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Aeromonas spp. IN FARMED FISH IN BRAZIL: A SYSTEMATIC LITERATURE REVIEW

Aeromonas spp. EM PEIXES DE CULTIVO NO BRASIL: UMA REVISÃO SISTEMÁTICA DA LITERATURA

Aeromonas spp. EN PECES DE CULTIVO EN BRASIL: UNA REVISIÓN SISTEMÁTICA DE LA LITERATURA

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Abstract

The genus *Aeromonas* comprises more than 30 species of bacteria widely distributed in aquatic environments and frequently associated with opportunistic infections in aquatic organisms, especially farmed fish. In aquaculture systems, these bacteria can cause septicemia, high mortality rates, and economic losses, and pose a potential risk to public health. Therefore, this study aimed to conduct a systematic review of the scientific literature on the occurrence of *Aeromonas* spp. in farmed fish in Brazil, from 2012 to 2022. Searches were conducted in the ScienceDirect, CAPES Journals, SciELO, and PubMed databases, using the English descriptors "*Aeromonas*," "aquaculture," "diseases," "fish," and "Brazil," combined with the Boolean operator "AND," according to the specificities of each database. Of the 151 studies identified, 10 articles met the established criteria and were included in the final analysis. The species *Aeromonas* bestiarum, *A. caviae, A. dhakensis, A. jandaei, A. hydrophila*, and *A. veronii* were identified in five species of farmed fish: tambaqui, jundiá, pacu, tilapia, and hybrid surubim, in the states of Amazonas, Mato Grosso do Sul, Pernambuco, Paraná, Rio Grande do Sul, and São Paulo. The isolates presented varied virulence profiles and resistance to different antibiotics. All *Aeromonas* species were isolated from tambaqui, 80% from tilapia, 60% from pacu, and 20% from jundiá and hybrid surubim. Additionally, isolates of the genus *Aeromonas* without species identification were reported in tambaqui and jundiá. The results highlight the scarcity of studies on *Aeromonas* spp. in farmed fish in Brazil, indicating a relevant scientific gap, especially

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considering the growth of national fish farming and the emergence of this bacterial genus as a pathogen of sanitary importance.
Keywords: *Colossoma macropomum*; diseases; fish farming; fish health; tilapia.

Resumo

O gênero *Aeromonas* compreende mais de 30 espécies de bactérias amplamente distribuídas em ambientes aquáticos e frequentemente associadas a infecções oportunistas em organismos aquáticos, especialmente em peixes de cultivo. Em sistemas aquícolas, essas bactérias podem causar quadros de septicemia, elevadas taxas de mortalidade e prejuízos econômicos, além de representarem um risco potencial à saúde pública. Diante disso, o presente estudo teve como objetivo realizar uma revisão sistemática da literatura científica sobre a ocorrência de *Aeromonas* spp. em peixes de cultivo no Brasil, no período de 2012 a 2022. As buscas foram conduzidas nas bases de dados ScienceDirect, Periódicos CAPES, SciELO e PubMed, utilizando os descritores em inglês "*Aeromonas*", "aquaculture", "diseases", "fish" e "Brazil", combinados pelo operador booleano "AND", de acordo com as especificidades de cada base. Do total de 151 estudos identificados, 10 artigos atenderam aos critérios estabelecidos e foram incluídos na análise final. As espécies *A. bestiarum*, *A. caviae*, *A. dhakensis*, *A. jandaei*, *A. hydrophila* e *A. veronii* foram identificadas em cinco espécies de peixes de cultivo, tambaqui, jundiá, pacu, tilápia e surubim híbrido, nos estados do Amazonas, Mato Grosso do Sul, Pernambuco, Paraná, Rio Grande do Sul e São Paulo. Os isolados apresentaram perfis variados de virulência e de resistência a diferentes antibióticos. Todas as espécies de *Aeromonas* foram isoladas em tambaqui, 80% em tilápia, 60% em pacu e 20% em jundiá e em surubim híbrido. Adicionalmente, foram relatados isolados do gênero *Aeromonas,* sem identificação ao nível de espécie, em tambaqui e jundiá. Os resultados evidenciam a escassez de estudos sobre *Aeromonas* spp. em peixes de cultivo no Brasil, indicando uma lacuna científica relevante, especialmente considerando o crescimento da piscicultura nacional e a emergência desse gênero bacteriano como patógeno de importância sanitária.
Palavras-chave: *Colossoma macropomum*; doenças; piscicultura; sanidade; tilápia.

Resumen

El género *Aeromonas* comprende más de 30 especies de bacterias ampliamente distribuidas en ambientes acuáticos y frecuentemente asociadas a infecciones oportunistas en organismos acuáticos, especialmente en peces de cultivo. En sistemas de acuicultura, estas bacterias pueden causar septicemia, altas tasas de mortalidad y pérdidas económicas, además de representar un riesgo potencial para la salud pública. Por lo tanto, este estudio tuvo como objetivo realizar una revisión sistemática de la literatura científica sobre la presencia de *Aeromonas* spp. en peces de cultivo en Brasil entre 2012 y 2022. Se realizaron búsquedas en las bases de datos ScienceDirect, CAPES Journals, SciELO y PubMed, utilizando los descriptores en inglés "*Aeromonas*", "aquaculture", "diseases", "fish" y "Brazil", combinados con el operador booleano "AND", según las especificidades de cada base de datos. De los 151 estudios identificados, 10 artículos cumplieron con los criterios establecidos y se incluyeron en el análisis final. Las especies *Aeromonas bestiarum, A. caviae, A. dhakensis, A. jandaei, A. hydrophila* y *A. veronii* se identificaron en cinco especies de peces de cultivo: tambaqui, jundiá, pacu, tilapia y surubim híbrido, en los estados de Amazonas, Mato Grosso do Sul, Pernambuco, Paraná, Rio Grande do Sul y São Paulo. Los aislados presentaron perfiles de virulencia variados y resistencia a distintos antibióticos. Todas las especies de *Aeromonas* se aislaron en tambaqui, 80% en tilapia, 60% en pacu y 20% en jundiá y surubim híbrido. Además, se reportaron aislados del género *Aeromonas* sin identificación de especie en tambaqui y jundiá. Los resultados resaltan la escasez de estudios sobre *Aeromonas* spp. en peces de cultivo en Brasil, lo que evidencia un vacío científico relevante, especialmente ante el crecimiento de la piscicultura nacional y el surgimiento de este género bacteriano como patógeno de importancia sanitaria.
Palabras clave: *Colossoma macropomum*; enfermedades; piscicultura; salud; tilapia.

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1. Introduction

Fishing and aquaculture have been increasingly recognized as sources of high-biological-value animal protein for global food security. In 2020, global aquatic animal production was estimated at 178 million tons, of which approximately 90% was destined for human consumption, with 56% coming from aquaculture. Even amid the impacts of the COVID-19 pandemic, the sector recorded 22.4% growth in global production between 2010 and 2020, corresponding to an average annual rate of 4.6%. During this period, farmed fish production reached 57.5 million tons, predominantly continental aquaculture (85.4%), followed by marine and coastal aquaculture (14.4%) (FAO, 2022).

In Brazil, fish farming reached approximately 860,000 tons in 2022, a 2.3% increase from the previous year. Tilapia (*Oreochromis niloticus*) stood out as the main species produced, accounting for about 64% of the total volume (550,000 tons) and 88% of Brazilian fish exports, positioning the country as the fourth-largest producer in the world. The Southern region leads national tilapia production, accounting for 43.5% of total production, followed by the Northeast and Southeast regions, with particular emphasis on the Northeast´s productive growth (Peixe BR, 2023).

Despite its high productive potential, the intensification of fish farming in Brazil, frequently associated with high stocking densities, inadequate feeding management, and compromised water quality, favors fish stress and the emergence of infectious diseases (Pessoa *et al.*, 2020; Sebastião *et al.*, 2022). In this context, infections caused by bacteria of the genus *Aeromonas* represent one of the main sanitary challenges for national fish farming, potentially causing mortality outbreaks, reduced zootechnical performance, and significant economic losses (Pessoa *et al.*, 2020; Wang *et al.*, 2022).

The genus *Aeromonas* comprises Gram-negative, motile, and opportunistic bacteria that are naturally distributed across various aquatic ecosystems and are frequently isolated from fish and crustaceans. Furthermore, they can be found in terrestrial environments, including soil, plants, and various organisms, including birds and amphibians. This wide environmental distribution exposes these bacteria

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to antimicrobial residues from urban and industrial effluents, contributing to the selection and dissemination of resistant strains, especially in aquatic environments (Pessoa *et al*., 2019; Wang *et al*., 2022).

Currently, this genus comprises more than 30 species, many of which exhibit diverse virulence factors, including extracellular enzymes, toxins, and membrane components involved in adhesion, colonization, and invasion of host cells. The expression of these factors varies among species and strains, resulting in different levels of pathogenicity. Furthermore, these bacteria are recognized for their ability to form biofilms, which favors environmental persistence, surface colonization, and the acquisition and horizontal transfer of antimicrobial resistance and virulence genes (Pessoa *et al*., 2019; Pessoa *et al*., 2020).

In addition to their relevance to aquaculture health, *Aeromonas* spp. are considered emerging pathogens in humans, being associated with gastrointestinal and extraintestinal infections, with water and aquatic foods as potential transmission routes. In aquaculture systems, the intensification of production and the recurrent use of antimicrobials favor the selection and persistence of resistant strains in the culture environment, sediments, and fish microbiota (Pessoa *et al*., 2020; Wang *et al*., 2022).

The biofilm-forming capacity and high genetic plasticity of these bacteria contribute to the maintenance and dissemination of antimicrobial resistance genes, increasing health risks at the environment-animal-human interface (Abe; Nomura; Suzuki, 2020). In this context, *Aeromonas* spp. have been identified as a growing threat to environmental health and aquaculture, reinforcing the need for systematic monitoring of this genus in culture environments, with emphasis on antimicrobial resistance profiles (Lin *et al*., 2022).

Given this scenario and considering the absence of a systematized synthesis on the occurrence of *Aeromonas* spp. in farmed fish in Brazil, the present study aimed to conduct a systematic review of the scientific literature published between 2012 and 2022, in order to compile and analyze national studies that address the isolation, identification, and virulence and antimicrobial resistance profiles of this bacterial genus in farmed fish.

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2. Methodology

After defining the problem, a qualitative systematic review of the scientific literature was conducted through a bibliographic survey of the ScienceDirect, CAPES Journals, SciELO, and PubMed databases. The searches covered studies published between 2012 and 2022.

The following descriptors were used in English: "*Aeromonas*", "aquaculture", and "diseases", associated with the terms "fish" and "Brazil", combined using the Boolean operator "AND", according to the methodological specificities of each database. This strategy was adopted to identify studies on the occurrence of *Aeromonas* spp. in farmed fish in Brazil.

The selection of articles was carried out in four stages. In the first stage, the titles and abstracts of the identified studies were read. In the second stage, the selected articles were evaluated through full-text reading. In the third stage, additional studies identified in the "recommended articles" section of the ScienceDirect database were included, adopted as a complementary search strategy, provided they met the same criteria as the previous stages. In the fourth stage, data extraction and qualitative and quantitative analysis were performed.

In the first three stages, previously defined inclusion criteria were applied, such as: 1. Article type: Short research and communication articles; and 2. Referring to the identification and analysis of the genus *Aeromonas* in any phase of the fish production chain (primary production, transport, processing, or trade). For exclusion, the following criteria were used: 1. Articles prior to 2012 and after 2022; 2. Studies on *Aeromonas* outside of Brazil; 3. Review articles, book chapters, dissertations, and monographs; and 4. Articles addressing other bacterial species besides *Aeromonas* in fish.

In the ScienceDirect database, 151 articles were initially identified during the analyzed period, a number reduced to 114 after applying document-type filters. In the CAPES Journals database, 9 articles were found, 2 of which were duplicates. In PubMed, three articles were identified, two of which were duplicates, while in SciELO, only one article was found, already identified in another database. The

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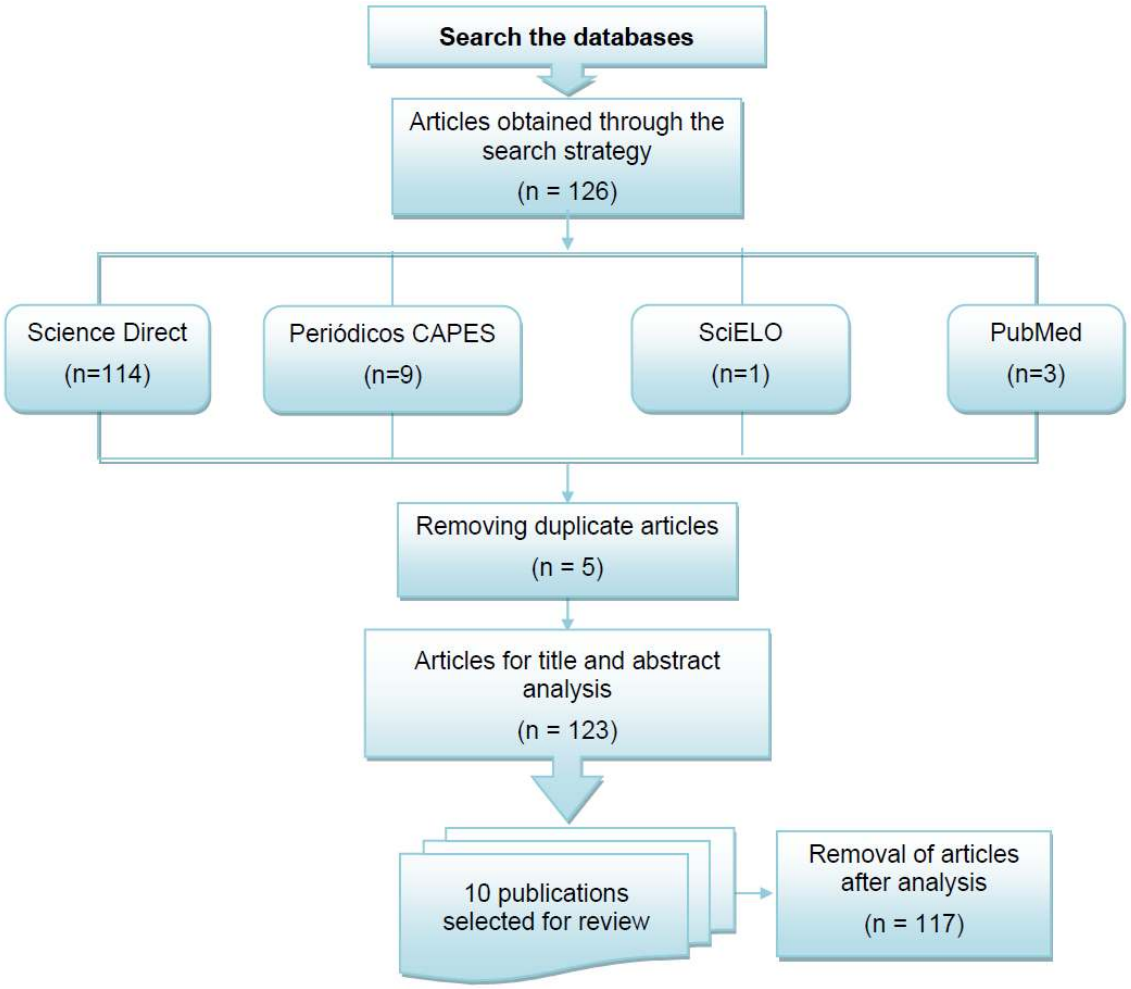
process of identifying, screening, and selecting the studies is represented in the flowchart (Figure 1).

Figure 1. Flowchart of the search process for selected articles on the study of *Aeromonas* in Brazil.



Source: Elaborated by the authors (2025).

Data extraction was performed systematically and recorded in an electronic spreadsheet (Microsoft Excel®), including the following variables: (I) authors and year of publication; (II) *Aeromonas* species identified; (III) fish species analyzed; (IV) origin of the fish; (V) method of bacterial identification; and (VI) study location.

3. Results and discussion

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The genus *Aeromonas* comprises opportunistic bacteria widely distributed in aquatic environments, with continuous contact with aquatic organisms often unavoidable (Pessoa *et al*., 2019). These bacteria can be isolated from both healthy and diseased fish, often acting as opportunistic pathogens in stressful conditions or as secondary agents following the establishment of primary infections (Pessoa *et al.,* 2019; Wang *et al.,* 2022).

Table 1 presents the studies included in this systematic review that addressed the identification of *Aeromonas* species isolated from farmed fish in Brazil, from 2012 to 2022. The analysis of the selected works showed that the collections were predominantly conducted at local fish farms distributed across five Brazilian states. Rio Grande do Sul (RS) concentrated 30% of the studies, while Amazonas (AM), Pernambuco (PE), and São Paulo (SP) each accounted for 20% of the research, and Mato Grosso do Sul (MS) for 10% (Figure 2).

Table 1. References used and classified by the qualitative data extraction technique from the selected articles.

States	Fish species	*Aeromonas* species	Identification	References
Amazonas	Tambaqui (*C. macropomum*)	*A. jandaei*	Spectrometry	Mielke *et al*. (2022)
	Tambaqui (*C. macropomum*)	*Aeromonas* spp.	Biochemical and molecular	Sebastião *et al*. (2022)
Pernambuco	Tambaqui (*C. macropomum*)	*A. bestiarum* e *A. caviae*	Biochemical	Marques *et al*. (2016)
	Tambaqui (*C. macropomum*)	*A. hydrophila, A. dhakensis, A. caviae, A. veronii* e *A. jandaei*	Biochemical	Pessoa *et al*. (2020)
São Paulo	Pacu *(P. mesopotamicus*)	*A. dhakensis*	Biochemical and molecular	Carriero *et al*. (2016)
	Tilápia *(O. niloticus)* e Pacu *(P. mesopotamicus)*	*A. caviae, A. hydrophila, A. jandaei, A. veronii*	Morphological, Biochemical and molecular	Assane *et al*. (2019)
Mato Grosso	Hybrid surubim *(P. corruscans* × *P. fasciatum*)	*A. hydrophila*	Biochemical and molecular	Silva *et al*. (2012)
Rio Grande do Sul	Jundiá (*R. quelen*)	*Aeromonas* spp.	Morphological e Biochemical	Sutili *et al*. (2015)
	Jundiá (*R. quelen*)	*A. hydrophila*	Biochemical and molecular	Bandeira-Júnior *et al*. (2019, 2021)

Source: Elaborated by the authors (2024).

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Figure 2. Map of Brazil indicating the points of origin of *Aeromonas* isolations.



Source: Elaborated by the author using Microsoft Bing.

The state of São Paulo ranks 2nd in the production of farmed fish in Brazil, with a productivity of 83,400 tons in 2022, followed by Mato Grosso do Sul in 8th (34,450 tons), Pernambuco in 10th (31,960 tons), Rio Grande do Sul in 12th (27,300 tons), and Amazonas in 15th place (21,300 tons). The Southern Region stands out as the main farming hub in the country, accounting for almost a third (32%) of the total produced, followed by the Northeast (approximately 20%), Southeast (18.5%), Northern region (16.9%), and Central-West (12.8%) (Peixe BR, 2023).

The higher concentration of studies in states with significant aquaculture production suggests a direct relationship between the economic importance of the activity and the scientific interest in investigating bacterial pathogens associated with aquaculture systems. On the other hand, the absence of studies in several federative units with significant aquaculture production highlights regional research gaps and underscores the need to expand research on *Aeromonas* spp. across different production contexts across the country.

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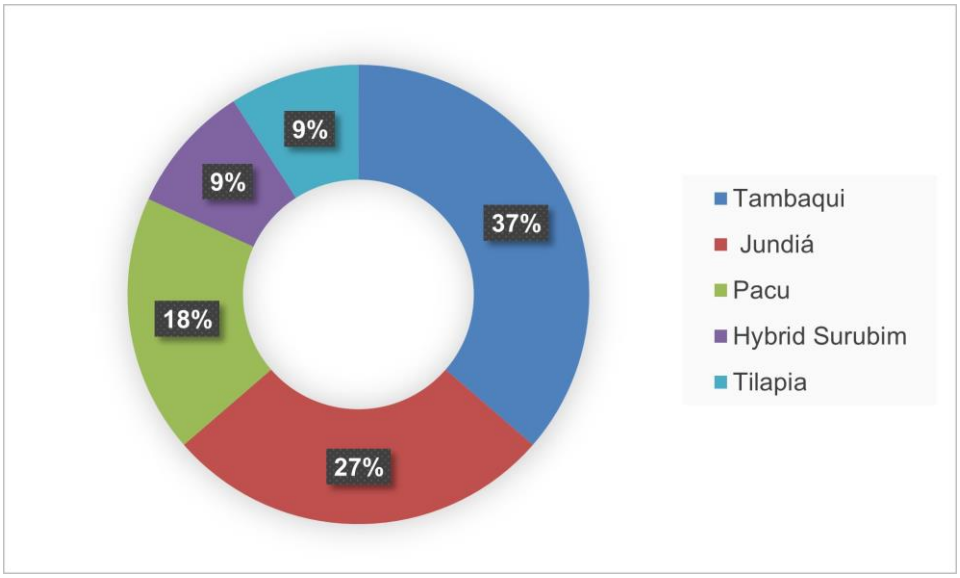
3.1. Isolation and identification of *Aeromonas* spp.

According to the studies included in this systematic review, tambaqui (*Colossoma macropomum*) was the fish species in which *Aeromonas* spp. were most frequently isolated, corresponding to 37% of the analyzed articles (Figure 3). Of these studies, 50% were conducted in the state of Amazonas in 2022, and the remainder in Pernambuco between 2016 and 2020. Tambaqui is a native Brazilian species, originating from the Amazon basin and widely distributed also in the São Francisco River basin, which includes areas of the states of Bahia and Pernambuco (Campeche; Guilherme, 2019). Amazonas stands out as the fifth-largest producer of native fish in Brazil, with production focused mainly on native species, especially tambaqui, which accounts for approximately 68.85% of the state's aquaculture activity (Peixe Br, 2023; Dassori, 2023).

Figure 3. Fish species affected by *Aeromonas* in Brazil, from 2012 to 2022.



Source: Elaborated by the authors (2024).

According to Pessoa *et al.* (2020), scientific interest in tambaqui is directly related to its high importance in Brazilian aquaculture, since the species is large, grows rapidly, has a high capacity for environmental adaptation, and is widely accepted commercially, mainly due to the sensory quality of its meat.

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The second most investigated species was the jundiá (*Rhamdia quelen*), present in 27% of the studies, all conducted in the state of Rio Grande do Sul between 2019 and 2020. The jundiá, also known as silver catfish, is one of the main native species cultivated in the Southern region of Brazil (Peixe BR, 2020), playing a relevant economic and social role, especially for small rural properties, contributing to food and income generation (Graeff, 2013). According to Bandeira-Júnior *et al.* (2021), *Aeromonas* spp. are the main etiological agents of diseases in this species, frequently causing skin ulcers and hemorrhagic septicemia.

Isolates of *Aeromonas* spp. from pacu (*Piaractus mesopotamicus*) were reported in 18% of the analyzed articles, all originating from the state of São Paulo. Assane *et al*. (2019) identified *Aeromonas* species in pacu in Nile tilapia (*O. niloticus*). Pacu is a native species that stands out in Brazilian fish farming due to its hardiness, adaptability to different production systems, rapid growth, and good acceptance in the consumer market, with production concentrated mainly in the southern region of the country, along with tambaqui, pirapitinga, and their hybrids (Tordin, 2021).

Nile tilapia is the most cultivated and exported species in Brazilian fish farming, with São Paulo as the second-largest producer (Peixe BR, 2020). Internationally, Brazil ranks fourth among the world´s largest tilapia producers, steadily advancing to third place. However, the expansion of the activity poses the challenge of increasing the risk of the spread of emerging diseases across the country´s production centers (Peixe BR, 2023).

The hybrid surubim, resulting from the crossbreeding of pintado (*P. corruscans*) and cachara (*P. fasciatum*), was reported in only one study conducted in Mato Grosso do Sul in 2012 (Silva *et al*., 2012). It should be noted that *P. fasciatum* was recently reclassified into *P. punctifer* (surubim) and *P. reticulatum* (cachara) (Matos; Meurer, 2021). The hybrid surubim is one of the largest freshwater fish in South America and is of increasing importance in Brazilian aquaculture, with Mato Grosso do Sul being one of the main centers of technological development for the production of larvae of this genus, especially *P. corruscans, P. reticulatum*, and their hybrids (Silva *et al*., 2011).

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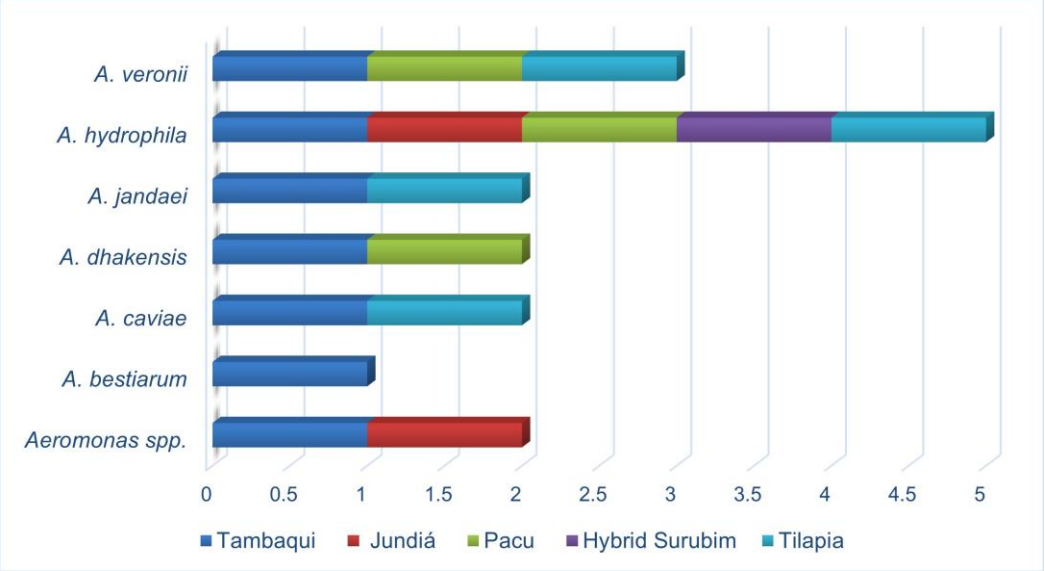
Among the studies analyzed, six *Aeromonas* species were identified as associated with five fish species farmed in Brazil: *A. bestiarum, A. cavie, A. dhakensis, A. jundaei, A. hydrophila*, and *A. veronii* (Figure 4). All *Aeromonas* species were isolated from tambaqui, while 80% were identified in tilapia, 60% in pacu, and 20% in jundiá and hybrid surubim. In addition, isolates of the genus *Aeromonas* without species identification were reported in tambaqui and jundiá. Among the identified species, *A. hydrophila* showed the greatest representation, being isolated from all evaluated fish species.

Figure 4. Species of *Aeromonas* isolated from fish in Brazil, from 2012 to 2022.



Source: Elaborated by the authors (2024).

Pessoa *et al.* (2020) identified *A. hydrophila* as the predominant species among the isolates from tambaqui, accounting for 41.2% of the strains analyzed. However, the concomitant detection of *Aeromonas* sp., *A. dhakensis* (20.6%), *A. caviae* (17.6%), *A. veronii* (11.8%), and *A. jandaei* (8.8%) highlights the high intraspecific diversity of this genus associated with tambaqui. These results indicate that, in addition to being highly susceptible to infection by *Aeromonas*, tambaqui can act as a reservoir of potentially pathogenic strains to humans, considering that *A. dhakensis* and *A. caviae* are frequently associated with human infections and that this fish species is widely consumed in the Northern region of Brazil.

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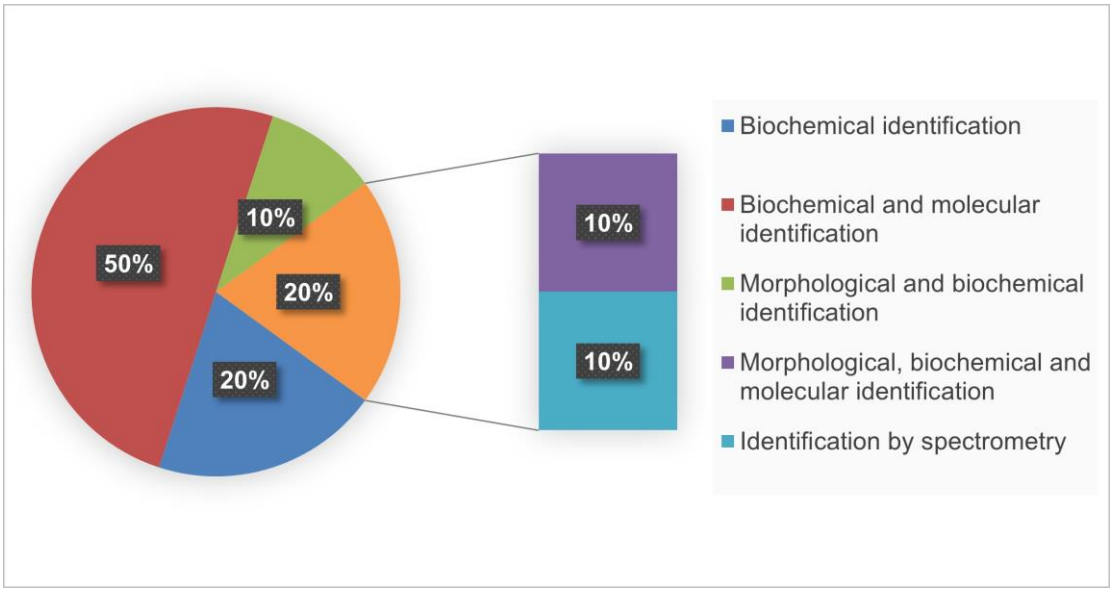
In Nile tilapia, Assane *et al.* (2019) reported that *A. hydrophila* predominated, accounting for approximately 70% of the isolated strains, followed by *A. jandaei* (16.7%), *A. veronii* (12.5%), and *A. caviae* (4.2%). In isolates from pacu, the authors observed an equitable distribution between *A. hydrophila* and *A. veronii* (50% each). In contrast, Carriero *et al.* (2016) identified all strains isolated from pacu as *A. dhakensis* or as subspecies previously classified as *A. hydrophila* or *A. aquariorum*, highlighting the taxonomic complexity of the genus and the need for more precise identification methods.

Regarding the methodologies employed for bacterial identification, 50% of the studies used combined biochemical and molecular approaches to characterize strains at the species level. In 20% of the articles, identification was based exclusively on biochemical tests, while 10% employed morphological methods in combination with biochemical tests. In the remaining studies (20%), in addition to these methods, advanced techniques such as mass spectrometry were used (Figure 5).

Figure 5. Method for identifying *Aeromonas* species in the analyzed articles.



Source: Elaborated by the authors (2024).

According to Pessoa *et al.* (2019), the correct identification of *Aeromonas* remains a challenge due to the high phenotypic and genetic diversity of the genus. Strain cultivation and maintenance can be carried out in various culture media, with

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Tryptone Soy Broth (TSB) widely used for preserving isolates from fish and aquatic environments. For presumptive identification, selective media such as MacConkey agar supplemented with ampicillin are frequently used. However, despite their wide application, biochemical tests have limitations in discriminating among some *Aeromonas* species, underscoring the need to integrate them with molecular techniques, corroborated by this review.

In this context, Carnahan, Behram, and Joseph (1991) developed the Aerokey II identification key, based on seven highly discriminatory tests: esculin hydrolysis, gas production from glucose, acid production from arabinose and sucrose, indole production, Voges-Proskauer reaction, and cephalothin resistance (30 µg). The authors demonstrated that the system correctly identified approximately 97% of 60 clinical isolates coded in an independent laboratory and 100% of the species-level reference strains, characterizing Aerokey II as a reliable and accurate method for taxonomic identification of *Aeromonas* spp.

More recently, Mielke *et al.* (2022) employed matrix-assisted laser desorption/ionization mass spectrometry (MALDI-TOF MS) to identify *Aeromonas* strains isolated from tambaqui following mortality outbreaks during transport. This technique is based on the ionization of samples and the analysis of the time-of-flight of the generated ions, allowing the differentiation of microorganisms based on specific protein profiles, mainly ribosomal and cytosolic proteins. Thus, MALDI-TOF MS has proven effective for taxonomic discrimination at both the genus and species levels, reinforcing its potential as a complementary or alternative tool to classical bacterial identification methods (Pessoa *et al*., 2019).

3.2. Virulence factors and correlated genes

The expression of virulence factors by pathogenic bacteria is directly related to the reduction of host immunity, favoring the establishment and progression of infectious processes. In the genus *Aeromonas*, virulence is multifactorial and complex, resulting from the wide diversity of structural components, toxins, and extracellular products that can act independently or synergistically during infection (Pessoa *et al*., 2019).

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The high genetic plasticity observed among *Aeromonas* species results from the presence of non-uniform genetic components, such as pseudogenes, insertion elements, and genomic rearrangements, which contribute significantly to the phenotypic and behavioral variability of this genus (Beaz-Hidalgo; Figueras, 2013). These virulence factors play essential roles in bacterial pathogenicity, acting at different stages of the infectious process, including tissue adhesion, evasion of the host immune response, and invasion of host cells (Bandeira-Junior *et al.,* 2019).

Bandeira-Júnior *et al.* (2019) evaluated the effects of *A. hydrophila* infection on behavior and stress-related gene expression in catfish (*R. quelen*) and observed that the infection induced stress-related hyperlocomotion. The authors also reported alterations in the hypothalamic-pituitary-interrenal (HPI) axis, with increased brain expression of heat shock protein 12A (hspa12a) and the cortisol synthesis pathway (crh), demonstrating the direct interference of bacterial infection with the physiological mechanisms of the stress response in fish.

In tambaqui (*C. macropomum*), Pessoa *et al.* (2020) identified five distinct *Aeromonas* species with varying virulence profiles, suggesting differences in the pathogenic behavior of the strains during the infectious process. Among the *A. hydrophila* isolates, virulence genes such as β-hemol, ser, and lip were detected, responsible for encoding β-hemolysin, serine protease, and lipase, respectively. The expression of these genes was associated with the production of hemolytic enzymes (HEM), proteolytic activity (PROT), and lipolytic activity (LIP), indicating a high virulence potential and sanitary risk for tambaqui production.

Bacterial proteases play a fundamental role in nutrient sequestration and microbial proliferation, as well as in promoting damage to fish tissues, such as scale discoloration and mucosal degradation, and facilitating pathogen penetration. Similarly, lipase production contributes to the hydrolysis of lipids in the outermost cell layers, acting as an important virulence factor by causing lesions in the intestinal epithelium of fish (Beaz-Hidalgo; Figueras, 2013).

In addition to determining pathogenicity, virulence profiles directly influence a bacterium´s ability to survive and multiply under adverse environmental conditions. The horizontal dissemination of genetic material between bacteria, favored in aquaculture environments, constitutes an essential adaptive mechanism for the

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persistence of the genus *Aeromonas* and contributes to the emergence of multidrug-resistant microorganisms, increasing the challenges for disease control in fish farming (Pessoa *et al.,* 2019).

3.3. Antimicrobial resistance

Antimicrobials are the main therapeutic tools used globally for the treatment and prevention of bacterial diseases in aquaculture systems. However, the use of these drugs in aquaculture is dynamic and heterogeneously regulated across countries, with classes such as oxytetracyclines, florfenicol, quinolones, and sulfonamides among the most frequently reported in aquaculture systems. Projections also indicate an increase in global antimicrobial consumption in aquaculture until 2030, driven by the expansion of aquaculture production worldwide (Schar *et al.,* 2020).

Although various antimicrobials are used in different countries, authorizations for their use in aquaculture vary widely across countries, depending on local legislation. In Brazil, only two antimicrobials are authorized by the regulatory body for use in fish farming (oxytetracycline and florfenicol), reflecting a more restrictive regulatory framework and reinforcing the need for responsible management of antimicrobial use in aquaculture production (Rosario *et al.,* 2024).

Sebastião *et al.* (2022) isolated seven strains of *Aeromonas* spp. from asymptomatic tambaqui and reported 100% resistance to ampicillin, as well as 28% resistance to erythromycin and sulfonamide. The isolates also showed minimum inhibitory concentrations (MICs) above the tested ranges for amoxicillin, penicillin, novobiocin, tylosin tartrate, and clindamycin, with 85% of the strains demonstrating resistance to erythromycin. These findings reinforce the pattern of intrinsic resistance of the genus *Aeromonas* to β-lactam antibiotics, especially ampicillin.

Similar results were observed by Carriero *et al*. (2016) when evaluating the antimicrobial susceptibility profile of *A. dhakensis* against 15 antimicrobials. The authors reported resistance to ampicillin (MIC ≥ 32 µg/mL) and to the ampicillin/sulbactam combination (MIC ≥ 32 µg/mL), as well as resistance to cefoxitin (MIC ≥ 64 µg/mL) and meropenem (MIC ≥ 16 µg/mL). Despite this, the

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strains showed susceptibility to most of the antimicrobials tested, highlighting relevant variations in resistance profiles among species and strains of the genus.

Given this scenario, alternatives to the conventional use of antimicrobials have been extensively investigated. Assane *et al.* (2019) evaluated the in vitro activity and in vivo therapeutic efficacy of the combination of thiamphenicol and florfenicol against *A. hydrophila*, demonstrating that this combination was effective in controlling aeromonosis even at reduced doses, maintaining therapeutic performance similar to the isolated use of the drugs. These results indicate that combined therapies can help reduce antimicrobial use during outbreaks in fish farms.

Other promising approaches include the use of natural compounds. Sutili *et al.* (2015) and Bandeira-Júnior *et al.* (2021) highlighted the potential of essential oils and the combination of florfenicol with linalool as therapeutic alternatives in the treatment of aeromonosis, showing positive effects on the survival and response of infected fish.

In addition to therapeutic strategies, host immunological mechanisms also play a relevant role in infection control. Marques *et al.* (2016) evaluated the serum lectin response in tambaqui challenged with Aeromonas spp. and observed that this component of the innate immune system responds differently to infection by different bacterial species. Lectins exhibit antimicrobial activity by recognizing carbohydrates expressed on the surface of pathogens, acting as opsonin's and stimulating processes such as phagocytosis and microbial lysis, reinforcing their potential as a complementary tool in fish farming sanitary management.

4. Final considerations

Based on the studies analyzed, it is observed that *A. hydrophila* is the species most frequently associated with infections in farmed fish in Brazil, and consequently, the most scientifically investigated. The widespread distribution of this pathogen, coupled with its diverse virulence factors and the increasing reports of antimicrobial resistance, reinforces its role as an emerging pathogen of importance to aquaculture and public health.

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This systematic review revealed a significant lack of national studies on the occurrence, diversity, virulence, and antimicrobial resistance of Aeromonas spp. in farmed fish, especially considering the rapid growth of Brazilian fish farming. This scientific gap limits the understanding of the health risks associated with aquaculture production and hinders the development of effective disease prevention and control strategies.

Therefore, it is essential to encourage integrated research that addresses the ecology, pathogenicity, and resistance profiles of *Aeromonas* spp., as well as the development and validation of alternatives to the indiscriminate use of antimicrobials, such as combination therapies, natural compounds, and strategies to strengthen fish immune responses. Such approaches are essential for the sustainability of national fish farming and for mitigating the risks associated with the spread of resistant bacteria in the aquatic environment.

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