

# Understanding Aeromonas: Virulence Factors, Clinical Implications, and Therapeutic Approaches

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## ABSTRACT

The genus *Aeromonas* includes over 30 species of Gram-negative bacteria that are naturally found in aquatic environments. Although they are commonly thought of as fish and other animal pathogens, these microorganisms have gained attention in medical trials because of their capacity to colonize and infect humans. In addition to water, *Aeromonas* can be found in a wide variety of sources, including soil, vegetables, and food. Despite their opportunistic nature, they can infect patients who are immunocompromised or immunocompetent. *Aeromonas hydrophila*, *Aeromonas veronii* *bv. sobria*, *Aeromonas caviae*, and *Aeromonas dhakensis* are typically considered potential human pathogens. The most common clinical signs and symptoms include septicemia, wound and soft tissue infections, and gastrointestinal tract diseases. When it comes to antibiotic reactions, the bacteria exhibit a varied sensitivity profile and ampicillin resistance. This article focused on the *Aeromonas* species, virulent factors, pathogenesis, diagnosis, and treatment.

**Keywords:** *Aeromonas*, Species, Virulent factors, Pathogenesis, Diagnosis

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## Introduction

*Aeromonas veronii* (*A. veronii*) is an opportunistic bacterium that affects both humans and animals (1). Which is under the family Aeromonadaceae, order Aeromonadales, and class of Gammaproteobacteria (2). It is a rod-shaped, gram-negative as seen in Fig. 1, and catalase and oxidase are positive (3). When it comes to people, *Aeromonas* species can cause diarrhea and wound infections to sepsis in those with weakened immune systems (4).



Fig. 1: *Aeromonas* spp. (5)

There are more than 30 species of *Aeromonas*, and the most commonly linked species of *Aeromonas* to human infection are *A. hydrophila*, *A. veronii* *bv. sobria*, *A. caviae*, and the newly discovered pathogen, *A. dhakensis* (6, 7). In order to definitively identify *Aeromonas* species, multiple housekeeping genes or whole genome sequencing are necessary, as routine microbiology laboratory phenotypic assays cannot reliably identify them to the species level. Several species of *Aeromonas* are regarded as emerging pathogens since they infect both immunocompetent and immunocompromised people and cause a variety of diseases, primarily gastroenteritis, wound infections, biliary tract infections, necrotizing fasciitis, meningitis, endogenous endophthalmitis, and bacteremia/septicemia (8, 9). Infection usually happens after consuming contaminated food or drink; however, wound infection is caused by contaminated water exposure (10). *Aeromonas* are found in a wide range of environments, including soil and vegetables, in addition to water and food (9, 10).

In order to definitively identify *Aeromonas* species, multiple housekeeping genes or whole genome sequencing are necessary, as routine microbiology laboratory phenotypic assays cannot reliably identify them to the species

level (11). *Aeromonas* has element diverse ranges, denominated virulence factors, which promote adhesion, colonization, and invasion into host cells. These virulence factors, such as membrane components, enzymes, and toxins, for example, are differentially expressed among species, making some strains more virulent than others. Due to their diversity, no single virulence factor was considered determinant in the infectious process generated by this microorganism (12). Currently, antibiotic therapy is the primary basis of its treatment. *Aeromonas* spp. new therapies are urgently needed as antibiotic resistance becomes a more significant problem (13). When it comes to antibiotic reactions, the bacteria exhibit a varied sensitivity profile and ampicillin resistance (13).

## Conclusion

There are several species of *Aeromonas*, and the most pathogenic for humans are *Aeromonas hydrophila*, *Aeromonas veronii* *bv. sobria*, *Aeromonas caviae*, *eromonas dhakensis*. The most common clinical signs and symptoms include septicemia, wound and soft tissue infections, and gastrointestinal tract diseases. When it comes to antibiotic reactions, the bacteria exhibit a varied sensitivity profile and ampicillin resistance.

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