3.88 g NaCl, 2.5 g Na₂SO₄, 2.91 g Na₂HPO₄·12H₂O, 0.25 g KH₂PO₄, 7.5 ml formalin 37%, 0.1 g crystal violet per 1000 ml distilled water, final pH: 7.3) was previously prepared and filtered using a Whatman filter paper (No. 2) after overnight incubation. Thereafter, 10 µL of the diluted sample were loaded on the hemacytometer counting chamber and the cells were allowed to settle in a pre-humid petri dish for 3-5 minutes. TEC was

performed in 5 squares (the middle square and 4 corner squares) within the large center square of the chamber using a light microscope (40× objective) under lowered condenser mood, while TLC was carried out in the 4 large corner squares of the chamber at 100× magnification (10× objective) under the same mood. Subsequently, TEC and TLC were calculated by means of the following formula:

$$\text{TEC} (\times 10^6/\mu\text{L}) = (\text{total number of red blood cells counted} \times \text{dilution factor}) / \text{volume of squares counted} (\text{mm}^3)$$

Where, the volume of squares counted was calculated by multiplying the total dimensions of the squares counted (0.2 mm²) to the distance between the coverslip and chamber (0.1 mm)

$$\text{TLC} (\times 10^3/\mu\text{L}) = (\text{total number of white blood cells counted} \times \text{dilution factor}) / \text{volume of squares counted} (\text{mm}^3)$$

Where, the volume of squares counted was measured by multiplying the total dimensions of the squares counted (4 mm²) to the distance between the coverslip and chamber (0.1 mm)

Innate immune parameters

Serum lysozyme activity was measured in turbidity as described by Ellis (1990). Serum anti-protease activity was performed by incubating 10 µL of serum with 20 µg of trypsin dissolved in 100 µL of Tris-HCl (50 mM, pH 8.2). In serum blank, 100 µL of Tris-HCl was added to 10 µL of serum, instead of trypsin in Tris-HCl, and in the positive control, no serum was added to trypsin. All tubes were made up to 200 µL with Tris-HCl and incubated for 1 hour at room temperature. After the incubation, 2 ml of 0.1 mM substrate BAPNA (N-benzoyl-DL-arginine-*p*-nitroanilide HCl, Sigma chemicals), dissolved in Tris-HCl (containing 20 mM calcium chloride), was added to all tubes and incubated for further 15 minutes. At the end of incubation, the

reaction was stopped by adding 500 µL of 30% acetic acid. The optical density was measured at 410 nm by using a UV-Visible spectrophotometer (Shimadzu UV-1601) (Sareyyupoglu *et al.* 2010). Total protein and albumin concentrations were determined (Zist Shimi kit, Iran) according to Nayak *et al.* (2010). The albumin content was estimated spectrophotometrically using a standard kit (Glaxo, India). The globulin content was estimated by subtracting the albumin content from the total protein content. In order to assess myeloperoxidase (MPO) activity, 15 µL of serum was diluted in 135 µL of Hanks' balanced salt solution (HBSS, modified without Ca²⁺ and Mg²⁺) in a 96-well plate. Subsequently, 25 µL of 3,3',5,5-tetramethylbenzidine (TMB, 20 mM,

Sigma-Aldrich) and 25 μ L of diluted hydrogen peroxide (H₂O₂, 5 mM, Sigma-Aldrich) were added to each well. The reaction was stopped precisely after 2 min by adding 25 μ L of diluted sulfuric acid (H₂SO₄, 4 M, Sigma-Aldrich) and the optical density was measured at 450 nm in a microplate reader (Mohapatra *et al.*, 2014).

Oxidative stress indicators

The serum SOD (*Superoxide dismutase*) activity was determined using a commercial kit (RANSOD kit, Randox Com, UK) on a microplate-reader (Synergy HT, BioTek, USA) according to the manufacturer's protocol, which measured the conversion of superoxide anion to hydrogen peroxide.

The activity of CAT (Catalase) was assayed according to the method described by Koroliuk *et al.* (1988). Serum CAT was determined based on the decomposition rate of hydrogen peroxide. Briefly, 5 μ L of the serum sample, 100 μ L of H₂O₂ (10 mM), 50 μ L of Tris HCl buffer (50 mM, pH=7.8), and were poured into microplate wells. After 10 min at room temperature, 100 μ L of 4% ammonium molybdate was added to wells. Then, the optical absorption rate of the samples against the control by a microplate analyzer was read at 410 nm and expressed as IU/mg protein.

The serum GSH (*Glutathione*) activity was assayed using the method of Ellman (1959). Briefly, the reaction solution consisted of 15 μ L of the serum sample, 260 μ L of sodium phosphate buffer (Na₂HPO₄, 0.1 M) containing EDTA (1 mM, pH=8) and DTNB reagent (0.01 M). 5 μ L of Elman's reagent was added to this solution. Then,

this solution was incubated at room temperature for 15 min and then read at 412 nm against the blank sample using the microplate reader. The GSH activity was stated as μ mol/L serum.

The serum MDA (*Malondialdehyde*) level was measured according to the method of Mihara and Uchiyama (1978). Briefly, 25 μ L of each sample was mixed with the working solution (250 ml of 20% trichloroacetic acid (TCA) and 100 ml of 0.6% TBA) and kept in a hot water bath for 30 min. The solution after cooling was centrifuged at 5,000g for 5 min. After that, the samples optical absorption was detected spectrophotometrically at 535 nm. Finally, the results were expressed as nmol/mg protein.

Challenge test

The *A. hydrophila*, AH04, was grown in nutrient broth and incubated at 37°C for 24 h. Lethal dose 50 % (LD₅₀) of *A. hydrophila* (i.e., able to kill 50 % of the *C. carpio* population) was determined by intraperitoneal injection of 60 fish with different doses of *A. hydrophila* (10⁶, 10⁷, 10⁸ and 10⁹CFU/fish) at 25°C. LD₅₀ was calculated using the method described by Reed and Muench (1938) with consideration of Koch's postulate. Sixteen days after experimental feeding, the fish from each group were divided into two subgroups (45 fish in each group), one as a challenge group to be infected with *A. hydrophila* and the other as an uninfected control. The challenge group was injected intraperitoneally with 0.2 mL PBS containing the LD₅₀ dose of live *A. hydrophila* determined above, while control fish received only 0.2 ml PBS. The

cumulative mortality was determined after 10 days post-infection (Mohammadian *et al.*, 2016).

Statistical analysis

All statistical tests were performed using SPSS software (SPSS, Release 16.0, SPSS, Chicago, IL, USA). Two-way analysis of variance (ANOVA) and a general linear model were used to evaluate the effect of time and treatments on each variable. One-way analysis of ANOVA was done to determine the differences between different variables. Differences were considered

statistically significant when $p<0.05$ and the results are expressed as mean \pm SD (Mohammadian *et al.*, 2016).

Result

Hematological indices and respiratory burst activity

As presented in Table 2, Hct was significantly enhanced in *C. carpio* supplemented with QQ1 and WQQ for 60 days compared to the control groups ($p<0.05$).

Table 2: Hematological indices of *C. carpio* fed either regular feed or feed supplemented with probiotics for 60 days.

| Parameters | Groups | Day 30 | Day 60 |
|-----------------------------------|---------|---------------------------------|---------------------------------|
| Hct (%) | QQ1 | 37.5 \pm 6.4 ^{Aa} | 40.1 \pm 2.7 ^{Aa} |
| | QQ2 | 39.9 \pm 4.11 ^{Aa} | 32.36 \pm 3.52 ^{ABa} |
| | WQQ | 35.6 \pm 3.52 ^{Aa} | 39.3 \pm 2.5 ^{Aa} |
| | QQ1+QQ2 | 30.17 \pm 2.2 ^{Aa} | 35.3 \pm 1.5 ^{ABa} |
| | Combine | 34. 4 \pm 6.32 ^{Aa} | 29.73 \pm 4.15 ^{Ba} |
| Hb (g/dl) | Control | 34.8 \pm 3.262 ^{Aa} | 30.36 \pm 1.5 ^{Ba} |
| | QQ1 | 29.2 \pm 6.4 ^{ABa} | 15.5 \pm 8.7 ^{Ab} |
| | QQ2 | 28.96 \pm 4.11 ^{ABa} | 14.27 \pm 2.56 ^{Ab} |
| | WQQ | 27.1 \pm 4.52 ^{ABa} | 11.43 \pm 3.55 ^{Aa} |
| | QQ1+QQ2 | 19.7 \pm 3.2 ^{Ba} | 13.5 \pm 4.9 ^{Ab} |
| TEC ($\times 10^6/\mu\text{L}$) | Combine | 33.54 \pm 11.32 ^{Aa} | 13.16 \pm 5.55 ^{Ab} |
| | Control | 26.8 \pm 2.262 ^{ABa} | 11.03 \pm 3.9 ^{Ab} |
| | QQ1 | 2.6 \pm 0.26 ^{A,b} | 4.07 \pm 0.12 ^{A,a} |
| | QQ2 | 2.5 \pm 0.11 ^{A,b} | 3.28 \pm 0.6 ^{A,a} |
| | WQQ | 2.86 \pm 0.32 ^{A,b} | 3.98 \pm 0.01 ^{A,a} |
| TLC ($\times 10^3/\mu\text{L}$) | QQ1+QQ2 | 2.62 \pm 0.2 ^{A,b} | 3.54 \pm 0.25 ^{A,a} |
| | Combine | 2.72 \pm 0.22 ^{A,a} | 3.24 \pm 0.1 ^{A,a} |
| | Control | 2.62 \pm 0.12 ^{A,a} | 3.098 \pm 0.05 ^{Aa} |
| | QQ1 | 1.25 \pm 0.04 ^{AB,a} | 1.06 \pm 0.1 ^{A,a} |
| | QQ2 | 1.05 \pm 0.09 ^{ABa} | 1.087 \pm 0.05 ^{A,a} |
| | WQQ | 1.41 \pm 0.02 ^{A,a} | 1.04 \pm 0.01 ^{A,b} |
| | QQ1+QQ2 | 0.51 \pm 0.06 ^{B,b} | 1.02 \pm 0.1 ^{Aa} |
| | Combine | 1.08 \pm 0.02 ^{AB,a} | 1.05 \pm 0.01 ^{A,a} |
| | Control | 0.83 \pm 0.06 ^{Ba} | 1.01 \pm 0.01 ^{A,a} |

* For each parameter, values (Mean \pm SD) bearing different uppercase letters or different lowercase letters represent significant differences within each column or each row, respectively ($p<0.05$). Hct: hematocrit, Hb: hemoglobin, TEC: total erythrocyte count, and TLC: total leucocyte count.

A significant increase in Hb content was observed in the combined (QQ1+QQ2+WQQ) probiotic treatments

when compared to the QQ1 and control groups at day 30, whereas Hb was not significantly different between

treatments at day 60 ($p>0.05$). A significant increase in TLC content was observed in WQQ treatment when compared to the QQ1+QQ2 and control groups at day 30, whereas TLC was not significantly different between treatments at day 60 ($p>0.05$). After 30 days of feeding the probiotic, the complement activity in the groups fed with the QQ2 was significantly increased in relation to the control and the other groups ($P<0.05$). At 60 day of probiotic feeding, only the QQ1+QQ2

group had a significant difference in complement activity with respect to QQ1 ($p<0.05$). At 30 day of probiotic feeding, QQ1+QQ2 group had higher serum lysozyme activity than that of other groups ($P<0.05$). At the end of the experimental period, only the QQ1 and QQ2 groups had a significant difference in lysozyme activity with the control group ($P<0.05$). The total plasma globulin levels were not different observed between treatments (Fig. 1; $p>0.05$).

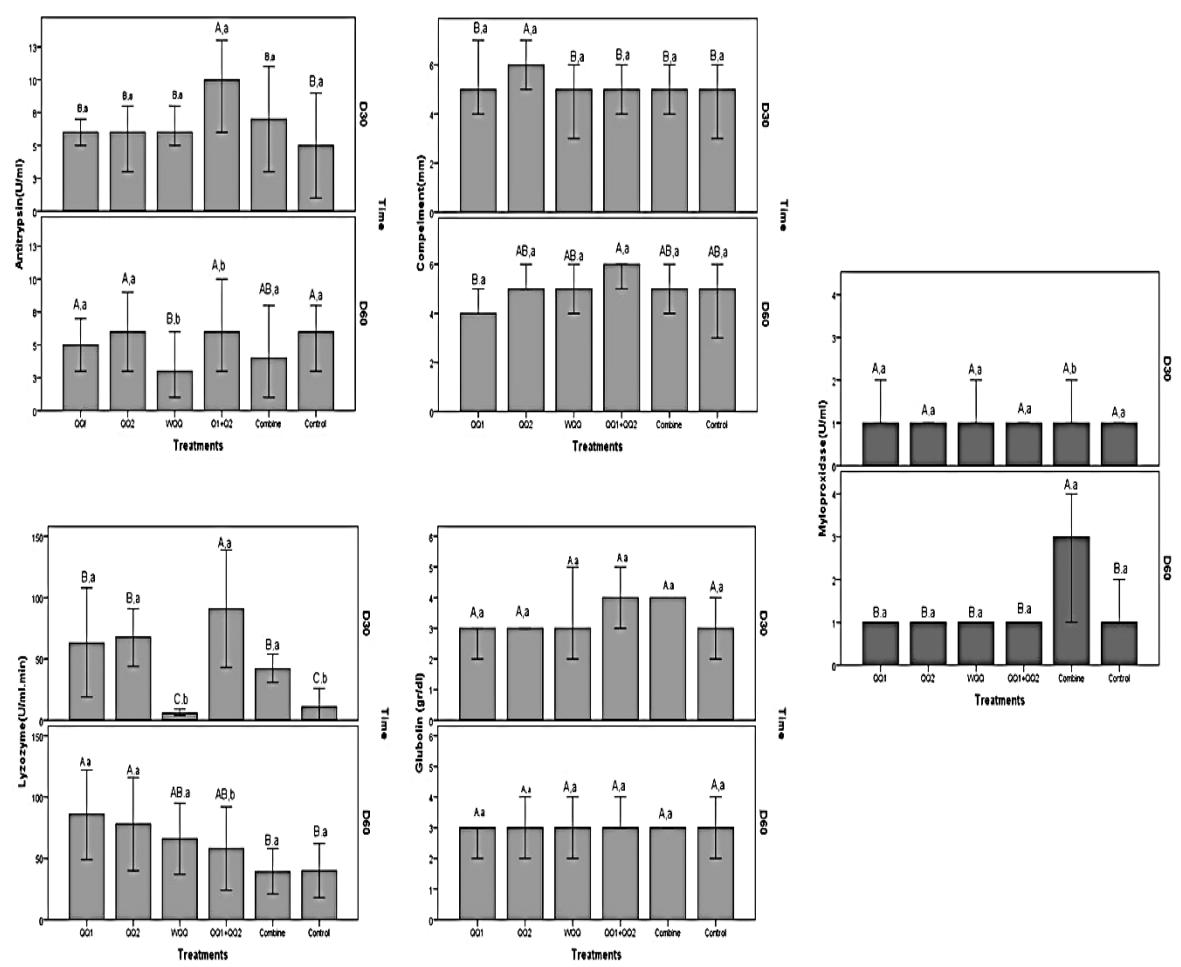


Figure 1: Innate immune parameters activity in *Cyprinus carpio* treated with QQ1 (*C. freundii* $\sim 1 \times 10^9$ cfu g $^{-1}$), QQ2 (*B. foraminis* $\sim 1 \times 10^9$ cfu g $^{-1}$), WQQ (*Lactobacillus plantarum* $\sim 1 \times 10^9$ cfu g $^{-1}$), QQ1+QQ2 (*C. freundii* and *B. foraminis* $\sim 1 \times 10^9$ cfu g $^{-1}$), QQ2 (*B. foraminis* $\sim 1 \times 10^9$ cfu g $^{-1}$), QQ1+QQ2+WQQ (*C. freundii* and *B. foraminis* and *Lactobacillus plantarum* $\sim 1 \times 10^9$ cfu g $^{-1}$) and without probiotic (control). Values is shown as means \pm standard error (n=9). Legends as mentioned in Figure 1. *For each parameter, values (Mean \pm SD) bearing different lowercase letters or different uppercase letters represent significant differences within each column or each row, respectively ($p<0.05$).

At 30 day of probiotic feeding, QQ1+QQ2 group had higher serum Antitrypsin activity than that of other groups ($p<0.05$). At the end of the experimental period, only the WQQ group had a significant difference in Antitrypsin activity with the other groups (except for the combine group) ($p<0.05$). A significant increase in myeloperoxidase content was observed in combine (QQ1+QQ2+WQQ) probiotic treatments when compared to the other groups at day 60, whereas myeloperoxidase was no significant differences between treatments at day 30 ($p>0.05$).

Liver oxidative stress indicators

The data in Figure 2 describe the liver antioxidant capacity of *C. carpio* fed with QQ probiotics. After 30 days of feeding, liver CAT activities were enhanced ($p<0.05$) in the QQ probiotic groups compared to the mixed probiotic groups (QQ1+QQ2 and combine), while no significant ($p>0.05$) difference was

observed in their levels between the probiotic treatments and control group. After 60 days of feeding, liver CAT activities were decreased ($p<0.05$) in all groups compared to 30 days of feeding, while a significant ($p<0.05$) difference was observed in level between the WQQ treatments and other groups. An enhancement in liver SOD activity was observed in the QQ2 and WQQ groups compared to the control group at days 30 and 60, however, the highest activity ($p<0.05$) was noticed in fish received *B. forminis* (QQ2). However, the WQQ groups displayed lower SOD activities in days 60 ($p<0.05$) relative to the days 30. After days 30 the level of GSH in the liver showed a reduction in all mixed groups relative to separated groups. Nevertheless, liver GSH at day 60 was significantly higher in combine group than the days 30. Moreover, MDA content in the liver was significantly ($p<0.05$) lower in the QQ1 and QQ2 groups compared to the QQ1+QQ2 group after 60 days (Fig. 2).

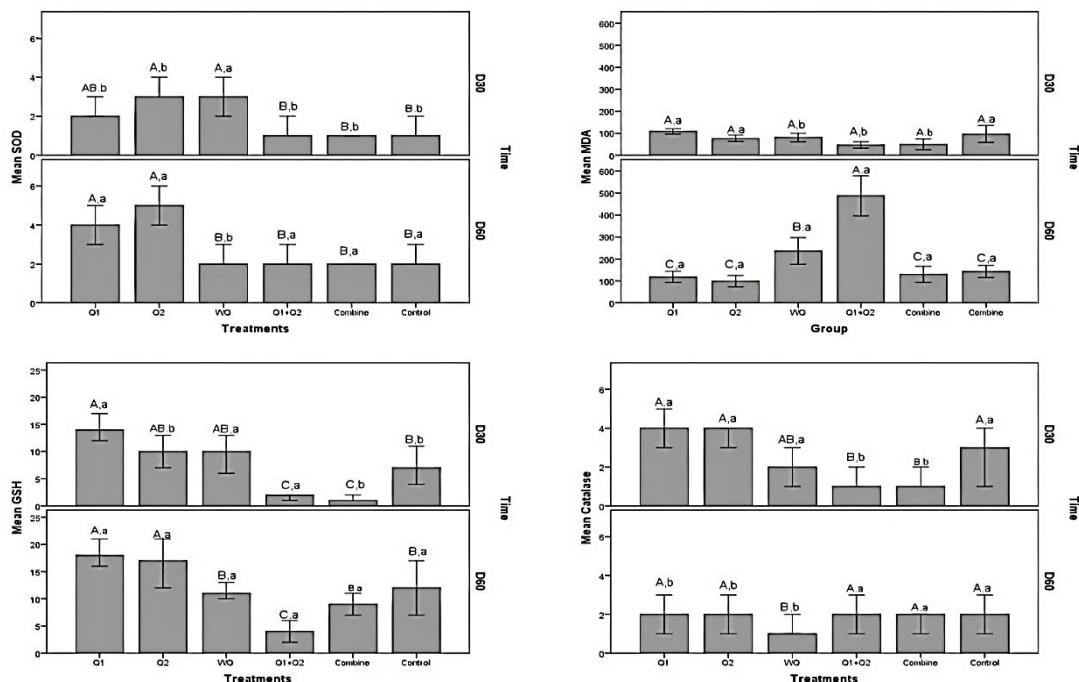


Figure 2: liver antioxidant capacity in *Cyprinus carpio* treated with QQ1 (*C. freundii* $\sim 1 \times 10^9$ cfu g $^{-1}$), QQ2 (*B. forminis* $\sim 1 \times 10^9$ cfu g $^{-1}$), WQQ (*Lactobacillus plantarum* $\sim 1 \times 10^9$ cfu g $^{-1}$), QQ1+QQ2 (*C. freundii* and *B. forminis* $\sim 1 \times 10^9$ cfu g $^{-1}$), QQ2 (*B. forminis* $\sim 1 \times 10^9$ cfu g $^{-1}$), QQ1+QQ2 +WQQ (*C. freundii* and *B. forminis* and *Lactobacillus plantarum* $\sim 1 \times 10^9$ cfu g $^{-1}$) and without probiotic (control). Values are shown as means \pm standard error (n=9). Legends as mentioned in Figure 2. *For each parameter, values (Mean \pm SD) bearing different lowercase letters or different uppercase letters represent significant differences within each column or each row, respectively ($p<0.05$).

Challenge test

Analysis of the rate of mortality showed that the LD50 on day 10 was 3.7×10^8 CFU/fish. After the challenge test, there were significant differences in the cumulative mortality rate among probiotic-treated and control groups. The first mortalities due to *A. hydrophila* began at 24 h post-infection (hpi) in all infected groups. The cause of death was confirmed

as *A. hydrophila* by bacterial isolation from the spleen and head kidney. Mortalities continuously occurred until 72 hpi. The highest mortality rate was recorded in the control group. Cumulative mortalities were significantly lower in the probiotic-treated groups than the control group (60.3% mortally) (Table 3).

Table 3: Mortality rate percentage in different treatments after challenge with *Streptococcus iniae*.

| Parameters | Treatments | | | | | |
|--------------------|-------------------|-------------------|------------------------------|-------------------|--------------------|-------------------|
| | QQ1 | QQ2 | <i>L. Plantarum</i> (WQQ) | QQ1+QQ2 | Combine | Control |
| Mortality rate (%) | 30.6 ^a | 30.6 ^a | 40.63 ^a | 30.6 ^a | 40.63 ^a | 60.3 ^b |

The data represent the Mean \pm SD of three tanks per treatment. Values with various lowercase letters in each row indicate significant differences ($p<0.05$).

Discussion

Probiotics can modulate the host immune responses through interaction with immune components within the gut or mucus, triggering immune-related signaling pathways and their effects on the production of cytokines (Thy *et al.*, 2017). According to our results, at 30 days, the QQ1+QQ2 group had significantly higher serum lysozyme activity compared to other groups, and by the end of the experiment, significant lysozyme differences were seen between the QQ1, QQ2, and control groups. Lysozyme activity was significantly higher in the QQ1+QQ2 group at 30 days, and the highest activity was observed in QQ1 and QQ2 at day 60. Lysozyme is a bacteriolytic enzyme that directly hydrolyze the peptidoglycan layer of Gram-positive bacteria. It has also a lytic activity against Gram-negative bacteria after damage by complement system which exposes the peptidoglycan cell wall (Nakanishi *et al.*, 2018). Furthermore, as an

opsonin, lysozyme activate phagocytes and the complement system. Our results are in line with those of Jiang *et al.* (2019) who reported that administration of dietary *B. cereus* QSI-1 at 5×10^8 CFU/g feed for 15 days could enhance lysozyme and complement activities in skin mucus of crucian carp. In this study, a reduction in lysozyme activity was observed in combine, as compared the other groups. Similar results were observed, dietary probiotic increased serum lysozyme activity in striped snakehead (*Channa striata*) (Talpur *et al.*, 2014); Asian sea bass (*L. calcarifer*) (Siddik *et al.*, 2022; Mozanzadeh *et al.*, 2023), *E. bruneus* (Harikrishnan *et al.*, 2010), *E. coioides* (Son *et al.*, 2009), Shabot (*Tor grypus*) (Mohammadian *et al.*, 2016) and *Labeo rohita* (Giri *et al.*, 2013).

Serum complement activity is an important humoral component of the non-specific immune system with bactericidal, chemotactic and opsonic activities (Budi-

no *et al.*, 2006). Lipopolysaccharides from Gram-negative bacteria and foreign red blood cells are among the known activators of this pathway (Nakanishi *et al.*, 2018; Ghanei-motlagh *et al.*, 2021). In this study, serum complement activity was significantly increased in fish fed with dietary QQ2 at 30 days. It has been previously reported that dietary *B. aerius* B81e significantly increased serum complement, lysozyme, bactericidal activities and RB in Pla-Mong (*Pangasius bocourti*), in a manner consistent with our present results (Meidong *et al.*, 2018). After day 60, complement activity was higher in the QQ1+QQ2 groups compared to the QQ1 group. In accordance with our results, a higher complement activity was reported in Asain sea bass (Mozanzadeh *et al.*, 2023), *Salmo trutta caspius* (Hoseinpouri Ghasemabad Sofla *et al.*, 2024) fed with mix probiotics, and olive founder (*Paralichthys olivaceus*) fed with diets containing probiotic and herbal extract (Harikrishnan *et al.*, 2011).

Serum protease inhibitors are involved in acute phase reactions, homeostasis of the body fluids and defense against protease-producing bacteria (Magnad' ottir, 2006). Our findings revealed that serum antiprotease activity was higher in fish fed with the mixed QQ probiotics (QQ1+QQ2) at days 30. In agreement with our results, Nile tilapia fed with diets containing *B. subtilis* and *B. licheniformis* had significantly enhanced levels of serum antiprotease in comparison with the untreated fish (Abarike *et al.*, 2018). Moreover, at the end of this study, the WQQ group showed a significant difference in antitrypsin activity compared

to all groups except the combined treatment group. In agreement with our result, feeding with dietary *L. sakei* BK19 promoted several immune parameters including serum antiprotease activity in fish (Harikrishnan *et al.*, 2011) also use of *Bacillus subtilis* AB1 in the diet of rainbow trout (*O. mykiss*) for two weeks could significantly increase antiprotease activity (Newaj-Fyzul *et al.*, 2007). Likewise, olive flounder (*Paralichthys olivaceus*) fed with *E. fascium* for 5 days had an increased levels of serum antiprotease activity (Kim and Kim, 2013).

Myeloperoxidase (MPO) is a major enzyme present in azurophilic (primary) granules of granulocytic cells (mostly neutrophils) and modulates the immune response and inflammatory processes. MPO is involved in both oxidative (chlorination and peroxidase activities) and antioxidant (superoxidase, SOD and CAT activities) activities. Under normal conditions, MPO and its derivatives provide an effective microbicidal system against pathogens. However, excessive production of MPO-derived oxidants has been associated with several pathological circumstances in higher-developed organisms (Winterbourn and Kettle, 2013). According to the results, a higher serum MPO activity was recorded in the combined treatment group (QQ1+QQ2+WQQ) compared to the control group at day 60. Consistent with our results, Zhang *et al.* (2017) showed that supplementation with *Lactobacillus delbrueckii* led to a significant elevation in the lysozyme and MPO activities compared to the control group. Also, improvement of the above-mentioned immune responses has been

documented following oral administration of probiotics in Nile tilapia (Makled *et al.*, 2019), pirarucu (*Arapaima gigas*) (Pereira *et al.*, 2019), catla (*Catla catla*) (Bhatnagar and Saluja, 2019), red seabream (*Pagrus major*) (Dawood *et al.*, 2019), striped catfish (*Pangasianodon hypophthalmus*) (Thy *et al.*, 2017), snakehead (*Channa striata*) (Talpur *et al.*, 2014), white carp (*Cirrhinus mrigala*) (Bhatnagar and Lamba, 2017), common carp (*C. carpio*) (Mohammadian *et al.*, 2022) and Japanese eel (*Anguilla japonica*) (Lee *et al.*, 2017).

Hematological variables are considered prognostic indicators and vital diagnostic tools for the assessment of fish health, reflecting the physiological and pathological responses in fish (Mohammadian *et al.*, 2022). Similarly to our findings, improvement of hematological indices using dietary supplementation with *Bacillus* spp. has been demonstrated in Asian seabass (Adoraian *et al.*, 2019; Ghanei Motlagh *et al.*, 2021; Mozanzadeh *et al.*, 2023), red seabream (Zaineldin *et al.*, 2018), Nile tilapia (Hassaan *et al.*, 2014; Abdel-Aziz *et al.*, 2020), African catfish (Reda *et al.*, 2018), Shabot (*Tor grypus*) (Mohammadian *et al.*, 2019a) and Rohu (Mukherjee *et al.*, 2019). It has been reported that probiotics could promote hematopoiesis which may be associated with diminished content of blood cortisol, provided essential micronutrients particularly B-Group vitamins and positively modulated gut microbiota (Carneveli *et al.*, 2006, Mohapatra *et al.*, 2013, Mohapatra *et al.*, 2014; Elshaghabee *et al.*, 2017). Probiotics can also interact with the components of the immune system

within the intestinal lumen, resulting in the stimulation of immune responses. In this study, TLC was significantly increased in WQQ group for 30 days (Table 2). Our results are in line with previous reports, suggesting that *lactobacillus* spp. can modulate innate immune responses in fish (Zaineldin *et al.*, 2018; Mohammadian *et al.*, 2019; Mozanzaeh *et al.*, 2023). A higher level of Hb was found in the combined group in 30 days post-feeding when compared to the control group. It was in agreement with the findings of Olayinka and Afolabi (2013) reported the association between Hb concentration and fish activity. Taking this finding, higher activity was observed in the probiotic-fed fish throughout the whole experiment than the control group. There was no significant differences between TEC and Hct levels (days 30) in the control and probiotic-fed groups during the experiment. This finding was in agreement with the results of previous works of Capkin and Altinok (2009). The probiotics indicate the increase of some blood parameters as a result of hemopoietic stimulation. Overall, our results suggest that the fish that received QQ and WQQ probiotics had healthier conditions compared to non-probiotic groups and, enhanced the host tolerance to possible stressors.

The modulatory effects of probiotics on the antioxidant defense system of fish have been demonstrated in previous studies (Mohammadian *et al.*, 2022; Mozanzadeh *et al.*, 2023). In the present research, higher hepatic activities of CAT and SOD were recorded in common carp fed with dietary QQ2 for 30 and 60 days, while higher hepatic activities of GSH were recorded in

common carp fed with dietary QQ1 for 30 and 60 days. In the current study, the malondialdehyde (MDA) analysis of fish fed with the QQ1+QQ2 (group 4) diets increased remarkably compared to the other groups only at day 60. In this regard, feeding gibel carp with an AHL-degrading probiotic (*B. frmus* sw40) led to an increased level of serum SOD but reduced contents of serum MDA and GSH (Li *et al.*, 2019). The elevated activities of serum SOD, CAT and GSH as well as the decreased level of MDA were observed in Pengze crucian carp (*Carassius auratus* var. Pengze) fed with *B. cereus* (Yang *et al.*, 2020). Moreover, dietary supplementation with *B. cereus* 39HN resulted in the highest levels of serum SOD in African catfish (*Clarias gariepinus*) (Reda *et al.*, 2018). These protective effects of dietary probiotics on prevention of oxidative stress may be attributed to their potential for direct scavenging active oxidants, production of enzymes and metabolites with antioxidant activity, positive modulation of intestinal microbiota composition, biosynthesis of essential micronutrients with antioxidant activity such as vitamins B12 and B6, increased bioavailability of dietary antioxidants from the gut and regulation of antioxidant-associated signaling pathways in host (Wang *et al.*, 2017 ; Hoseinpouri Ghasemabad Sofla, *et al.*, 2024). SOD, CAT, GSH and MDA are among the most reliable markers associated with oxidative stress response. SOD and CAT are two essential components of the antioxidant enzyme system catalyzing the dismutation of the superoxide anion radical to hydrogen peroxide and water, and the decomposition

of hydrogen peroxide into oxygen and water, respectively (Peixoto *et al.*, 2016). GSH is a non-enzymatic antioxidant with a high abundance of sulfhydryl (thiol) groups that plays a key role in maintaining of intracellular oxidoreductive balance through scavenging reactive oxygen species (such as hydrogen peroxide in conjunction with glutathione peroxidase GPx) and detoxification of organic hydroperoxides (Zengin and Yilmaz, 2016). The reduction in hepatic GSH is associated with depletion during oxidative stress, decreased synthesis and increased utilization (Lu, 2020). MDA is one of the end products of lipid peroxidation and is frequently used as a biomarker of cell membrane injury. In this study, elevated activities of CAT and SOD, reduced contents of GSH, and increased levels of MDA were observed in QQ1+QQ2 and control groups compared to the other groups, especially at day 60. The mix QQ probiotics (QQ1+QQ2) in this study resulted in higher MDA levels in the liver as well as lower SOD activity in the liver that probably supported the worst antagonistic effect of two QQ bacteria compared to single use.

The results of the present study also demonstrate that the level of mortality in fish fed with the diets supplemented by *C. freundii* (QQ1) and *B. foraminis* (QQ2) decreased by 30.6 compared to the control group. However, no clear mechanism has been suggested for this protection and for the difference in protectiveness between QQ bacteria. A possible explanation may be differences in the probiotic's capabilities to modulate physiological responses in fish. *L. plantarum*, included as a without

characteristics QQ, caused a 40 % decrease in the level of mortality seen in the probiotic-fed fish compared to the control group (60.3 %), but did not give better protection compared to the experimental QQ isolated from the intestine of *C. carpio*. Our results were similar to the findings of Takafoyan *et al.* (2024), Chen *et al.* (2020a, 2020b), Torabi Delshad *et al.* (2019), Ghanei-Motlagh *et al.* (2019), Bhatnagar and Lamba (2017) and Bhatnagar and Aly *et al.* (2008), Giri *et al.* (2013), who recorded higher survival rate in fish fed with a diet containing probiotics compared with those fed with normal diet. Dietary supplementation with defined probiotics may be an effective biotherapeutic or prophylactic means in aquaculture (Mohammadain *et al.*, 2016). Our results showed that *C. carpio* fed with the probiotic isolated from *C. carpio* intestine raised the survival rate when challenged with *A. hydrophilla*, suggesting that feeding with the probiotics for eight or more weeks is effective in helping to control *Aeromonas* infections in fish. There are many reports relating to enhanced protection against various diseases by feeding probiotic-containing food. The effects of probiotic bacteria have been studied in relation to the fish species and their genetic makeup, the feeding lengths, dosage and the type and origin of probiotic strain (Takafoyan *et al.*, 2024). These results collectively suggest that dietary supplementation of gut QQ of *C. carpio* in form mix (QQ1+QQ2) not only improved their immune responses as well as the common probiotics like *Lactobacillus* bacteria but also in some respects is better. The observed improvement in the immune parameters

measured here as a result of feeding the probiotic bacteria may be useful indicators for screening new strains of probiotic bacteria for use in aquaculture. When selecting a potential probiotic both its safety and its efficacy should be considered, both of the experimental species used here were originally isolated from the GI tract of *C. carpio* and are therefore autochthonous to the species and environment, and these probiotics could be useful because they are safety. The probiotic bacteria have to be administered at an optimal dose depending on the size and species of fish and probiotic strain used; thus, further investigation into the effectiveness of these probiotics is warranted.

Conclusion

The results obtained in this study suggest that, after full validation of their efficacy in the field and safety considerations, the application of QQ bacteria with high probiotic potential could be developed commercially as novel dietary supplements for control of infections caused by *Aeromonas* pathogens in the aquaculture industry. Moreover, the characteristic of spore formation by a certain QQ probiotic (*Bacillus* spp.) protects these kinds of strains from pressure and heat during the manufacturing processes, which simplifies their incorporation into commercial pellets.

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Conflicts of interest

The authors declare that they have no conflict of interest.

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