



Review Article

Aeromonas veronii as an emerging pathogen of aquatic animals: Ecology, genomics, virulence, host–pathogen interactions, antimicrobial resistance, and sustainable control strategies

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Abstract

Aeromonas veronii is a Gram-negative, motile bacterium widely distributed in aquatic environments and increasingly recognized as an important pathogen of freshwater fish and an opportunistic pathogen of humans. In aquaculture, infections caused by *A. veronii* are associated with septicaemia, ulcerative lesions, systemic disease, and mortality, particularly under intensive culture conditions and environmental stress. Its pathogenicity is multifactorial and involves a diverse range of mechanisms, including adhesion, motility, biofilm formation, quorum sensing, iron acquisition, secretion systems, toxin production, and modulation of host immune responses. Advances in genomic research have revealed substantial genetic diversity within *A. veronii*, with variation in virulence-associated traits and antimicrobial-resistance determinants among isolates from different hosts and geographical regions. Antimicrobial resistance is an increasing concern, particularly in aquaculture systems where antimicrobial use may promote the selection and dissemination of resistant strains. The persistence of *A. veronii* in aquatic environments, its capacity to acquire adaptive traits, and its ability to infect diverse hosts further increase its epidemiological and veterinary significance. Accurate identification is essential because phenotypic characteristics may overlap among closely related *Aeromonas* species, highlighting the importance of molecular and genomic approaches for reliable characterization. This review provides an integrated overview of the ecology, epidemiology, taxonomy, genomic characteristics, virulence mechanisms, host–pathogen interactions, disease manifestations, antimicrobial resistance, molecular diagnostics, and current control strategies associated with *A. veronii*. Particular attention is given to emerging and sustainable approaches, including vaccination, probiotics, immunostimulants, bacteriophages, phytochemicals, functional feeds, anti-biofilm strategies, and anti-virulence interventions. The review further examines the implications of *A. veronii* from a One Health perspective and identifies key knowledge gaps and research priorities for improved disease surveillance, antimicrobial stewardship, and sustainable management of infections in aquaculture.

Keywords: *Aeromonas veronii*; aquaculture; aquatic animal health; virulence factors; antimicrobial resistance; genomics; host–pathogen interactions; molecular diagnostics; sustainable disease control; One Health

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Introduction

The genus *Aeromonas* comprises Gram-negative, facultatively anaerobic bacteria that are widely distributed in freshwater and other aquatic environments. Members of the genus are increasingly recognized as important bacterial pathogens in aquaculture, where infections can result in septicemia, ulcerative lesions, tissue damage, and mortality in susceptible fish. Motile *Aeromonas* species, including *Aeromonas hydrophila*, *A. veronii*, *A. caviae*, *A. jandaei*, *A. sobria*, *A. bestiarum*, *A. dhakensis*, and *A. schubertii*, have been associated with disease outbreaks in cultured fish and other aquatic animals (Dien *et al.*, 2023). The widespread occurrence of these bacteria in aquatic environments, together with their capacity to persist under diverse environmental conditions, makes motile *Aeromonas* infections an important constraint to the health and productivity of aquaculture systems. Among the motile *Aeromonas* species, *A. veronii* has emerged as an important pathogen because of its broad ecological distribution, diverse host range, and capacity to cause severe disease. The bacterium occurs predominantly in aquatic environments and has been recovered from freshwater habitats, fish farms, aquatic animals, and other environmental sources. In fish, *A. veronii* has been associated with septicemia, haemorrhagic lesions, ulceration, and systemic disease, with infections reported in several economically important species. Its pathogenic importance is not restricted

to aquaculture, as the organism has also been associated with human gastrointestinal and extraintestinal infections, making it relevant to both veterinary and public health (Liu *et al.*, 2022; Maia *et al.*, 2023).

The ecological versatility of *A. veronii* is particularly important for understanding its epidemiology. Aquaculture systems provide multiple opportunities for bacterial persistence and transmission because fish, water, sediment, organic matter, and equipment can act as interconnected components of the microbial environment. Temperature changes, water quality, stocking density, nutrition, and host physiological condition may influence the ability of opportunistic bacteria to colonize and infect susceptible fish. Consequently, disease caused by *A. veronii* should be considered as the outcome of interactions among the pathogen, host and environment rather than simply the presence of the bacterium in culture water (Dien *et al.*, 2023). Recent investigations of aquaculture-associated isolates have further demonstrated that pathogenic *A. veronii* can be recovered from both diseased fish and surrounding production environments, emphasizing the importance of environmental surveillance.

The pathogenicity of *A. veronii* is multifactorial and depends on a complex collection of bacterial attributes that facilitate attachment, colonization, tissue invasion, and persistence within the host. Important virulence-associated characteristics include motility, adhesion, biofilm formation, secretion

systems, extracellular enzymes, hemolysins, aerolysin, cytotoxic proteins, iron-acquisition systems, and mechanisms involved in evasion or modulation of host immune responses. Experimental studies in fish have demonstrated the presence of multiple virulence genes, including genes associated with hemolysins, aerolysin, proteases, adhesins, and other pathogenicity-related functions (Youssef *et al.*, 2023). The simultaneous occurrence of several virulence determinants suggests that disease severity may arise from the combined activity of multiple bacterial systems rather than from an individual toxin or gene.

Comparative genomic investigations have provided further evidence for substantial variation in the virulence potential of *A. veronii*. Analysis of 41 genomes identified numerous genes associated with adhesion, secretion, iron acquisition, immune evasion, antiphagocytosis and toxin production. Conserved components of type I and type II secretion systems, type IV pili, and flagellar systems were identified across the analyzed genomes. In contrast, type III, type V and type VI secretion systems displayed greater variability (Tekedar *et al.*, 2019). Genome sequencing of fish-associated strains has similarly identified genes encoding aerolysin, RtxA, secretion systems, adherence and motility, together with several antimicrobial-resistance determinants (Das *et al.*, 2021). These findings indicate that differences in the genetic composition of

individual isolates may contribute to variation in pathogenicity and disease outcome.

Genomic diversity within *A. veronii* is also evident from comparative analyses of strains originating from different hosts and geographical locations. Song *et al.* (2021) analyzed 39 *A. veronii* strains from diverse sources and identified a conserved core genome containing 1,993 genes, while also demonstrating differences in virulence-associated characteristics among strains. Importantly, the study found no clear relationship between genetic relatedness and geographical isolation site, whereas some associations were observed between host source and virulence-factor distribution (Song *et al.*, 2021). These observations suggest that host-associated selection and genetic adaptation may contribute to the diversification of *A. veronii* populations.

Human-associated *A. veronii* isolates provide additional evidence of the species' genomic diversity and pathogenic potential. Liu *et al.* (2022) analyzed newly sequenced strains obtained from patients with gastrointestinal disease together with globally available genomes. Numerous putative virulence factors were identified, including aerolysin, microbial collagenase, and multiple hemolysins. The study also identified a type III secretion system located within a genomic island and provided evidence that this region may have been acquired through horizontal gene transfer from other *Aeromonas* species (Liu *et al.*, 2022). Such findings demonstrate that

horizontal acquisition of genetic material may contribute to the evolution of virulence-associated traits within the species.

The expanding availability of whole-genome data has also revealed important challenges in the taxonomic identification of *A. veronii*. Closely related *Aeromonas* species may share phenotypic and biochemical characteristics, potentially resulting in inaccurate species assignments when identification relies exclusively on conventional methods. Comparative genomic analysis of isolates from fish, environmental sources, and humans demonstrated that some genomes deposited in public databases as *A. veronii* were subsequently considered misclassified based on genome-level comparisons. The use of average nucleotide identity and other genomic approaches was therefore recommended for more reliable species-level assignment (Maia *et al.*, 2023). Antimicrobial resistance represents another major challenge associated with *A. veronii*. The use of antimicrobial agents in intensive aquaculture can impose selection pressure on bacterial populations, potentially favoring resistant strains and facilitating the persistence of resistance determinants within aquatic production systems. Genomic studies have identified resistance mechanisms involving antibiotic efflux, enzymatic inactivation, and modification of antimicrobial targets in *A. veronii* (Tekedar *et al.*, 2019). Genome sequencing of fish-pathogenic *A. veronii* strains has similarly identified

genes associated with antibiotic inactivation, target-site alteration, and efflux mechanisms, together with multiple virulence-associated systems.

The One Health relevance of *A. veronii* has become increasingly apparent as resistance and virulence determinants have been detected among isolates from aquatic animals, environmental sources and humans. Maia *et al.* (2023) identified extensive virulence-associated and resistance-associated gene repertoires among globally distributed genomes, including determinants associated with clinically important resistance mechanisms. The coexistence of these characteristics in isolates from different ecological sources emphasizes the possibility of transmission and genetic exchange across environmental, animal, and human compartments.

Disease management has traditionally relied heavily on antimicrobial therapy; however, increasing antimicrobial resistance and concerns regarding antimicrobial residues have stimulated interest in alternative control approaches. Vaccination has been investigated as a preventive strategy, with studies examining virulence-associated antigens and both live and inactivated vaccine approaches against *A. veronii* in important cultured fish such as Nile tilapia (Youssef *et al.*, 2023). In parallel, non-antibiotic approaches including probiotics, immunostimulants, functional feeds, bacteriophages and other biological interventions are receiving increasing attention as

components of sustainable aquaculture disease management (Dien *et al.*, 2023). Natural products and phytochemicals also represent promising areas for future intervention because they may provide antibacterial, antibiofilm, or immunomodulatory effects while reducing dependence on conventional antibiotics. However, evidence for many alternative approaches remains heterogeneous, and differences in experimental design, pathogen strain, fish species, treatment dose, and route of administration make direct comparison difficult. Therefore, future research should move beyond simple in vitro inhibition studies and establish the efficacy, safety, pharmacokinetics, and reproducibility of promising interventions under controlled and farm-level conditions.

Despite substantial progress in understanding *A. veronii*, important questions remain concerning the relationships among environmental persistence, genomic variation, virulence expression, host susceptibility, and antimicrobial resistance. The mechanisms by which environmental stressors influence virulence and transmission require further investigation, while the contribution of mobile genetic elements to dissemination of resistance and virulence determinants warrants greater genomic and epidemiological attention. Therefore, a comprehensive understanding of *A. veronii* requires integration of microbiology, genomics, molecular epidemiology, pathology, immunology, antimicrobial-resistance

research, and aquaculture management. The present review examines these interconnected aspects, with particular emphasis on ecology and epidemiology, genomic diversity, virulence mechanisms, host–pathogen interactions, disease development, antimicrobial resistance, molecular diagnostics and emerging control strategies.

Taxonomy, nomenclature and biological characteristics of *Aeromonas veronii*

Aeromonas veronii belongs to the genus *Aeromonas*, family Aeromonadaceae, order Aeromonadales and class Gammaproteobacteria. The species was formally described by Hickman-Brenner *et al.* (1987) as a new ornithine decarboxylase-positive *Aeromonas* species that may cause diarrhoea. The type strain is ATCC 35624 (Hickman-Brenner *et al.*, 1987). Current taxonomic databases place the species within the lineage Bacteria–Pseudomonadota–Gammaproteobacteria–Aeromonadales–Aeromonadaceae–*Aeromonas*–*A. Veronii* (Schoch *et al.*, 2020). The taxonomic history of *A. veronii* has been complicated by the use of different names and phenotypic groupings. Historically, isolates now assigned to *A. veronii* were associated with hybridization groups and phenotypically defined taxa. Subsequent DNA–DNA hybridization and molecular studies demonstrated that *Aeromonas ichthiosmia* is conspecific with *A. veronii*, while other historical names have also been associated with

closely related taxonomic groups (Huys *et al.*, 2001). These historical designations remain relevant when interpreting older literature and sequence databases because publications may describe organisms now recognized as *A. veronii* under earlier taxonomic names.

A. veronii has traditionally been divided phenotypically into two biovars, biovar *veronii* and biovar *sobria*. The two biovars have historically been differentiated using biochemical characteristics, although their close genetic relationship makes discrimination based solely on conventional phenotypic methods difficult (Janda and Abbott, 2010). The difficulty in distinguishing closely related *Aeromonas* species has important implications for epidemiological and clinical studies. Conventional biochemical identification systems may incorrectly assign uncommon *Aeromonas* species to more frequently encountered taxa, particularly within closely related groups. Consequently, molecular methods have increasingly become important for reliable species-level identification. The application of genomic approaches has provided substantially improved resolution of *A. veronii* taxonomy. Whole-genome comparisons, particularly average nucleotide identity (ANI), can distinguish closely related species more accurately than phenotypic characteristics alone. Maia *et al.* (2023) demonstrated that several genomes previously assigned to *A. veronii* were incorrectly classified when reassessed

using genome-level comparisons, emphasizing the importance of ANI and related approaches.

Morphologically, *A. veronii* is a Gram-negative, rod-shaped bacterium that generally occurs as individual cells or short arrangements. The organism is typically motile through polar or lateral flagellar structures and is capable of growth under both aerobic and facultatively anaerobic conditions. Like other members of the genus, it is non-spore-forming and possesses a Gram-negative cell envelope consisting of an inner cytoplasmic membrane, periplasmic space, and outer membrane. The organism displays physiological characteristics that contribute to its ecological versatility. *A. veronii* can occur in freshwater environments and has been isolated from water, sediment, aquatic animals, and aquaculture-associated environments. Its ability to survive outside the host is particularly important because environmental populations can serve as reservoirs from which susceptible fish may become exposed.

A notable biological characteristic of *A. veronii* is its ability to express multiple surface-associated structures involved in motility and host colonization. Flagella contribute not only to movement but also to chemotaxis, attachment, and biofilm development. Comparative genomic studies have identified conserved genes associated with flagellar assembly and type IV pili among numerous *A. veronii* genomes, supporting the importance of these systems in species biology.

Another important characteristic is the capacity of *A. veronii* to form biofilms. Biofilm formation enables bacterial populations to establish structured communities attached to biotic or abiotic surfaces and can enhance persistence under unfavorable environmental conditions. In aquaculture systems, biofilm-associated populations may occur on tank surfaces, equipment, sediments, and other interfaces, potentially contributing to environmental persistence and recurrent exposure of fish. At the genomic level, *A. veronii* exhibits considerable diversity. Comparative analysis of 41 genomes demonstrated an open pangenome consisting of a conserved core genome together with a large accessory genome containing genes that vary among strains (Tekedar *et al.*, 2019). This genomic architecture provides a potential basis for differences in environmental adaptation, host association, virulence, and antimicrobial resistance.

The genome of *A. veronii* therefore represents more than a static collection of species-specific genes; rather, it reflects an adaptable bacterial population capable of maintaining conserved biological functions while acquiring variable traits. Genes associated with secretion, adhesion, motility, iron acquisition, toxin production, and antimicrobial resistance may occur within different genomic backgrounds, resulting in considerable phenotypic variation between isolates (Tekedar *et al.*, 2019; Maia *et al.*, 2023). Overall, the taxonomy and biology of *A.*

veronii demonstrate why accurate species identification is essential for understanding its epidemiology and pathogenicity. Its historical nomenclatural complexity, phenotypic similarity to related *Aeromonas* species, extensive genomic diversity, and ability to persist in aquatic environments collectively complicate conventional characterization.

Ecology, environmental reservoirs and epidemiology

Aeromonas veronii is an environmentally versatile bacterium that is particularly associated with freshwater ecosystems and aquatic production systems. Unlike pathogens that depend primarily on a specific host for persistence, *A. veronii* can occur within the surrounding aquatic environment and subsequently colonize fish and other aquatic animals. This environmental lifestyle is important epidemiologically because water can function simultaneously as a reservoir, transmission medium, and selective environment for the organism. Global genomic analyses have confirmed that *A. veronii* isolates originate from diverse sources, including aquatic animals, environmental samples and humans, supporting the ecological flexibility of the species (Liu *et al.*, 2022).

Aquatic reservoirs and environmental persistence

Freshwater bodies, aquaculture ponds, rearing water and sediments represent important environmental reservoirs of *A.*

veronii. The organism has been recovered not only from diseased fish but also from apparently healthy aquatic systems, demonstrating that environmental detection does not necessarily indicate an active disease outbreak. A study from the Poyang Lake aquaculture region of China examined 46 *A. veronii* isolates collected from diseased fish, aquaculture water, and pond sediment during 2016–2020. The isolates represented 36 ERIC-PCR genotypes, demonstrating substantial genetic diversity rather than the dominance of a single epidemic clone. Differences in virulence-associated gene distribution between environmental and clinical isolates further suggested that environmental populations may constitute a diverse reservoir from which pathogenic variants can emerge. The persistence of *A. veronii* within aquaculture systems is further supported by its detection across different components of production environments. In the Poyang Lake investigation, isolates were obtained from aquaculture water and pond sediment as well as multiple freshwater fish species, including grass carp, silver carp, bighead carp, and Pengze crucian carp. Such findings emphasize that the epidemiology of *A. veronii* should not be considered solely as a fish-to-fish transmission process; rather, it involves continuous interaction among fish hosts, water, sediments, and management practices (Xu *et al.*, 2022).

Association with aquaculture systems

The importance of *A. veronii* has increased with the expansion and intensification of freshwater aquaculture. High stocking densities, accumulation of organic matter, deterioration of water quality, handling stress, and other husbandry-related pressures can increase the opportunity for opportunistic bacteria to colonize susceptible fish. In India, a pathogenic *A. veronii* strain was isolated from diseased *Labeo rohita*, and experimental challenge reproduced clinical manifestations similar to those observed during natural infection (Tyagi *et al.*, 2022). The complete genome of the strain also contained multiple virulence-associated and antimicrobial-resistance-related determinants. An investigation of commercial rainbow trout farms in southeastern Anatolia, Türkiye, demonstrated considerable spatial variation in *A. veronii* detection and highlighted the importance of reliable species-level identification (Filiz, 2023). More recently, an epidemiological survey of farmed largemouth bass in major aquaculture regions of China identified *A. veronii* among important bacterial isolates recovered from diseased fish. Twenty-three of 39 bacterial isolates were identified as *A. veronii*, while multilocus sequence typing revealed 13 sequence types, including 12 previously unreported sequence types (Chen *et al.*, 2024).

Geographical distribution and regional diversity

The epidemiology of *A. veronii* is geographically heterogeneous. Although the species is broadly distributed, individual aquaculture regions may contain distinct genetic populations shaped by host composition, environmental conditions, animal movement, water connectivity and antimicrobial exposure. Movement of fish and fish seed may contribute to dissemination. In regions where fry, fingerlings or broodstock are transferred between farms, bacteria associated with fish surfaces, intestinal contents or transport water can potentially be introduced into new production units. Environmental disturbances may also facilitate bacterial redistribution. Recent evidence has also expanded the recognized geographical and ecological range of *A. veronii* to marine aquaculture environments. A 2025 report documented an outbreak associated with farmed European seabass in the Ionian Sea region, demonstrating that suitable ecological and host conditions can permit disease emergence beyond traditional freshwater systems.

Environmental and epidemiological drivers

The epidemiology of *A. veronii* is influenced by the interaction of environmental reservoirs, host susceptibility and aquaculture management. Factors that increase organic loading or microbial abundance can create favorable conditions for *Aeromonas* proliferation, while

physiological stress may compromise host barriers and immunity. Temperature fluctuations, poor water quality, crowding, nutritional imbalance, transportation and handling are therefore relevant factors when assessing the risk of disease associated with *A. veronii*. Importantly, environmental abundance and pathogenicity are not necessarily equivalent. Environmental and clinical isolates may differ in their frequency of virulence-associated genes and antimicrobial-resistance determinants, suggesting that environmental populations can act as reservoirs of adaptive traits even when they do not exhibit the same virulence profile as clinical isolates.

Transmission pathways

Transmission of *A. veronii* in aquatic production systems is likely multifactorial. Waterborne exposure represents an important route because fish are continuously exposed through their skin, gills and gastrointestinal tract. Direct contact between infected and susceptible fish can further facilitate transmission, particularly in densely stocked systems. Contaminated equipment, transport water, sediments and movement of infected or carrier animals may also contribute to dissemination between production units. The ability of *A. veronii* to occur simultaneously in environmental compartments and aquatic hosts creates a potentially self-sustaining transmission cycle. Fish may shed bacteria into the surrounding environment, where the organism can

persist and subsequently encounter new hosts.

Epidemiological significance

Taken together, current evidence indicates that *A. veronii* should be regarded as an environmentally persistent and epidemiologically dynamic pathogen rather than a bacterium restricted to individual disease outbreaks. Its occurrence in water, sediments and diverse aquatic hosts provides multiple opportunities for persistence and transmission, while genetic diversity allows different populations to acquire or maintain

distinct combinations of virulence and antimicrobial-resistance determinants (Liu *et al.*, 2022).

From an aquaculture perspective, disease prevention therefore requires more than treatment of clinically affected fish. Routine monitoring of water and sediment, appropriate stocking density, quarantine of introduced animals, biosecurity, management of organic loading and responsible antimicrobial use are important components of reducing the ecological opportunities available to *A. veronii* (Table 1; Fig. 1).

Table 1: Ecological reservoirs, geographical occurrence, host associations and epidemiological characteristics of *Aeromonas veronii*

Region/setting	Host or environmental source	Major observation	Epidemiological significance	Reference
Poyang Lake, China	Diseased fish, aquaculture water and pond sediment	46 isolates representing 36 ERIC-PCR genotypes	Demonstrates substantial environmental and clinical genetic diversity	Xu et al. (2022)
Poyang Lake, China	Grass carp, silver carp, bighead carp and Pengze crucian carp	Association with freshwater aquaculture	Broad host association within intensive freshwater production	Xu et al. (2022)
India	Diseased <i>Labeo rohita</i>	Pathogenic strain isolated and experimentally confirmed	Demonstrates pathogenic potential in an important Indian carp	Tyagi et al. (2022)
Türkiye	Commercial rainbow trout farms	Detection varied among farms	Indicates spatial heterogeneity	Filiz (2023)
China	Farmed largemouth bass	23 <i>A. veronii</i> strains among 39 bacterial isolates; 13 sequence types	Indicates regional genetic diversity	Chen et al. (2024)
Shrimp aquaculture	Rearing water and shrimp gut	Outbreak-associated <i>A. veronii</i> abundance monitored quantitatively	Supports environmental surveillance and predictive risk assessment	2024 study
Ionian Sea, Greece	Farmed European seabass	Regional outbreak associated with <i>A. veronii</i>	Demonstrates emergence beyond traditional freshwater aquaculture	2025 study
Global	Aquatic animals, environmental sources and humans	Genomes from multiple ecological sources	Supports broad ecological adaptability	Liu et al. (2022)

The bacterium persists in aquatic environments, sediments, organic matter, biofilms, and aquaculture infrastructure and can subsequently colonize susceptible aquatic animals. Fish may acquire infection through waterborne exposure, damaged epithelial surfaces, gills or the gastrointestinal tract. Infected animals can release bacteria back into the environment, allowing continued

transmission and environmental persistence. Movement of fish, contaminated equipment, water, and farm effluents may facilitate dissemination between production systems and surrounding ecosystems.

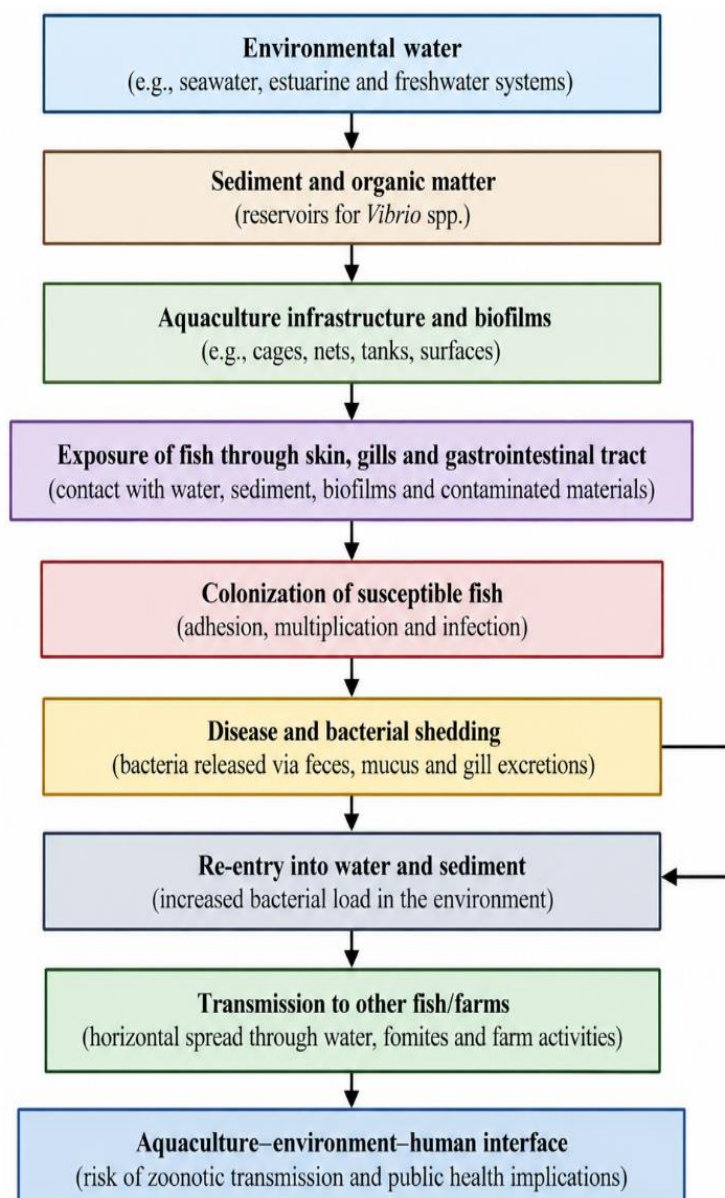


Figure 1: Ecology, environmental reservoirs and transmission cycle of *Aeromonas veronii*.

Host range and disease spectrum

Aeromonas veronii has a broad host range and has been recovered from numerous freshwater and marine-associated aquatic animals, as well as from humans. Its importance in aquaculture is largely related to its ability to infect economically important fish species belonging to different taxonomic groups. Disease expression can range from localized skin lesions and ulceration to systemic septicaemia and extensive mortality. The outcome of infection depends on the bacterial strain, infectious dose, host species, developmental stage, environmental conditions, and physiological status of the host.

Fish hosts

Fish represent the most extensively documented aquatic hosts of *A. veronii*. The bacterium has been associated with disease in carps, tilapia, catfish, ornamental fish, and several marine or euryhaline species. Important freshwater hosts include *Labeo rohita*, *Oreochromis niloticus*, *Oreochromis mossambicus*, *Channa punctata*, *Pelteobagrus fulvidraco*, *Cyprinus carpio* and *Odontobutis potamophila*. In Indian aquaculture, *A. veronii* has been repeatedly associated with disease in major cultured fish. Tyagi *et al.* (2022) isolated a pathogenic strain from diseased *Labeo rohita* and demonstrated its pathogenicity experimentally. More recent Indian research demonstrated the occurrence of *A. veronii* in naturally infected *Channa punctata*. Diseased fish displayed a bacterial septicaemic

syndrome characterized by ulcerative lesions and mortality, and both *A. veronii* and *A. hydrophila* were identified from naturally infected fish (Das *et al.*, 2023).

A. veronii has also been associated with disease in tilapia. Coinfection involving *A. veronii* and viral pathogens illustrates how bacterial disease can be amplified when fish are already compromised by other infectious agents. Recent work in cultured *Oreochromis niloticus* further demonstrates the epidemiological importance of the species. Fadel *et al.* (2025) reported *A. veronii* infection in Nile tilapia farms, with substantial prevalence and mortality and clinical signs including erratic swimming, skin haemorrhages, and corneal opacity. The host spectrum extends to scaleless freshwater fish such as yellow catfish (*Pelteobagrus fulvidraco*), an economically important cultured species in China. Infection with *A. veronii* has been associated with motile *Aeromonas* septicaemia and ulcerative disease.

Carp and ornamental fish

Carp species represent another important host group. *A. veronii* has been isolated from common carp and koi carp and may cause external ulceration, haemorrhage, abdominal distension and systemic disease. The occurrence of *A. veronii* in ornamental fish is epidemiologically important because international ornamental fish trade can facilitate movement of bacterial pathogens between geographic regions. Experimental studies have also demonstrated that isolates originating

from ornamental fish can infect economically important cultured species.

Marine and euryhaline fish

Although *A. veronii* is traditionally associated with freshwater environments, recent evidence demonstrates that its host range extends into marine and euryhaline aquaculture. An outbreak associated with farmed European seabass in the Ionian Sea demonstrated that environmental salinity does not necessarily prevent establishment of pathogenic *A. veronii* populations under suitable ecological and host conditions.

Disease manifestations

Clinical manifestations associated with *A. veronii* are highly variable. External signs commonly include skin haemorrhages, ulceration, fin erosion, scale loss, petechial lesions and abnormal swimming behaviour. As infection progresses, affected fish may develop abdominal distension, ascites, exophthalmia, anaemia and lethargy. Internal pathological changes may include hepatomegaly or hepatic degeneration, splenomegaly, renal lesions, intestinal inflammation and generalized congestion. The progression from localized infection to systemic disease reflects the invasive potential of pathogenic *A. veronii* strains. Once host epithelial barriers are compromised, bacteria can gain access to underlying tissues and subsequently disseminate through the bloodstream, resulting in septicaemia and multi-organ damage.

Coinfections and disease complexity

An important feature of *A. veronii* epidemiology is its occurrence in coinfections. Disease outbreaks in aquaculture rarely occur under completely controlled conditions, and infected fish may simultaneously harbour viruses, bacteria, parasites or fungi. Coinfection can increase disease severity by damaging epithelial barriers, suppressing immune responses or altering the host microbiota. Therefore, isolation of *A. veronii* from diseased fish should not automatically be interpreted as proof of a single-agent outbreak. Epidemiological investigations should consider other pathogens, environmental stressors and host-related factors.

Human infections and zoonotic relevance

The host range of *A. veronii* is not restricted to aquatic animals. The species is also recognized as an opportunistic human pathogen. Human infections are particularly associated with exposure to aquatic environments, contaminated food or water and damaged skin, although severe systemic infections can occur in susceptible individuals.

Clinical manifestations may include gastroenteritis, wound and soft-tissue infections, bacteraemia and sepsis. Severe infections have been reported particularly among immunocompromised individuals (Zhao *et al.*, 2024). Global genomic analyses have further strengthened the One Health relevance of *A. veronii*. Comparative analysis of worldwide genomes has identified isolates from

human gastrointestinal disease alongside strains from aquatic and environmental sources (Liu *et al.*, 2022).

Host susceptibility and disease outcome

Host susceptibility is determined by several interacting factors. Fish species, age, nutritional status, immune competence and physiological condition can influence disease severity. Environmental conditions such as temperature, ammonia, pH, dissolved oxygen, salinity and organic loading can further modify both bacterial growth and host resistance.

Consequently, *A. veronii* disease should be viewed as the outcome of a pathogen–host–environment interaction rather than simply the presence of the bacterium.

Overall host and disease spectrum

Available evidence demonstrates that *A. veronii* possesses a broad and expanding host range. Its disease spectrum extends from localized skin lesions and ulcerative disease to systemic septicaemia and mortality. The species has been reported in freshwater carp, tilapia, catfish and ornamental fish and, more recently, in marine farmed European seabass. Its ability to occur in coinfections and its recognized association with human disease further increase its epidemiological significance.

Genomics, pangenome and genetic diversity

The increasing availability of whole-genome sequences has substantially improved understanding of the biology, evolution and pathogenic potential of

Aeromonas veronii. Conventional phenotypic identification provides useful preliminary information, but genomic approaches have revealed considerable genetic diversity within the species and have identified differences in virulence-associated genes, antimicrobial-resistance determinants, mobile genetic elements and metabolic capabilities among isolates.

Expansion of whole-genome resources

The number of publicly available *A. veronii* genomes has increased rapidly during the last decade. Early genomic studies focused on individual strains associated with fish disease or human infection, whereas more recent studies have compared genomes originating from multiple hosts and geographical regions. Tekedar *et al.* (2019) compared 41 *A. veronii* genomes and identified a large pangenome containing approximately 8,710 genes, while the core genome consisted of approximately 2,855 genes. The predicted open nature of the pangenome indicated that additional genomes were likely to contribute previously unrecognized accessory genes. Song *et al.* (2021) subsequently performed comparative genomic analysis of 39 *A. veronii* strains from different sources. Their analysis identified 1,993 shared core genes and approximately 8,396 homologous protein groups. The relatively stable core genome was associated with fundamental biological functions, whereas accessory genomic variation contributed to differences among strains.

Pangenome architecture

The pangenome of a bacterial species consists of the complete collection of genes observed across its available genomes and can be divided broadly into core, accessory, and strain-specific components. The core genome contains genes conserved among most or all members of the species, whereas accessory genes may be present in only a subset of isolates. The large pangenome observed in *A. veronii* indicates substantial genomic plasticity. The open pangenome reported by Tekedar *et al.* (2019) suggests that sequencing additional isolates is likely to reveal further genetic diversity. Lawal *et al.* (2024) further demonstrated extensive gene-content variation among hundreds of publicly available *A. veronii* genomes and newly sequenced freshwater isolates. Their dataset contained a relatively small core genome compared with a very large accessory component.

Phylogenomic diversity

Whole-genome phylogenetic analysis has demonstrated that *A. veronii* is genetically diverse but does not exhibit a simple relationship between genetic lineage and geographical location. Song *et al.* (2021) reported that isolates from different sources could be closely related despite originating from geographically separated locations. Lawal *et al.* (2024) similarly demonstrated considerable global diversity among isolates collected from multiple countries and sources, including humans, animals, freshwater fish and aquatic environments.

Genomic evidence for taxonomic complexity

Genomic approaches have exposed problems associated with historical identification of *A. veronii*. Phenotypic characteristics within the genus *Aeromonas* can overlap considerably, and database-associated misidentification may occur when genomes are assigned using limited markers or incomplete taxonomic information. Maia *et al.* (2023) demonstrated that several genomes previously deposited as *A. veronii* were incorrectly assigned when reassessed using genome-level methods. This finding emphasizes the importance of accurate species assignment before comparative genomic analysis.

Genomic diversity among aquaculture-associated isolates

Aquaculture-associated *A. veronii* isolates show substantial genomic variation. Whole-genome studies have identified different combinations of virulence-associated genes, antimicrobial-resistance determinants, and mobile genetic elements among strains isolated from different fish species. Rahman *et al.* (2023) sequenced a multidrug-resistant *A. veronii* isolate recovered from ulcerative lesions of stinging catfish (*Heteropneustes fossilis*) during an outbreak in Bangladesh. Genome analysis was used to investigate virulence factors, antimicrobial-resistance genes, and phylogenetic relationships. A recent example comes from *Macrobrachium rosenbergii*. Zhou *et al.* (2026) characterized a pathogenic

A. veronii strain associated with mortality and identified a chromosome, plasmids, predicted virulence-associated genes, and antimicrobial-resistance determinants.

Mobile genetic elements and horizontal gene transfer

The accessory genome of *A. veronii* is influenced by mobile genetic elements, including plasmids, prophages, insertion sequences and other genomic regions capable of facilitating horizontal gene transfer. These elements can contribute to acquisition and dissemination of genes associated with antimicrobial resistance, virulence and environmental adaptation.

Horizontal gene transfer is particularly important from a One Health perspective because aquatic environments can contain diverse bacterial populations exposed to antimicrobial compounds and other selective pressures.

Biosynthetic and metabolic diversity

Genomic diversity in *A. veronii* extends beyond virulence and antimicrobial resistance. Accessory genes can encode metabolic pathways and biosynthetic gene clusters that allow individual strains to exploit different ecological niches. Lawal *et al.* (2024) identified unique biosynthetic gene clusters among environmental *A. veronii* isolates, indicating that environmental strains may possess specialized metabolic capabilities that are not uniformly distributed across the species.

Relationship between genomic diversity and virulence

One of the most important questions arising from comparative genomics is why some *A. veronii* strains cause severe disease while others remain environmental or opportunistic organisms. Current evidence indicates that virulence is not determined by a single genetic determinant. Instead, pathogenic potential reflects the combined presence, regulation, and interaction of multiple genes involved in motility, adhesion, secretion, toxin production, iron acquisition, biofilm formation, and host interaction. Importantly, the presence of a virulence gene does not necessarily demonstrate functional expression or clinical pathogenicity. Genomic prediction should therefore be complemented by phenotypic characterization, experimental infection studies and transcriptomic or proteomic approaches.

Genomics and one health surveillance

The genomic diversity of *A. veronii* has direct implications for One Health surveillance. The species has been recovered from humans, fish, aquatic environments, and other animals, while comparative genomic studies demonstrate that isolates from different ecological sources can occur within related phylogenetic groups. Maia *et al.* (2023) emphasized the global distribution of virulence and resistance genes across isolates from fish, environmental and human sources. Together, these findings support integrated genomic surveillance capable

of linking bacterial populations across environmental, animal and human compartments.

Future directions in A. veronii genomics

Future genomic research should move beyond simple genome sequencing toward integrated population genomics. Long-read sequencing could improve characterization of plasmids, repetitive regions and genomic islands, while hybrid assemblies may provide more complete representations of mobile genetic elements. Metagenomic approaches could additionally identify *A. veronii* populations directly from water, sediment and host-associated microbiomes without requiring culture. Combining WGS with transcriptomics, proteomics, metabolomics and experimental infection models would provide a more complete understanding of how genomic variation translates into differences in phenotype.

Overall, genomic evidence demonstrates that *A. veronii* is not a genetically uniform pathogen. Instead, it represents a highly diverse population characterized by a relatively conserved core genome and a large, variable accessory genome. This genomic plasticity provides the foundation for adaptation to different hosts and environments and may facilitate acquisition of virulence and antimicrobial-resistance traits.

Virulence factors and molecular pathogenesis

The pathogenicity of *Aeromonas veronii* is multifactorial and results from the

coordinated activity of several bacterial determinants rather than a single virulence factor. These determinants include surface structures involved in adhesion and motility, extracellular toxins and hydrolytic enzymes, iron-acquisition systems, secretion systems, biofilm-associated mechanisms, and regulatory networks. The relative contribution of individual factors varies among strains and hosts, consistent with the considerable genomic diversity observed within the species (Liu *et al.*, 2022; Maia *et al.*, 2023).

Adhesion and initial colonization

Adhesion is an essential early stage of *A. veronii* infection because successful colonization requires attachment to host epithelial surfaces before tissue invasion and systemic dissemination. The bacterium possesses multiple surface-associated structures that contribute to attachment, including polar and lateral flagella, type IV pili, mannose-sensitive haemagglutinin-associated pili and outer-membrane-associated adhesins. Flagella have traditionally been considered primarily motility structures; however, increasing evidence indicates that they also contribute to adhesion, biofilm formation and host colonization. The coordinated activity of motility and adhesion allows *A. veronii* to reach favourable host surfaces and maintain contact with epithelial tissues. Genetic studies of the *mshK* gene demonstrated that disruption of this component reduced swimming ability, biofilm formation, and pilus-associated phenotypes, while also reducing

virulence. These findings support an important role for MSHA-associated structures in pathogenicity.

The type III secretion system also contributes to colonization. Tang *et al.* (2024) demonstrated that deletion of *ascR*, an export-apparatus component of the T3SS, altered biofilm formation, swimming motility, and host colonization and reduced virulence.

Motility and chemotaxis

Motility is an important component of the infectious process because it allows bacteria to move through the aquatic environment and toward host surfaces. *A. veronii* possesses polar flagella that support swimming motility and may also produce lateral flagella under particular environmental conditions. Flagellar structures contribute to more than movement. They can influence adhesion, biofilm formation, surface colonization, and interactions with host immune components. Consequently, disruption of flagellar assembly can produce pleiotropic effects on bacterial pathogenicity. The ferric uptake regulator Fur provides an important example of this regulatory connection. In *A. veronii* TH0426, deletion of *fur* affected polar flagellar assembly and reduced biofilm formation. The mutant also exhibited reduced pathogenicity, demonstrating that iron regulation can influence motility and virulence simultaneously (Gong *et al.*, 2024). Similarly, the QseC sensor of the QseBC two-component regulatory system influences chemotaxis, motility, biofilm formation, and virulence. Deletion of

qseC reduced swimming motility and flagellar expression and attenuated cytotoxicity and virulence in experimental models (Luo *et al.*, 2024).

Toxins and cytotoxic factors

Toxin production represents another major component of *A. veronii* pathogenicity. The species produces several extracellular toxins and enzymes capable of damaging host cells and tissues. Among the best characterized are aerolysin, haemolysins, cytotoxic enterotoxins and extracellular proteases.

Aerolysin

Aerolysin is a pore-forming toxin encoded by the *aerA* gene and is one of the most widely investigated virulence-associated determinants in *Aeromonas*. The toxin interacts with susceptible host-cell membranes and forms transmembrane pores, resulting in cellular damage and lysis. Liu *et al.* (2022) identified aerolysin among the virulence-associated determinants of human gastrointestinal isolates, demonstrating the widespread distribution of this determinant among clinically relevant strains. However, the presence of *aerA* alone should not be interpreted as proof of high virulence. Disease severity depends on the combined action of multiple determinants and their expression under particular host and environmental conditions.

Haemolysins

Haemolysins are membrane-damaging toxins that can contribute to erythrocyte

destruction and tissue injury. Genes encoding haemolytic activity, including *hly* and related determinants, have been detected in pathogenic *A. veronii* isolates. Recent studies of fish-associated isolates demonstrate considerable variation in virulence-gene profiles, reinforcing the concept that *A. veronii* pathogenicity is strain-dependent.

Extracellular enzymes

A. veronii produces a range of extracellular hydrolytic enzymes that can facilitate tissue invasion and nutrient acquisition. These include proteases, lipases, phospholipases, collagenases, and other degradative enzymes. Proteases can degrade host proteins and extracellular matrix components, weaken tissue barriers and facilitate bacterial dissemination. Collagenases may contribute to degradation of connective tissue, while lipases and phospholipases can interfere with cellular membranes and provide access to nutrients. Genomic characterization has revealed widespread occurrence of protease and enzyme-associated genes among *A. veronii* isolates (Maia *et al.*, 2023).

Secretion systems

Secretion systems are central to *A. veronii* pathogenesis because they enable bacteria to export enzymes and toxins or deliver effector proteins directly into host or neighbouring cells. Genomic studies have identified multiple secretion systems in *A. veronii*, including type I, type II, type III, type

IV, and type VI systems. The type II secretion system is particularly important for extracellular release of enzymes and toxins. The type III secretion system is especially important because it can deliver bacterial effector proteins directly into host cells. Tang *et al.* (2024) demonstrated that deletion of *ascR*, an essential T3SS export-apparatus component, markedly reduced bacterial colonization and increased the LD50 of the bacterium. Type VI secretion systems may additionally contribute to interbacterial competition and host interactions.

Iron acquisition

Iron is essential for bacterial growth but is strongly restricted within vertebrate hosts. Consequently, successful pathogens require mechanisms that enable them to obtain iron under conditions of nutritional immunity. *A. veronii* possesses several iron-acquisition mechanisms, including siderophore-associated systems and iron-regulatory pathways. The ferric uptake regulator Fur acts as a central transcriptional regulator of iron homeostasis and connects iron availability with other virulence-associated processes. The role of Fur extends beyond iron acquisition. In *A. veronii* TH0426, Fur influenced flagellar assembly and biofilm formation, while deletion of *fur* reduced pathogenicity (Gong *et al.*, 2024).

Biofilm-associated virulence

Biofilm formation provides *A. veronii* with an important survival strategy in

both environmental and host-associated settings. Within a biofilm, bacterial cells are embedded in an extracellular matrix that can improve persistence, promote cell-to-cell interactions and reduce susceptibility to environmental stress and antimicrobial exposure. Several virulence-associated structures contribute to biofilm formation. Flagella, pili, outer membrane proteins and regulatory systems can collectively influence the transition from free-living cells to surface-associated communities.

Quorum sensing and regulatory networks

The coordinated expression of virulence factors requires sophisticated regulatory mechanisms. Quorum sensing enables bacterial populations to respond to cell density through chemical signalling and regulate collective behaviours such as motility, biofilm formation, enzyme production and host interaction. The QseBC two-component regulatory system represents one important regulatory mechanism in *A. veronii*. Recent deletion studies demonstrated that QseC influences chemotaxis, swimming, biofilm formation, secretion-associated pathways, and virulence (Luo *et al.*, 2024). These findings illustrate an important principle of *A. veronii* pathogenesis: virulence determinants do not function independently. Instead, regulatory networks coordinate their

expression according to environmental signals, bacterial population density, and host-associated conditions.

Integrated molecular pathogenesis The molecular pathogenesis of *A. veronii* can therefore be conceptualized as a multistage process. The bacterium first encounters the host through contaminated water or direct contact and uses motility and chemotaxis to approach susceptible tissues. Surface structures such as flagella and pili facilitate adhesion and colonization. Biofilm formation may enhance persistence at epithelial or environmental surfaces. Following colonization, secretion systems and extracellular enzymes facilitate tissue interaction and invasion. Toxins such as aerolysin and haemolysins can damage host cells, while proteases and other hydrolytic enzymes contribute to tissue degradation. Iron-acquisition systems support bacterial multiplication under nutrient-limited host conditions. Regulatory systems such as Fur and QseBC coordinate these processes and allow the bacterium to adjust its phenotype according to environmental conditions. Consequently, virulence should be viewed as an interconnected network rather than a collection of independent genes (Table 2; Fig. 2).

Table 2. Major virulence determinants of *Aeromonas veronii* and their functional roles

Virulence determinant/system	Representative genes/components	Principal function	Contribution to pathogenesis
Polar flagella	<i>fla</i> -associated genes	Swimming motility and surface interaction	Host approach, colonization and dissemination
Lateral flagella	Lateral flagellar genes	Surface-associated motility	Colonization and biofilm development
Type IV pili/MSHA	<i>msh</i> genes including <i>mshK</i>	Adhesion, twitching and biofilm formation	Attachment and persistence
Aerolysin	<i>aerA</i>	Pore-forming cytotoxin	Membrane damage and cell lysis
Haemolysins	<i>hly</i> and related genes	Membrane damage	Haemolysis and tissue injury
Cytotoxic enterotoxin	<i>act</i>	Cytotoxic/enterotoxin activity	Cellular damage
Cytotoxic enterotoxins	<i>alt</i> , <i>ast</i>	Alteration of intestinal signalling	Enteric disease
Metalloprotease	<i>stcE</i> and protease-associated genes	Protein degradation	Tissue invasion
Collagenase	Collagenase-associated genes	Collagen degradation	Tissue destruction
Lipases/phospholipases	Lipase-associated genes	Lipid degradation	Membrane disruption
T2SS	T2SS-associated genes	Extracellular secretion	Release of enzymes and toxins
T3SS	<i>asc</i> genes	Effector delivery	Cytotoxicity and immune modulation
T6SS	T6SS-associated genes	Effector delivery/interbacterial competition	Host interaction and ecological fitness
Iron-acquisition systems	Siderophore/iron transport genes	Iron uptake	Growth and persistence
Fur	<i>fur</i>	Iron and virulence regulation	Controls motility, biofilm and pathogenicity
QseBC	<i>qseB/qseC</i>	Environmental signal regulation	Controls chemotaxis, motility and virulence
Biofilm matrix	Multiple components	Structured community formation	Persistence and tolerance
OMPs/adhesins	Multiple OMP-associated genes	Host attachment	Colonization and persistence

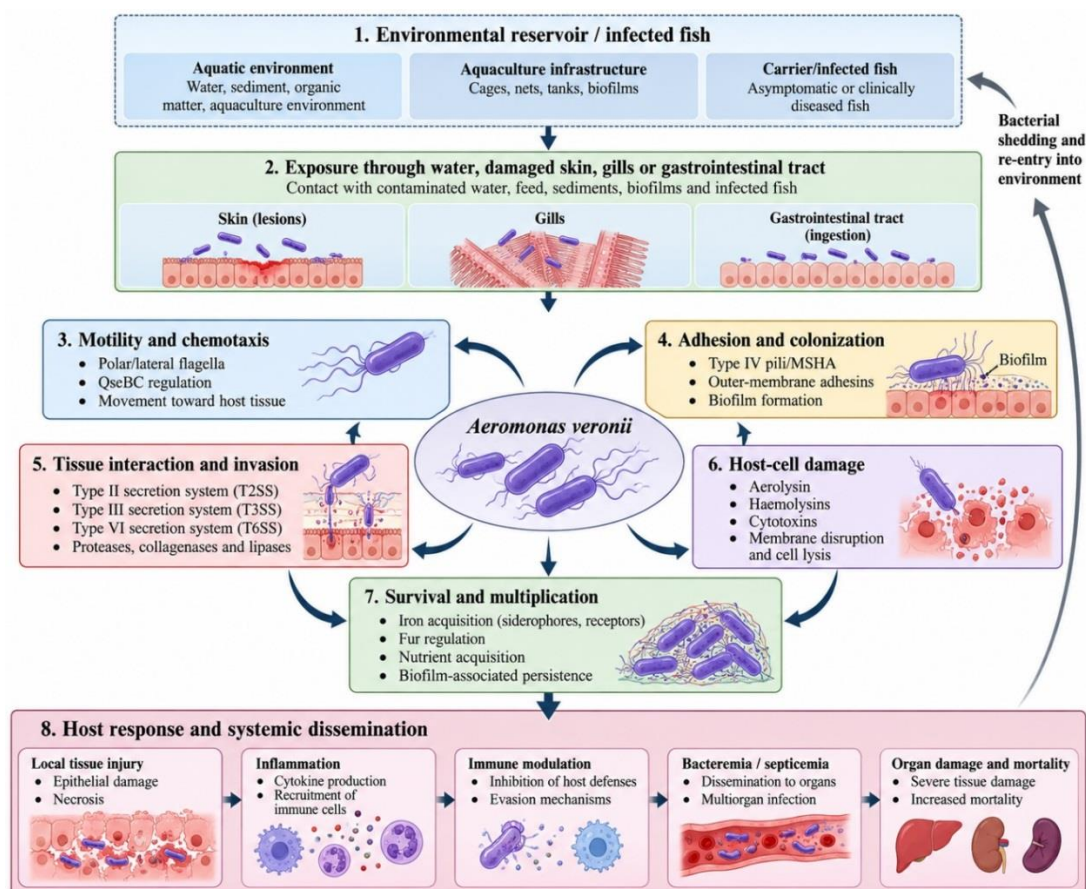


Figure 2: Integrated molecular pathogenesis of *Aeromonas veronii*.

Infection begins with environmental exposure followed by motility, chemotaxis, and adhesion to host surfaces. Flagella, type IV pili and outer-membrane-associated structures facilitate colonization and biofilm formation. Secretory systems, including T2SS, T3SS and T6SS, contribute to extracellular enzyme release, effector delivery and host interaction. Aerolysin, haemolysins, proteases, collagenases and other extracellular products promote cellular and tissue damage. Iron-acquisition systems and regulatory pathways such as Fur and QseBC support bacterial survival, persistence and coordinated expression of virulence-associated traits.

Host–pathogen interactions and immune responses

The outcome of *Aeromonas veronii* infection is determined by a dynamic interaction between bacterial virulence mechanisms and host defence responses. Following exposure, fish rely primarily on physical and chemical barriers, mucosal immunity and innate immune mechanisms to restrict bacterial colonization. When these barriers are compromised, *A. veronii* can invade tissues, multiply and disseminate systemically.

Mucosal barriers and the first line of defence

Fish are continuously exposed to microorganisms through the skin, gills

and gastrointestinal tract. Consequently, mucosal surfaces represent critical sites of host–pathogen interaction. The skin mucus contains lysozyme, complement components, antimicrobial peptides, lectins, immunoglobulins and other molecules capable of inhibiting bacterial attachment and growth. Experimental vaccination studies further demonstrate the importance of this compartment. Sukkarun *et al.* (2024) showed that immersion vaccination of red tilapia with a chitosan polymer-based nanovaccine against *A. veronii* enhanced specific IgM responses and bactericidal activity in serum and mucus.

Recognition of A. veronii by the innate immune system

Innate immune recognition represents an early response to *A. veronii*. Conserved bacterial components such as lipopolysaccharide, flagellar proteins and other pathogen-associated molecular patterns can be detected by host pattern-recognition receptors. NOD1, lipopolysaccharide-binding protein, natural killer-lysin and IL-1 β participate in early responses to bacterial infection, with changes observed across spleen, liver, gills and intestine.

Inflammatory responses

Inflammation is a central component of the host response to *A. veronii*. Following recognition of bacterial components, inflammatory signalling stimulates production of cytokines and chemokines that recruit leukocytes and activate antimicrobial mechanisms. Early cytokine activation can help

restrict bacterial growth, but excessive or prolonged inflammation may contribute to tissue damage.

Complement system

The complement system represents an important component of innate immunity in teleost fish. Complement proteins can recognize and opsonize pathogens, promote phagocytosis and contribute to direct bacterial killing. Vaccination studies provide functional evidence for the importance of complement-associated protection. Red tilapia receiving a chitosan-based *A. veronii* nanovaccine exhibited increased alternative complement pathway activity together with increased lysozyme activity and specific antibody responses (Sukkarun *et al.*, 2024).

Phagocytosis and cellular defence

Phagocytic cells such as macrophages and neutrophil-like granulocytes are essential for controlling bacterial infections in fish. These cells recognize, engulf and destroy invading bacteria. Bacterial virulence factors may interfere with these responses. Toxins, secretion-system effectors, oxidative stress and other bacterial products can alter host-cell function and potentially interfere with bacterial clearance.

Oxidative stress and antioxidant defence

Reactive oxygen species are important components of antimicrobial responses. Activated phagocytes can generate ROS as part of the respiratory burst, contributing to bacterial killing. However, excessive ROS production

can damage host lipids, proteins and nucleic acids. Fish therefore require antioxidant systems including superoxide dismutase, catalase and glutathione peroxidase to maintain redox balance during infection.

Intestinal immune response

The intestine represents a major portal of entry for waterborne and food-associated pathogens and contains an extensive mucosal immune system. Infection with *A. veronii* can therefore produce substantial changes in intestinal immune pathways. Integrated transcriptomic and proteomic analysis has demonstrated extensive changes in immune-related genes and proteins following infection, including activation of complement, coagulation, phagosome, MAPK and NOD-like receptor pathways (Han *et al.*, 2024).

Systemic immune responses

When *A. veronii* crosses epithelial barriers and enters internal tissues, systemic immune responses become increasingly important. The spleen and head kidney are major immune organs in teleosts and participate in systemic pathogen recognition, leukocyte production and antibody responses.

Humoral immunity and antibody responses

Adaptive immunity in fish includes production of immunoglobulins and development of immunological memory. IgM represents a major systemic antibody in teleosts, whereas IgT/IgZ has an important role in mucosal

immunity. The development of specific antibodies following exposure to *A. veronii* has been demonstrated in vaccination studies. Sukkarun *et al.* (2024) reported enhanced *A. veronii*-specific IgM concentrations and bactericidal activity following immersion vaccination. Earlier work also demonstrated that oral administration of an extracellular lectin derived from *A. veronii* could stimulate mucosal immune responses and provide measurable protection following challenge (Merino-Contreras *et al.*, 2001).

Immune evasion and modulation

The ability of *A. veronii* to cause systemic disease suggests that the bacterium can overcome or modulate host defence mechanisms. Toxins, secretion systems, biofilm formation, iron acquisition and surface structures can influence immune recognition and bacterial persistence. Biofilm formation may reduce exposure of bacterial cells to immune effectors, while extracellular polysaccharides and surface-associated structures may alter recognition by host immune molecules.

Host–pathogen interaction at the mucosal interface

The interaction between *A. veronii* and mucosal surfaces is a particularly important determinant of disease progression. Mucus and epithelial barriers can prevent bacterial attachment and invasion. If these barriers are overcome, pathogen-associated molecular patterns stimulate innate

receptors and initiate inflammatory responses.

Interaction between immunity and environmental stress

Environmental conditions can strongly influence host response to *A. veronii*. Temperature, dissolved oxygen, ammonia, stocking density, handling and nutritional status can affect immune competence and may alter the balance between bacterial proliferation and host resistance.

Implications for immunoprophylaxis

Understanding host-pathogen interactions have direct implications for vaccine development and immunostimulatory strategies. Traditional whole-cell inactivated vaccines can stimulate systemic antibody responses, but their effectiveness may be improved through appropriate adjuvants and mucosal delivery systems.

Current understanding and research gaps

Several aspects of the *A. veronii* host response remain incompletely understood. Most available studies have focused on individual fish species and short experimental infection periods. Future research should integrate transcriptomics, proteomics, metabolomics and microbiome analysis with controlled infection experiments.

Concluding perspective

The host response to *A. veronii* is a coordinated process involving physical

barriers, mucosal immunity, innate recognition, inflammation, complement activation, phagocytosis, oxidative responses and adaptive immunity. Disease outcome therefore reflects a dynamic balance between bacterial pathogenicity and host defence.

Biofilm formation and quorum sensing

Biofilm formation is an important adaptive strategy that enables *Aeromonas veronii* to persist in aquatic environments, colonize host surfaces and withstand adverse environmental conditions. Aquaculture systems provide numerous surfaces for bacterial attachment, including tank walls, pipes, nets, sediments, biofilters and fish-associated tissues.

Stages of biofilm development

Biofilm development is generally initiated by reversible attachment of planktonic bacteria to a suitable surface. In *A. veronii*, motility-associated structures such as flagella and type IV pili facilitate movement toward surfaces and contribute to initial attachment. The extracellular matrix provides structural stability and creates a localized microenvironment in which bacterial cells can communicate, exchange metabolites and tolerate environmental fluctuations.

Flagella, pili and surface adhesion

Flagella and pili have functions extending beyond bacterial movement. Flagellar motility can facilitate migration toward favourable

microenvironments, while type IV pili contribute to surface attachment, aggregation and bacterial interactions. Mutation of *mshK* has been associated with reduced biofilm formation and altered pilus abundance, demonstrating that disruption of the MSHA pilus system can affect biofilm phenotype and pathogenicity.

Quorum sensing and population-level coordination

Quorum sensing enables bacterial cells to coordinate gene expression according to population density through production, release and detection of chemical signalling molecules. In *A. veronii*, QS is increasingly recognized as an important regulatory mechanism linking bacterial communication with biofilm formation, motility, colonization and virulence. AHL-mediated signalling has been shown to influence biofilm formation and intestinal colonization (Li *et al.*, 2022).

AHL-mediated regulation of chemotaxis and colonization

Further work has provided insight into how AHL-mediated QS promotes intestinal colonization. The *ahyI* mutant showed altered expression of chemotaxis-associated genes, while *cheA* was identified as an important downstream component. Disruption of *cheA* reduced chemotaxis, intestinal dispersion and colonization (Li *et al.*, 2024).

LuxS/AI-2 signalling

Increasing evidence indicates that the LuxS/autoinducer-2 system also contributes to the biology of *A. veronii*. AI-2 is a broadly distributed bacterial signalling molecule that can participate in interspecies communication and regulation of collective bacterial behaviours. Li *et al.* (2025) demonstrated that AI-2 signalling contributes to intestinal colonization and host responses. Dietary supplementation with *Priestia* sp. PPB30 reduced AI-2-associated signalling and several virulence-related phenotypes (Gao *et al.*, 2025).

Two-component regulatory systems and biofilm formation

Two-component systems can integrate environmental signals and modify gene expression associated with motility, stress adaptation, biofilm development and virulence. In *A. veronii*, QseBC and EnvZ/OmpR represent examples of regulatory systems that influence biofilm-associated phenotypes. Wang *et al.* (2023) demonstrated that OmpR affects biofilm formation and is associated with antimicrobial resistance, stress resistance and virulence.

Biofilms and antimicrobial tolerance

Biofilm formation can contribute to persistence during antimicrobial treatment even when a bacterial population does not possess a corresponding resistance gene. The biofilm matrix can limit antimicrobial penetration, while nutrient limitation and slow growth can reduce the

effectiveness of drugs targeting actively dividing cells. Biofilm-associated tolerance should therefore be distinguished from genetically encoded antimicrobial resistance, although both phenomena can occur simultaneously.

Biofilm formation, virulence and environmental persistence

Biofilm formation should be considered an integrated component of *A. veronii* pathogenicity rather than an independent survival trait. The same bacterial structures and regulatory pathways can contribute to motility, adhesion, biofilm development and host colonization.

Biofilm dispersal and recolonization

Although mature biofilms provide persistence, dispersion is essential for dissemination to new ecological niches. Changes in nutrient availability, environmental stress, bacterial signalling or host-associated conditions may promote release of cells from established biofilms.

Anti-biofilm and quorum-sensing-based control

The regulatory nature of biofilm formation and QS creates opportunities for alternative disease-control strategies. Potential approaches include quorum-sensing inhibitors, signal degradation, competitive probiotics, phytochemicals, enzymes targeting the extracellular matrix and compounds that interfere with surface attachment.

Research gaps

Several questions remain unresolved concerning the relative contribution of different QS systems, composition of the biofilm matrix, relationship between QS and antimicrobial resistance, and behaviour of biofilms under realistic aquaculture conditions.

Concluding perspective

Biofilm formation and quorum sensing represent interconnected adaptive mechanisms that enhance the ecological persistence and pathogenic potential of *A. veronii*. Targeting bacterial communication and biofilm-associated processes may therefore represent an important complement to conventional antimicrobial therapy.

Antimicrobial resistance

Antimicrobial resistance has become an increasingly important concern in *Aeromonas veronii* because of the organism's capacity to acquire, maintain and disseminate resistance determinants in aquatic environments. The problem is particularly relevant to aquaculture, where repeated antimicrobial exposure, high stocking densities, environmental contamination and exchange of microorganisms can create conditions favourable for selection and persistence of resistant bacteria.

Phenotypic antimicrobial resistance

The antimicrobial susceptibility of *A. veronii* varies substantially among geographical regions, hosts and individual strains. Resistance has been reported against β -lactams,

tetracyclines, quinolones, sulfonamides, aminoglycosides, phenicols and other antimicrobial classes. A recent investigation of farmed largemouth bass in China demonstrated considerable multidrug resistance among *A. veronii* isolates, with multiple sequence types and regional differences in susceptibility patterns (Chen *et al.*, 2024). Studies from Indian aquaculture systems have similarly identified multidrug-resistant *Aeromonas* populations and β -lactamase-associated resistance, highlighting the relevance of *A. veronii* to AMR surveillance.

Major antimicrobial-resistance mechanisms

Resistance in *A. veronii* can arise through enzymatic antimicrobial inactivation, modification or protection of antimicrobial targets, reduced membrane permeability and active efflux. Comparative genomic analysis identified resistance determinants associated with antimicrobial efflux, antimicrobial inactivation, target alteration, target replacement and target protection (Maia *et al.*, 2023).

β -Lactam resistance and β -lactamases

β -lactam resistance is particularly important because β -lactam antibiotics are frequently used in clinical and veterinary settings. *A. veronii* can harbour several β -lactamase-associated determinants, including chromosomal and acquired resistance genes. More concerningly, acquired β -lactamases have also been documented. A multidrug-resistant *A. veronii* strain

recovered from hospital sewage in China was reported to carry clinically important resistance determinants, demonstrating the potential connection between environmental and clinical resistance reservoirs.

Tetracycline and quinolone resistance

Tetracyclines and quinolones are important antimicrobial classes in aquaculture, and resistance against both groups has been reported in *A. veronii*. Resistance to tetracyclines may involve efflux systems or ribosomal protection, whereas quinolone resistance may result from target mutations, plasmid-mediated resistance mechanisms and altered drug efflux. Integrated phenotypic and genomic approaches are preferable for comprehensive AMR characterization because detection of an ARG does not always translate directly into the same magnitude of phenotypic resistance.

Sulfonamide, aminoglycoside and other resistance determinants

Resistance-associated genes belonging to several antimicrobial classes have been identified in *A. veronii*. Commonly reported determinants include *sul* genes associated with sulfonamide resistance, *aadA* and related aminoglycoside-associated determinants, and multiple tetracycline-associated genes. The coexistence of resistance determinants is epidemiologically important because exposure to one antimicrobial may indirectly select bacteria carrying resistance to several other antimicrobial classes.

Efflux systems

Efflux systems can reduce intracellular antimicrobial concentrations by actively exporting compounds from bacterial cells. These systems may contribute to resistance against several structurally unrelated antimicrobial classes and can therefore produce multidrug-resistant phenotypes.

Mobile genetic elements

Plasmids, integrons, transposons and other mobile genetic elements can facilitate acquisition and dissemination of resistance determinants. The presence of mobile resistance elements increases the potential for horizontal gene transfer within aquatic microbial communities.

Biofilm-associated resistance and tolerance

Biofilm-associated cells may survive antimicrobial exposure because of restricted drug penetration, altered metabolic states, slow growth and stress-response mechanisms. Therefore, biofilm management should be integrated with antimicrobial stewardship.

Aquaculture as an AMR selection environment

Aquaculture systems can create conditions favourable for selection and persistence of resistant bacteria. Antimicrobial exposure can occur through therapeutic treatment, prophylactic practices or inappropriate administration. Organic matter accumulation, high fish density, contaminated water sources and

inadequate biosecurity can further increase bacterial transmission.

*One health significance of *A. veronii* AMR*

The One Health significance of *A. veronii* AMR arises from its ability to occupy aquatic environments while infecting fish and, under appropriate circumstances, humans. Genomic analyses have identified overlapping resistance determinants among isolates from human, fish and environmental sources (Maia *et al.*, 2023). The detection of resistant *A. veronii* in hospital sewage further demonstrates the potential connection between clinical and environmental reservoirs.

Molecular surveillance and genomic monitoring

Traditional antimicrobial susceptibility testing remains essential for determining the phenotype of individual isolates. However, whole-genome sequencing provides additional information about resistance genes, mutations, plasmids, genomic islands and other mobile genetic elements. Genomic surveillance is particularly valuable when combined with phylogenetic analysis because it can distinguish widespread resistance determinants from those associated with particular clones (Table 3; Fig. 3).

Antimicrobial exposure creates selection pressure that favours resistant and tolerant bacterial populations. Resistance may arise through antimicrobial inactivation, active efflux, target modification or protection and reduced permeability. Mobile genetic

elements can facilitate acquisition and dissemination of antimicrobial-resistance genes. Biofilm formation may further enhance persistence under antimicrobial stress. Resistant *A. veronii* populations can circulate among fish, water, sediment, aquaculture

infrastructure and wastewater, creating interconnected environmental, veterinary and human AMR reservoirs.

Table 3: Major antimicrobial-resistance phenotypes, genes and mechanisms reported in *Aeromonas veronii*.

Antimicrobial class	Representative determinants/mechanisms	Principal mechanism	Relevance
β-Lactams	<i>cphA</i> , <i>blaOXA</i> , <i>blaTEM</i> , <i>blaSHV</i> , <i>blaCTX-M</i> , <i>blaKPC-2</i>	Enzymatic hydrolysis	Important intrinsic/acquired resistance
Carbapenems	<i>cphA</i> , OXA-related determinants	Carbapenemase activity	Reduced therapeutic options
Tetracyclines	<i>tetA</i> , <i>tetB</i> , <i>tetC</i> , <i>tetM</i>	Efflux/ribosomal protection	Commonly detected
Quinolones	<i>qnr</i> , target mutations, efflux	Target protection/alteration	Important resistance phenotype
Sulfonamides	<i>sulI</i> and related genes	Altered dihydropteroate synthase	Often part of MDR profiles
Aminoglycosides	<i>aadA</i> and related genes	Enzymatic modification	Often co-occurs with other resistance
Phenicol	Efflux/inactivation mechanisms	Reduced concentration/modification	Detected in resistomes
Polymyxins/colistin	<i>mcr</i> -family genes	Lipid A modification	Emerging One Health concern
Macrolides	Efflux/target mechanisms	Reduced accumulation/target modification	Reported in resistomes
Multidrug resistance	Multiple ARGs and mechanisms	Combined mechanisms	Increasingly reported

Note: The presence of a resistance gene does not necessarily indicate the same magnitude of phenotypic resistance. Phenotypic susceptibility testing and genomic characterization should therefore be interpreted together.

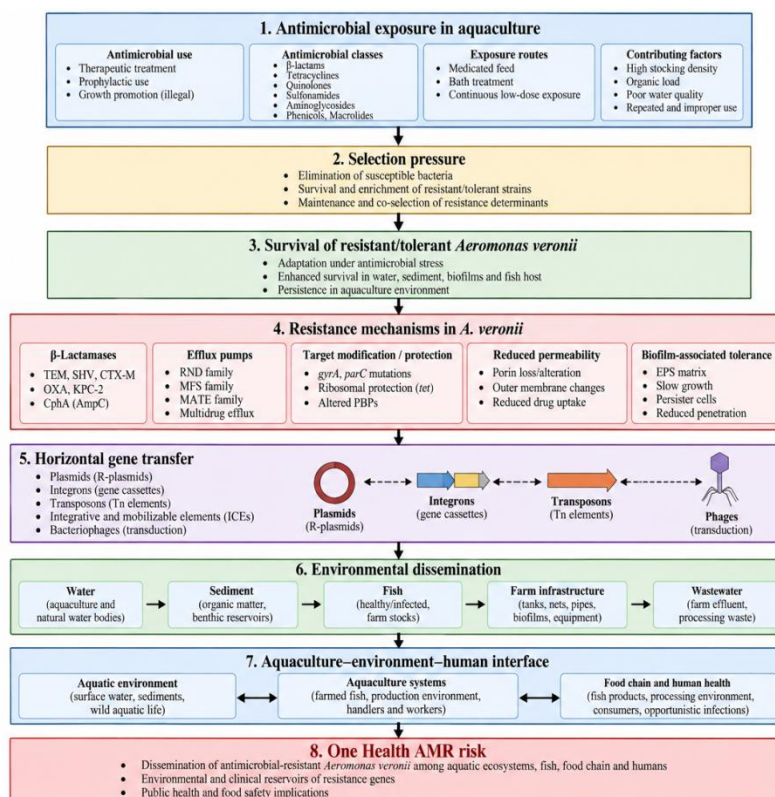


Figure 3: Development and dissemination of antimicrobial resistance in *Aeromonas veronii*.

Research gaps and future priorities

Several major gaps remain in understanding AMR in *A. veronii*. Large-scale longitudinal surveillance is required to determine temporal trends and identify emerging resistance hotspots. Greater attention should be given to the relationship between antimicrobial use and resistance development. The mobility and expression of resistance genes also require further investigation. Detection of an ARG through PCR or genome sequencing provides evidence of genetic potential, but functional studies are needed to establish whether the determinant contributes substantially to the observed phenotype. One Health surveillance should integrate aquaculture farms, natural water bodies,

wastewater, fish products and human-associated environments.

Concluding perspective

AMR in *A. veronii* represents a complex interaction between bacterial genetics, environmental selection, antimicrobial use and ecological connectivity. Sustainable management requires improved biosecurity, antimicrobial stewardship, routine susceptibility testing, genomic surveillance, environmental monitoring and non-antibiotic interventions.

Molecular diagnostics and identification

Accurate identification of *Aeromonas veronii* is essential for epidemiological surveillance, disease diagnosis, antimicrobial-resistance monitoring and

selection of appropriate control strategies. However, species-level identification within the genus *Aeromonas* can be challenging because closely related species frequently share phenotypic and biochemical characteristics.

Conventional culture-based identification

Initial detection of *A. veronii* generally involves isolation on appropriate bacteriological media followed by examination of colony morphology and biochemical characteristics. Members of the genus are typically Gram-negative, oxidase-positive, facultatively anaerobic, rod-shaped bacteria. Although these approaches are useful for preliminary identification, their ability to reliably distinguish *A. veronii* from closely related *Aeromonas* species is limited.

Limitations of 16S rRNA gene sequencing

16S rRNA gene sequencing is widely used for bacterial identification. It is valuable for confirming that an isolate belongs to the genus *Aeromonas*, but the high sequence similarity among several species limits its discriminatory power at species level. Comparative analysis of clinical *Aeromonas* isolates demonstrated that 16S rRNA sequencing was less reliable for species-level assignment than multilocus or genome-based approaches (Chen *et al.*, 2015).

Housekeeping gene-based identification

Sequencing of conserved housekeeping genes provides greater discriminatory power than 16S rRNA sequencing. Genes such as *gyrB*, *rpoB*, *rpoD*, *dnaJ*, *gltA* and *recA* have been evaluated for discrimination among closely related *Aeromonas* species. The *gyrB* gene is particularly useful because it generally contains greater sequence variation than the 16S rRNA gene while retaining sufficient conservation for phylogenetic analysis. Similarly, *rpoB* sequencing can improve resolution of closely related taxa.

Species-specific PCR

PCR-based detection provides a rapid alternative to sequencing when appropriate species-specific or gene-targeted primers are available. Conventional PCR, multiplex PCR and quantitative PCR have been used to detect *A. veronii* or its virulence-associated genes. Targets commonly investigated include *aerA*, *hly*, *act*, *alt*, *ast* and secretion-associated genes. However, detection of a virulence gene should not automatically be interpreted as proof of active expression or disease causation.

Multiplex PCR and rapid molecular detection

Multiplex PCR can simultaneously detect several targets within a single reaction, potentially allowing differentiation among *Aeromonas* species or simultaneous screening for virulence-associated genes. For aquaculture applications, molecular

assays can reduce the time required between sampling and confirmation.

MALDI-TOF mass spectrometry

Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry provides rapid identification based on characteristic bacterial protein spectra. The method has become increasingly important in clinical microbiology. MALDI-TOF MS has demonstrated substantial utility for *Aeromonas* identification, but its performance depends strongly on the reference spectral database. Earlier comparative work showed useful concordance between MALDI-TOF and molecular identification, although misidentifications can occur among closely related species. Consequently, MALDI-TOF MS is valuable as a rapid diagnostic screening tool, but unusual or epidemiologically important isolates should be confirmed using higher-resolution molecular methods.

Multilocus sequence typing

Multilocus sequence typing characterizes isolates using sequences from multiple conserved housekeeping genes. For *A. veronii*, MLST has been applied to investigate population structure, genetic diversity, geographical distribution and relationships among clinical and environmental isolates. Maia *et al.* (2023) used an MLST scheme involving *gyrB*, *groL*, *gltA*, *metG*, *ppsA* and *recA* to characterize *A. veronii* genomes.

Average nucleotide identity and genome-based species identification

Average nucleotide identity has become one of the most useful approaches for species-level identification of bacterial genomes. ANI measures the average nucleotide similarity between homologous genomic regions and provides greater resolution than many traditional phenotypic methods. Maia *et al.* (2023) demonstrated that several genomes previously deposited as *A. veronii* had been incorrectly assigned when evaluated using ANI.

Whole-genome sequencing

Whole-genome sequencing provides comprehensive genetic information for bacterial characterization. In *A. veronii*, WGS can simultaneously provide information on species identity, genomic diversity, virulence-associated genes, antimicrobial-resistance determinants, plasmids, prophages, secretion systems and adaptive traits. The integration of ANI, core-genome phylogeny and MLST therefore provides a powerful framework for characterizing *A. veronii* isolates.

Core-genome and SNP-based phylogenetics

Beyond species identification, genome-scale approaches can characterize evolutionary relationships among *A. veronii* isolates. Core-genome alignments identify conserved regions shared by most isolates, while SNP-based analyses provide higher resolution for closely related strains.

Metagenomic and culture-independent approaches

Culture-dependent isolation remains important for obtaining viable bacterial strains for antimicrobial susceptibility testing and experimental characterization. However, metagenomic approaches provide opportunities to detect *Aeromonas* populations directly from environmental or host-associated samples. Metagenomic detection of *A. veronii* DNA does not necessarily demonstrate active infection and should therefore be interpreted alongside culture, quantitative molecular assays, clinical signs and histopathological evidence.

Diagnostic integration for aquaculture

For practical aquaculture diagnosis, no single technique is ideal for every situation. A tiered strategy can provide both speed and reliability. An appropriate workflow begins with clinical observation and sampling of affected fish, followed by bacterial culture and preliminary biochemical characterization. PCR or MALDI-TOF MS can then provide rapid identification, while sequencing of discriminatory housekeeping genes can be used when species-level confirmation is uncertain. For epidemiological studies, multidrug-resistant isolates, unusual clinical presentations or suspected outbreaks, WGS with ANI and core-genome analysis provides a more comprehensive solution.

*Recommended diagnostic hierarchy**Level 1 – Preliminary identification*

- Clinical signs and lesion examination
- Culture and colony morphology
- Gram staining
- Oxidase and catalase tests
- Basic biochemical characterization

Level 2 – Molecular confirmation

- 16S rRNA sequencing for preliminary taxonomic confirmation
- Species-discriminatory housekeeping genes such as *gyrB*, *rpoB* or *rpoD*
- Species-specific PCR where validated primers are available

Level 3 – Rapid advanced identification

- MALDI-TOF MS using an updated reference database
- MLST for population and epidemiological characterization

Level 4 – Definitive genomic characterization

- Whole-genome sequencing
- ANI-based species confirmation
- Core-genome phylogeny
- SNP analysis
- Virulome and resistome characterization
- Plasmid and mobile genetic element analysis

Diagnostic challenges and research priorities

Several challenges continue to limit accurate identification of *A. veronii*. High genetic similarity among closely related species complicates species-level identification using conventional biochemical tests and 16S rRNA sequencing. Commercial identification

systems depend heavily on database quality, while public genomic databases may contain incorrectly annotated isolates. Future diagnostic development should focus on validated species-specific PCR assays, improved MALDI-TOF databases, portable sequencing technologies, automated genomic classification and standardized WGS-based surveillance pipelines.

Concluding perspective

Accurate identification of *A. veronii* requires recognition of the limitations associated with conventional phenotypic methods and low-resolution molecular markers. Culture-based techniques remain valuable for initial recovery and phenotypic characterization, while 16S rRNA sequencing provides useful genus-level confirmation. Housekeeping gene sequencing, particularly targeting discriminatory loci such as *gyrB* and *rpoB*, improves species-level resolution. MALDI-TOF MS provides rapid identification and is highly useful for routine diagnostics, whereas WGS combined with ANI, core-genome phylogeny and SNP analysis offers a comprehensive framework for definitive species identification and epidemiological investigation.

One Health significance

The significance of *Aeromonas veronii* extends beyond its role as an important pathogen of cultured and wild aquatic animals. Its widespread distribution in aquatic environments, ability to infect multiple hosts, capacity to acquire antimicrobial-resistance determinants

and association with human disease place this species within a broader One Health framework.

Veronii at the aquaculture–environment–human interface

Aquaculture provides an important setting in which the ecological and pathogenic characteristics of *A. veronii* intersect. The organism can persist in water, sediments and biofilms while also colonizing fish-associated surfaces and internal tissues. Water quality, organic loading, stocking density, biosecurity, animal movement and microbial contamination can all influence the likelihood of disease emergence (Behera *et al.*, 2023).

Environmental reservoirs and transmission pathways

Water represents an important component of the *A. veronii* transmission cycle. The bacterium can occur in freshwater environments and may persist in association with sediment, organic matter and biofilms. Aquaculture facilities may therefore function as amplification environments when susceptible fish, high microbial loads and favourable environmental conditions occur simultaneously. Environmental surveillance should complement fish-health monitoring because environmental populations may persist before clinical disease becomes apparent.

Fish health and aquaculture productivity

The direct economic importance of *A. veronii* arises from its ability to cause disease and mortality in commercially important fish. Clinical manifestations can include hemorrhage, ulceration, fin erosion, exophthalmia, ascites, internal organ lesions and systemic septicaemia. The consequences of infection extend beyond mortality. Disease can reduce growth, feed utilization, reproductive performance and market value, while treatment and increased farm-management costs can further reduce profitability.

Food safety and seafood consumption

Aquatic food represents an important source of animal protein worldwide. Consequently, bacterial pathogens associated with aquaculture have potential food-safety implications. The risk associated with *A. veronii* should not be interpreted as meaning that consumption of properly handled and cooked fish routinely causes human infection. Rather, the food-chain pathway represents one of several potential exposure routes through which aquatic bacteria and antimicrobial-resistance determinants may reach humans.

Human health significance

Although *A. veronii* is primarily associated with aquatic environments and animals, it can act as an opportunistic human pathogen. Human infections have been associated with gastrointestinal disease, wound infections, bacteremia and systemic infections, particularly among susceptible individuals. Comparative

genomic studies have identified virulence and resistance genes across environmental, animal and human-associated isolates, demonstrating that the species cannot be considered exclusively a fish pathogen (Maia *et al.*, 2023).

Antimicrobial resistance as a One Health threat

AMR represents perhaps the strongest connection between *A. veronii* and the One Health framework. Antimicrobial exposure in aquaculture can select for resistant bacterial populations, while environmental contamination can facilitate persistence and exchange of resistance determinants. A recent review of AMR in aquaculture emphasized that aquatic environments can function as reservoirs of resistant bacteria and resistance genes, while fish production systems can connect environmental, animal, food and human compartments (Milijasevic *et al.*, 2024).

Environmental contamination and wastewater

Wastewater represents another important connection between *A. veronii*, antimicrobial resistance and environmental health. Aquaculture effluents may contain bacteria, resistance genes, antimicrobial residues and organic material. Environmental bacteria may acquire resistance determinants and subsequently contribute to the wider environmental resistome. Wastewater treatment should therefore be considered part of pathogen and AMR control.

Aquaculture practices and antimicrobial stewardship

Prevention of *A. veronii* infections should prioritize disease prevention rather than routine antimicrobial dependence. Poor water quality, excessive stocking density, nutritional deficiencies, handling stress and inadequate biosecurity can increase disease susceptibility and consequently promote antimicrobial use. Antimicrobial stewardship should include accurate diagnosis, susceptibility testing, appropriate antimicrobial selection, correct dosage and duration, and avoidance of unnecessary prophylactic treatment.

Food security and sustainable aquaculture

The One Health importance of *A. veronii* also extends to food security. Aquaculture is an increasingly important contributor to global food production, particularly in regions where aquatic foods provide affordable animal protein. Disease outbreaks threaten this contribution by reducing survival and productivity. Sustainable disease management should therefore seek to maintain fish productivity while minimizing ecological and public-health consequences.

Climate and environmental change

Environmental change may further modify the epidemiology of *A. veronii*. Temperature, dissolved oxygen, salinity, organic matter and other environmental parameters can influence bacterial growth, host physiology and immune competence. Future disease-risk models

should integrate pathogen abundance, host susceptibility and environmental variables rather than relying solely on historical disease occurrence.

Surveillance within a One Health framework

Effective surveillance should integrate:

Aquatic animals

- Clinical disease surveillance
- Mortality monitoring
- Bacterial isolation
- Antimicrobial susceptibility testing
- Virulence profiling

Aquaculture environment

- Water
- Sediment
- Biofilms
- Farm infrastructure
- Effluents

Food chain

- Farmed fish
- Processing environments
- Retail seafood
- Food-contact surfaces

Human health

- Clinical isolates
- Gastrointestinal infections
- Wound infections
- Bloodstream infections

Genomic surveillance

- Whole-genome sequencing
- ANI-based species confirmation
- Resistome analysis
- Virulome analysis
- Plasmid and mobile-element characterization
- Phylogenomic comparison

Barriers to One Health implementation

Several barriers limit effective One Health surveillance. Surveillance programmes are often sector-specific, diagnostic capacity varies considerably among regions, environmental surveillance is less developed than clinical surveillance, and antimicrobial-use data in aquaculture may be incomplete. Addressing these limitations will require collaboration among microbiologists, fish-health specialists, veterinarians, clinicians, environmental scientists, epidemiologists, aquaculture producers and public-health authorities.

One Health research priorities

Future research should prioritize comparative genomics of fish-associated, environmental and human-associated populations, longitudinal sampling across production cycles, environmental surveillance, investigation of wastewater and aquaculture effluents, standardized genomic surveillance pipelines and evaluation of non-antibiotic interventions.

An integrated One Health perspective

The One Health significance of *A. veronii* can be conceptualized as a continuous ecological network:

Aquatic environment
↓
Water • sediment • biofilms
↓
Aquaculture system
↓
Fish colonization and disease
↓
Farm management and antimicrobial exposure

↓
Selection of resistant populations
↓
Farm effluent and environmental dissemination
↓
Natural aquatic ecosystems
↓
Food chain and occupational exposure
↓
Potential human exposure
↓
Human clinical infections and AMR surveillance
↓
Genomic and epidemiological feedback to aquaculture and environmental management

This framework emphasizes that interventions at a single point may be insufficient.

Concluding perspective

Aeromonas veronii represents a relevant One Health organism because it occupies the intersection of aquatic ecosystems, aquaculture production, food systems, antimicrobial resistance and human health. A coordinated One Health strategy should therefore combine environmental surveillance, fish-health management, food-safety practices, antimicrobial stewardship, genomic monitoring and alternative disease-control technologies.

Conventional and emerging control strategies

Control of *Aeromonas veronii* infections in aquaculture is becoming increasingly challenging because of the organism's broad host range, environmental persistence, biofilm-forming ability,

virulence diversity and increasing antimicrobial resistance. Consequently, modern control programmes increasingly emphasize prevention, immunoprophylaxis, nutritional management, probiotics, phytochemicals, bacteriophages, anti-biofilm approaches and integrated farm management (Dien *et al.*, 2023; Milijasevic *et al.*, 2024). No single intervention is likely to provide universal protection against *A. veronii*. The most sustainable strategy is therefore an integrated approach in which environmental management reduces pathogen pressure, vaccination and immunostimulation improve host resistance, probiotics and functional feeds support mucosal health, and targeted alternatives such as bacteriophages are used when appropriate.

Environmental management and biosecurity

Environmental management represents the first line of defence against *A. veronii*. The organism is widely distributed in aquatic environments and can persist in water, sediment and biofilms. Consequently, reducing environmental bacterial loads and minimizing opportunities for transmission can substantially reduce disease pressure (Xu *et al.*, 2022; Liu *et al.*, 2022). Important management measures include maintaining appropriate stocking densities, monitoring water quality, removing dead or moribund fish rapidly, controlling organic accumulation,

disinfecting equipment and preventing movement of contaminated water between culture units.

Antimicrobial chemotherapy

Antimicrobials remain useful for treating severe bacterial disease when susceptible pathogens have been accurately identified. However, treatment should ideally follow bacterial isolation and antimicrobial susceptibility testing rather than empirical repeated administration. The increasing occurrence of multidrug-resistant *A. veronii* makes indiscriminate antimicrobial use particularly problematic. Resistance to multiple antimicrobial classes has been documented among isolates from aquaculture and clinical environments (Maia *et al.*, 2023; Chen *et al.*, 2024).

Vaccination

Vaccination is one of the most promising approaches for reducing antimicrobial dependence in aquaculture. Vaccine platforms investigated against *A. veronii* include formalin-inactivated whole-cell vaccines, extracellular antigen preparations, recombinant antigens, oral vaccines, immersion vaccines and nanoparticle-based delivery systems (Youssef *et al.*, 2023; Sukkarun *et al.*, 2024). Sukkarun *et al.* (2024) demonstrated that a chitosan polymer-based nanovaccine enhanced systemic and mucosal immune responses and provided substantial protection following bacterial challenge.

Oral and feed-based vaccination

Oral vaccination provides an attractive approach because antigens can be incorporated into feed and administered without handling individual fish. However, antigens may undergo degradation within the gastrointestinal tract. Encapsulation, mucoadhesive materials, nanoparticles and adjuvants may improve antigen stability and uptake.

Nanovaccine and adjuvant-based approaches

Nanotechnology provides opportunities to improve antigen delivery and stimulate stronger immune responses. Chitosan is particularly attractive for aquatic vaccines because of its biocompatibility and mucoadhesive properties. Nevertheless, vaccine efficacy can vary according to antigenic diversity, bacterial strain, fish species, age, environmental conditions and vaccination route.

Probiotics

Probiotics represent one of the most extensively investigated alternatives to conventional antimicrobial treatment. Beneficial bacteria can reduce pathogen abundance through competitive exclusion, production of antimicrobial compounds, alteration of intestinal microbial communities, improvement of epithelial integrity and stimulation of host immunity.

Next-generation probiotics

Traditional probiotics are increasingly complemented by defined strains,

engineered microorganisms, postbiotics and microbiome-based interventions. Future research may move toward precision probiotics designed for specific fish species, production systems and pathogen populations.

Immunostimulants and functional nutrition

Immunostimulants enhance innate defence mechanisms without necessarily inducing pathogen-specific adaptive immunity. They include β -glucans, polysaccharides, vitamins, minerals, nucleotides, amino acids, herbal compounds and microbial derivatives. Functional feeds can combine nutritional support with immunostimulatory, antimicrobial, antioxidant or microbiome-modulating effects.

Phytochemicals and herbal extracts

Plant-derived compounds have received increasing attention because many possess antibacterial, antioxidant, anti-inflammatory and immunomodulatory properties. Phytochemicals may act through disruption of bacterial membranes, inhibition of bacterial enzymes, suppression of biofilm formation, interference with quorum sensing and modulation of host antioxidant and immune responses. However, plant-based interventions require careful standardization because chemical composition can vary according to plant genotype, geographical origin, harvesting stage,

extraction solvent, extraction method and storage conditions.

Functional feeds and phytogetic aquafeeds

The integration of plant extracts into aquafeeds offers a practical approach because feed is routinely administered in intensive aquaculture. Phytogetic feeds can potentially deliver bioactive compounds continuously and may simultaneously improve nutritional status and disease resistance. Thermal degradation is particularly relevant when phytochemicals are incorporated into pelleted feeds. Studies should therefore assess stability of active compounds after feed processing.

Bacteriophage therapy

Bacteriophages provide a highly specific alternative to conventional antibiotics. Lytic phages infect susceptible bacterial cells, replicate within them and cause bacterial lysis. Recent studies have demonstrated promising prophylactic and therapeutic effects of *A. veronii*-specific phages in fish. Mucus-associated phages may provide a protective barrier at the host–environment interface.

Limitations of phage therapy

Phages often have narrow host ranges, meaning that a single phage may not be effective against genetically diverse *A. veronii* populations. Bacteria may also evolve phage resistance through receptor modification and other defence systems. Phage cocktails containing several complementary lytic phages may

broaden host coverage. However, only strictly lytic phages without undesirable virulence, lysogenic or antimicrobial-resistance-associated genes should be considered for therapeutic development.

Anti-biofilm and quorum-sensing interventions

Potential approaches include inhibition of bacterial adhesion, disruption of extracellular polymeric substances, quorum-sensing interference, enzymatic degradation of the biofilm matrix, competitive probiotics and phytochemical anti-biofilm compounds. The relationship between quorum sensing, biofilm formation, motility and virulence provides a strong rationale for anti-virulence approaches (Li *et al.*, 2024; Luo *et al.*, 2024).

Anti-virulence strategies

Potential targets include type III secretion systems, type VI secretion systems, aerolysin and haemolysins, iron-acquisition pathways, flagellar assembly, type IV pili, quorum-sensing systems, biofilm formation and regulatory systems such as Fur and QseBC. Targeting virulence rather than bacterial survival could theoretically reduce selective pressure for resistance, although the evolutionary consequences of long-term anti-virulence treatment remain uncertain.

Integrated disease management

The most realistic strategy for sustainable control of *A. veronii* is an integrated disease-management programme rather than dependence on a

single intervention. A preventive programme should begin with environmental management, including maintenance of appropriate water quality, stocking density, oxygen availability and organic-load control. Biosecurity should include quarantine of new fish, disinfection of equipment and prevention of contaminated-water transfer. Nutritional management should provide balanced diets and, where evidence supports their use, functional feed additives. Probiotics and other microbiome-management approaches may support intestinal health. Vaccination should be considered before high-risk periods. Surveillance should include clinical signs, mortality, water quality and pathogen prevalence. When disease occurs, rapid diagnostic confirmation and antimicrobial susceptibility testing should guide treatment (Table 4; Fig. 4).

Combination strategies should nevertheless be evaluated experimentally because interactions between treatments may be positive, neutral, or antagonistic.

Regulatory and practical considerations

Before widespread implementation, emerging interventions require evaluation of safety, efficacy, stability, scalability and regulatory acceptability. For probiotics, candidate strains should be taxonomically characterized and screened for undesirable antimicrobial-resistance or virulence determinants. For phages, complete genome analysis is important to exclude lysogenic, virulence-associated, or antimicrobial-resistance-associated genes. Plant extracts require standardization, while vaccines require assessment of safety, antigen stability and protection against genetically diverse isolates.

Combination therapies and future directions

The future of *A. veronii* control is likely to involve combinations of interventions rather than replacement of one treatment with another. For example, vaccination can provide pathogen-specific immunity, while probiotics can support mucosal health. Functional feeds may improve nutritional and antioxidant status, while phages can directly reduce susceptible bacterial populations during outbreaks. Anti-biofilm compounds may increase bacterial accessibility to phages or conventional antimicrobials.

Table 4: Conventional and emerging control strategies for *Aeromonas veronii*.

Strategy	Principal mechanism	Major advantages	Key limitations	Development status
Antimicrobial chemotherapy	Direct bacterial inhibition/killing	Rapid action	AMR, residues, environmental impact	Established; stewardship required
Biosecurity	Reduces pathogen introduction/transmission	Low resistance-selection pressure	Requires consistent implementation	Essential
Water-quality management	Reduces stress and pathogen amplification	Broad fish-health benefits	Continuous monitoring required	Established
Vaccination	Antigen-specific systemic/mucosal immunity	Long-term protection	Antigenic variation	Increasingly advanced
Nanovaccines	Improved antigen delivery	Enhanced immune response	Cost and stability	Emerging
Probiotics	Competitive exclusion and immune modulation	Supports microbiome health	Strain/environment dependence	Increasingly investigated
Immunostimulants	Enhances innate immunity	Feed-compatible	Nonspecific effects	Widely investigated
Functional feeds	Nutritional and immunomodulatory effects	Practical	Bioavailability/processing stability	Promising
Phytochemicals	Antibacterial, antioxidant and anti-biofilm activity	Multifunctional	Dose, toxicity, standardization	Rapidly expanding
Bacteriophages	Specific bacterial lysis	High specificity	Narrow host range	Experimental/development
Phage cocktails	Multiple lytic activities	Broader strain coverage	Formulation complexity	Experimental
Anti-biofilm strategies	Prevent/disrupt biofilms	Targets persistence	Limited field validation	Emerging
Quorum-sensing inhibition	Disrupts bacterial communication	Anti-virulence potential	Signal diversity	Emerging
Anti-virulence therapy	Blocks toxins/secretion/regulation	Potentially lower selection pressure	Complex biology	Experimental
Integrated management	Combines multiple interventions	Most comprehensive	Requires coordination	Preferred sustainable model

Research priorities

Future research should prioritize:

1. Development of broadly protective vaccines.
2. Identification of conserved protective antigens.
3. Development of stable oral and immersion vaccine platforms.
4. Selection of host-associated and pathogen-targeted probiotic strains.

5. Development of standardized phytogetic and functional-feed formulations.
6. Identification of safe anti-biofilm and quorum-sensing inhibitors.
7. Development of phage cocktails with broad strain coverage.
8. Investigation of phage-probiotic and phage-phytochemical combinations.
9. Integration of WGS surveillance
10. Evaluation of intervention effectiveness under commercial aquaculture conditions.
11. Development of standardized protocols for non-antibiotic disease-control technologies.
12. Assessment of environmental and ecological consequences of long-term intervention use.

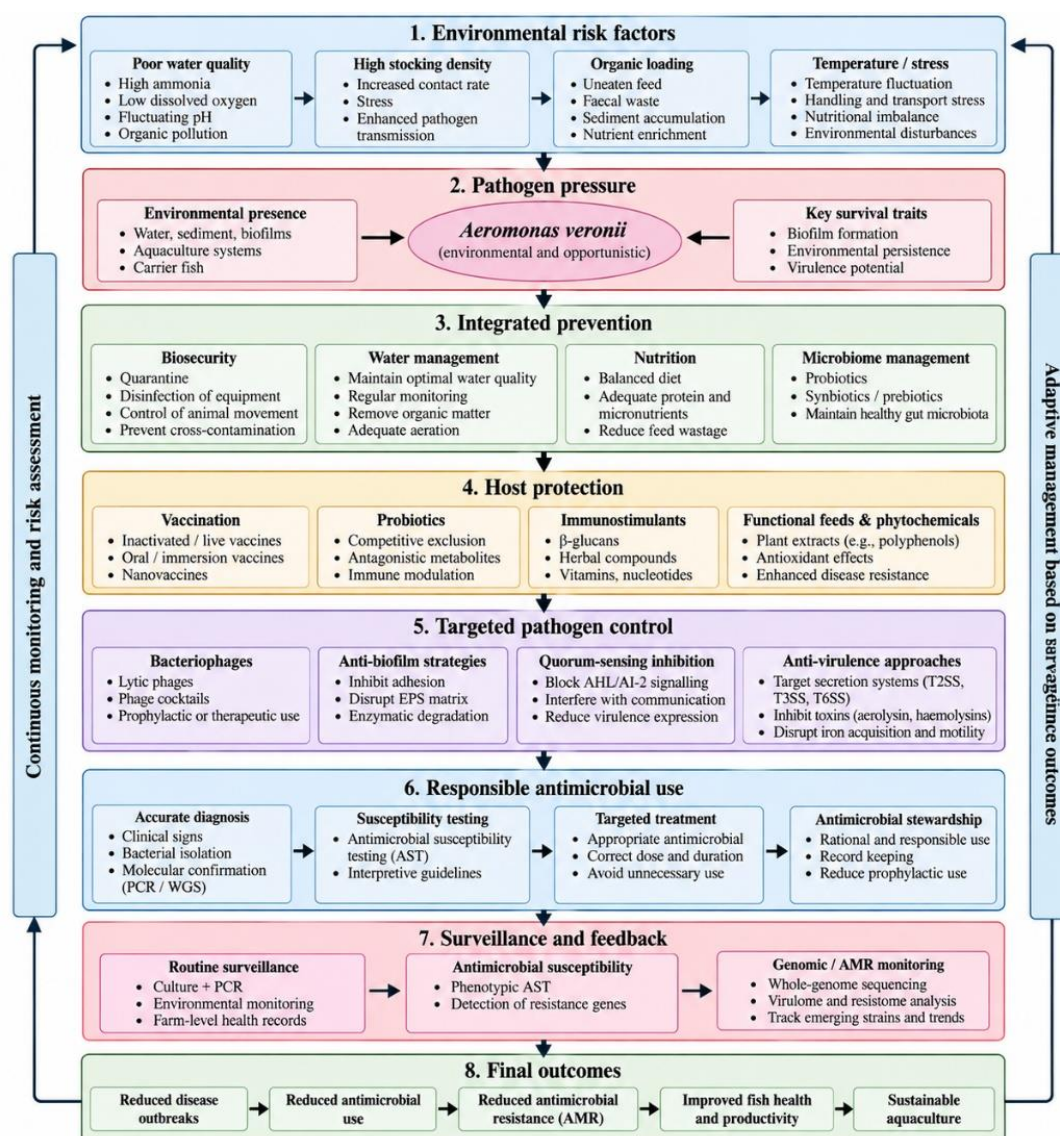


Figure 4: Integrated sustainable control strategy against *Aeromonas veronii*.

Concluding perspective

Control of *A. veronii* is moving from an antimicrobial-dependent model toward a more integrated disease-management framework. Antibiotics remain useful when appropriately selected and administered, but increasing antimicrobial resistance makes exclusive reliance on chemotherapy unsustainable (Maia *et al.*, 2023; Milijasevic *et al.*, 2024). Vaccination, probiotics, immunostimulants, functional feeds, and phytochemicals provide complementary approaches. Bacteriophages offer highly specific biological control, while anti-biofilm, quorum-sensing, and anti-virulence strategies provide opportunities to interfere with bacterial persistence and pathogenicity. Ultimately, successful control will depend on moving from reactive treatment toward predictive and preventive health management.

Research gaps and future perspectives

Despite substantial progress in understanding *Aeromonas veronii*, important gaps remain in epidemiology, comparative genomics, virulence, host–pathogen interactions, antimicrobial resistance, diagnostics, and disease control.

Need for improved global epidemiological surveillance

Although *A. veronii* has been reported from numerous geographical regions and aquatic hosts, its true global distribution remains incompletely understood. Existing studies often use

different isolation, identification, antimicrobial susceptibility and virulence-testing methods. Future surveillance should integrate standardized microbiological sampling with molecular identification, antimicrobial susceptibility testing and genomic characterization.

Linking genotype with virulence phenotype

One major challenge is that the presence of a virulence-associated gene does not necessarily indicate equivalent pathogenic potential. Future research should move toward integrated genotype–phenotype analyses using genome-wide association studies, transcriptomics, proteomics, metabolomics and targeted gene-editing approaches.

Functional genomics and regulatory networks

Although numerous genes associated with motility, adhesion, secretion, toxins, iron acquisition, biofilm formation and quorum sensing have been identified, the regulatory relationships connecting these systems remain incompletely understood. Recent studies demonstrate that regulatory components such as Fur and QseC influence motility, biofilm formation, chemotaxis, colonization and virulence (Gong *et al.*, 2024; Luo *et al.*, 2024).

Host-specific virulence and cross-species transmission

A. veronii is capable of infecting a wide range of aquatic hosts, but mechanisms

determining host specificity remain poorly understood. Future research should investigate host-specific adaptations using comparative infection models, transcriptomics, metabolomics and microbiome analysis.

Understanding environmental persistence

The ability of *A. veronii* to survive in water, sediment, biofilms and aquaculture infrastructure is central to its epidemiology. Future research should investigate how combinations of temperature, dissolved oxygen, pH, organic matter, salinity, nutrient availability, stocking density and microbial community composition influence persistence and virulence.

Biofilm and quorum-sensing research

Future research should determine how biofilm development differs between environmental and highly virulent isolates and whether specific genomic signatures predict strong biofilm-forming capacity. Anti-biofilm and quorum-sensing interventions should be evaluated under realistic aquaculture conditions rather than exclusively in laboratory models.

Antimicrobial resistance and mobile genetic elements

AMR represents one of the most important future challenges associated with *A. veronii*. Genomic studies have demonstrated diverse resistance determinants and mobile genetic elements. Future research should give particular attention to plasmids,

integrations, transposons, genomic islands, phages and other elements capable of transferring resistance determinants.

Standardization of antimicrobial susceptibility testing

Comparison of AMR data among *A. veronii* studies remains difficult because different antimicrobial panels, interpretive standards, inoculum concentrations and susceptibility-testing methods are frequently used. Future studies should report complete susceptibility profiles together with testing methodology, interpretive criteria, isolate source, geographic origin and genomic resistance determinants.

Development of rapid and accurate diagnostics

Reliable identification remains important because phenotypic characteristics may overlap among closely related *Aeromonas* species. Future diagnostic systems should combine rapid detection with high taxonomic accuracy. Species-specific PCR, multiplex PCR, MALDI-TOF MS, multilocus sequence analysis, whole-genome sequencing and metagenomic approaches each have potential applications depending on the diagnostic context.

Need for better vaccine strategies

Vaccination remains one of the most promising approaches for reducing dependence on antibiotics, but broadly protective vaccines are complicated by genomic and antigenic diversity. Future research should identify conserved

surface and secreted antigens shared among pathogenic lineages. Reverse vaccinology, comparative genomics, structural biology and immunoproteomics may help identify candidates.

Probiotics, postbiotics and microbiome-based approaches

Probiotics have shown considerable promise, but their effects are frequently strain-specific and influenced by environmental and host factors. Future studies should compare probiotics, synbiotics, postbiotics and defined microbial metabolites under standardized conditions.

Phage therapy and phage engineering

Bacteriophage therapy is an attractive alternative for controlling antimicrobial-resistant *A. veronii*, but narrow host range, phage resistance, environmental instability and regulatory requirements remain important challenges. Future research should prioritize phage cocktails containing genetically distinct lytic phages and evaluate phage–probiotic and phage–phytochemical combinations.

Phytochemicals and functional feeds

Plant-derived compounds represent an important area for future research because many possess multiple biological activities. However, reproducibility remains a major limitation. Future research should emphasize chemical standardization, identification of active constituents, pharmacokinetic studies, dose

optimization, toxicity assessment and stability during feed processing.

Integration of multi-omics

The future understanding of *A. veronii* will increasingly depend on integration of multiple omics approaches. Genomics can identify genetic diversity and potential virulence or resistance determinants. Transcriptomics can reveal genes activated during infection, proteomics can identify expressed proteins and metabolomics can reveal changes in metabolic pathways and host–microbe interactions.

Artificial intelligence and predictive disease surveillance

The increasing availability of genomic, environmental, clinical and production data creates opportunities for predictive disease modelling. Machine-learning approaches could potentially integrate water-quality parameters, temperature, stocking density, historical mortality, pathogen abundance, AMR profiles and genomic information to predict outbreak risk. Artificial intelligence should therefore complement, rather than replace, microbiological and epidemiological surveillance.

One Health research priorities

Future surveillance should include:

- Aquaculture production systems
- Hatchery and farm water
- Sediment and wastewater
- Fish and other aquatic animals
- Retail aquatic products
- Food-processing environments
- Hospital and community wastewater

- Human clinical isolates

Comparative WGS analysis could determine whether particular resistance or virulence determinants are shared among these compartments.

Translating laboratory findings to commercial aquaculture

A major limitation of current research is the frequent dependence on laboratory-scale experiments. Many promising vaccines, probiotics, phytochemicals,

phages and anti-biofilm compounds have demonstrated activity under controlled conditions but have not been sufficiently evaluated in commercial production environments.

Future studies should progress through:

Laboratory screening → Controlled challenge → Pilot-scale evaluation → Commercial farm trial → Long-term ecological assessment

Development of standardized experimental frameworks

Standardization should extend to experimental infection models. Differences in bacterial dose, exposure route, fish age, fish size, water temperature, observation period, and mortality endpoints can make results difficult to compare. Future studies should establish standardized reporting guidelines for *A. veronii* challenge experiments.

Towards precision aquaculture

The long-term objective should be development of precision disease management in aquaculture. Future systems could combine pathogen genomics, host genetics, microbiome composition, environmental monitoring and historical disease information to determine the most appropriate intervention for each production system.

Priority research questions

1. Which genomic determinants reliably distinguish highly virulent strains from environmental or low-virulence populations?
2. Which conserved antigens can provide broad protection against genetically diverse *A. veronii* lineages?
3. How do environmental conditions regulate the transition between environmental persistence and active pathogenicity?
4. Which mobile genetic elements are primarily responsible for antimicrobial-resistance dissemination?
5. How frequently are resistance and virulence determinants transferred between aquatic, environmental and clinical bacterial populations?
6. Can phage cocktails provide stable protection against genetically diverse *A. veronii* populations?
7. Which probiotic strains or postbiotic metabolites provide

- reproducible protection across different fish species?
8. Which phytochemicals retain their activity after feed processing and long-term storage?
 9. Can anti-virulence interventions reduce disease without producing unintended evolutionary consequences?
 10. How can genomic, environmental, microbiome and host-health data be integrated into practical early-warning systems?

Future perspective

The next generation of *A. veronii* research should move beyond describing the presence of the bacterium toward understanding and predicting its behaviour within complex aquaculture ecosystems. Genomic diversity, antimicrobial resistance, environmental persistence, host susceptibility, microbiome composition and bacterial virulence should be studied as interconnected components. Whole-genome sequencing and comparative genomics will remain central to surveillance, but genomic data should increasingly be linked to experimental phenotype, environmental information and clinical outcomes.

Ultimately, the most important future shift will be from reactive treatment to predictive prevention. A combination of genomic surveillance, environmental monitoring, rapid diagnostics, host-health assessment, microbiome management, vaccination, responsible antimicrobial use and targeted biological interventions could provide a more

sustainable framework for controlling *A. veronii*.

Conclusion

Aeromonas veronii has emerged as an important bacterial pathogen of freshwater and cultured aquatic animals, with increasing relevance to aquaculture production, antimicrobial resistance, environmental health and One Health. Its epidemiological importance is closely associated with its broad environmental distribution, diverse host range, ability to persist under changing environmental conditions and capacity to acquire and express multiple virulence and antimicrobial-resistance determinants (Janda and Abbott, 2010; Liu *et al.*, 2022; Maia *et al.*, 2023).

Advances in comparative genomics and whole-genome sequencing have substantially improved understanding of the genetic diversity of *A. veronii*. Genomic studies demonstrate considerable variation in core, accessory and mobile genetic components, with virulence and resistance determinants distributed among isolates from different geographical regions and hosts (Tekedar *et al.*, 2019; Song *et al.*, 2021; Lawal *et al.*, 2024). However, the presence of a particular gene does not necessarily predict disease severity, emphasizing the need to integrate genomic information with experimental virulence, transcriptomic, proteomic and environmental data.

The pathogenicity of *A. veronii* is multifactorial and involves coordinated interactions among motility, adhesion, pili, secretion systems, toxins,

extracellular enzymes, iron acquisition, biofilm formation, quorum sensing and regulatory pathways. These mechanisms allow the bacterium to colonize host surfaces, overcome environmental and host barriers, acquire nutrients, evade or modulate host defence mechanisms and disseminate systemically (Maia *et al.*, 2023; Tang *et al.*, 2024).

Antimicrobial resistance represents one of the most significant challenges for future management. Increasing resistance to multiple antimicrobial classes and detection of transferable resistance determinants highlight the potential for *A. veronii* to act as an important reservoir of antimicrobial-resistance genes within aquatic ecosystems (Maia *et al.*, 2023; Milijasevic *et al.*, 2024). Aquaculture environments may facilitate selection and persistence of resistant bacteria when antimicrobials are used excessively or without appropriate diagnostic guidance.

Accurate diagnosis is equally important. Conventional biochemical identification and single-gene approaches may be insufficient for reliable discrimination among closely related *Aeromonas* species. The increasing application of species-specific PCR, MALDI-TOF MS, multilocus approaches, ANI and whole-genome sequencing provides improved resolution for pathogen identification and epidemiological surveillance (Chen *et al.*, 2015; Maia *et al.*, 2023).

Disease control is also moving toward a more sustainable model. Although antimicrobials remain useful

when appropriately indicated, long-term dependence on chemotherapy is increasingly difficult to justify because of antimicrobial resistance and environmental concerns. Vaccination, particularly mucosal and immersion approaches, represents an important preventive strategy, while probiotics, immunostimulants, functional feeds, phytochemicals, bacteriophages and anti-biofilm approaches provide complementary alternatives (Dien *et al.*, 2023; Sukkarun *et al.*, 2024).

From a One Health perspective, *A. veronii* should not be considered solely as a fish pathogen. Its presence across aquatic environments, aquaculture systems, food-associated environments and human infections, together with its capacity to harbour antimicrobial-resistance determinants, creates opportunities for interactions among animal, environmental and human microbial populations (Liu *et al.*, 2022; Milijasevic *et al.*, 2024).

Future research should focus on linking bacterial genotype with phenotype, identifying conserved protective antigens, understanding environmental regulation of virulence, characterizing mobile resistance elements, improving mucosal vaccines, developing robust probiotics and functional feeds, optimizing phage cocktails and validating emerging interventions under commercial aquaculture conditions.

Overall, sustainable control of *A. veronii* will require a transition from reactive antimicrobial treatment toward predictive, preventive and integrated disease management. Combining

biosecurity, water-quality management, vaccination, nutritional and microbiome-based interventions, rapid diagnostics, responsible antimicrobial use, genomic surveillance and targeted biological control offers the most promising pathway for reducing disease losses while limiting antimicrobial resistance. Such an integrated framework will be essential for protecting aquatic animal health, improving food security, safeguarding environmental health and supporting the long-term sustainability of aquaculture.

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Conflict of interest

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Author cContributions

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evidence, and preparation and revision of the manuscript. All authors have read and approved the final version of the manuscript.

Data availability statement

No new experimental datasets were generated or analyzed in this review. All information discussed in this article was obtained from previously published literature cited within the manuscript.

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