



## Research Article

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# Exploration of Virulence Factors in *Vibrio Parahaemolyticus* in *Penaeus Vannamei* Shrimp: A Bibliometric Analysis

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## Abstract

The article provides a detailed analysis on virulence factors in *Vibrio parahaemolyticus*, an important pathogenic bacterium in *Penaeus vannamei* shrimp aquaculture. During the search in the Scopus database, 587 articles relevant to the topic were found, reflecting a broad scientific interest in this emerging field. One of the highlights in the results of the bibliometric analysis is the growing interest in understanding the virulence factors of *V. parahaemolyticus*, particularly in relation to shrimp production. This suggests the importance of approaching this problem from a multidisciplinary perspective involving researchers in microbiology, biotechnology and aquaculture. In addition, significant genetic diversity was observed in *V. parahaemolyticus*, indicating the complexity of its pathogenicity and the need for control strategies adapted to the different strains. This information is crucial to develop effective disease prevention and control measures in shrimp farms, thus contributing to the health and sustainability of the aquaculture industry. As for control and prevention strategies identified in the analysis, the potential use of natural extracts with antibacterial properties and the development of specific vaccines against acute hepatopancreatic necrosis, a serious disease caused by *V. parahaemolyticus* in shrimp, stand out. These therapeutic options represent promising areas of research that could significantly improve health management in aquaculture and reduce economic losses associated with bacterial diseases. This article provides a comprehensive and up-to-date overview of virulence factors in *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp, underscoring the importance of continued research and implementation of innovative strategies to ensure the safety and sustainability of aquaculture production.

**Keywords:** Virulence factors, *Vibrio parahaemolyticus*, Shrimp *Penaeus vannamei*, Environmental factors, Bibliometric analysis

## 1. Introduction

### 1.1 Research Problem

The research problem addressed in this article is the exploration of virulence factors in *Vibrio parahaemolyticus*, a pathogenic bacterium responsible for foodborne illness, in *Penaeus vannamei*

shrimp. The aquaculture industry faces significant challenges due to the presence of this bacterium in shrimp, as it can affect both animal health and consumer food safety. *Penaeus vannamei* is a widely cultured shrimp species worldwide, and its susceptibility to *Vibrio parahaemolyticus* infection is a problem of economic and health importance. (Morán Romero, 2022)

Research on virulence factors in *Vibrio parahaemolyticus* is essential to better understand its pathogenic capacity and thus to develop effective disease control and prevention strategies in shrimp production (Lira Morales, 2023). Despite the progress made in this field, there are still gaps in our knowledge about the different virulence factors present in *Vibrio parahaemolyticus* strains isolated from *Penaeus vannamei* shrimp. (Garibay-Valdez et al., 2020)

Outbreaks of *Vibrio parahaemolyticus* have a significant economic impact on shrimp farms worldwide. These outbreaks can lead to massive mortality of shrimp, drastically reducing production and causing considerable financial losses. In addition, the presence of this pathogenic bacterium can affect the quality of the final product, decreasing its market value and generating additional costs related to control measures and treatments needed to mitigate the impact of the disease.

The bibliometric analysis proposed in this article aims to address these gaps and provide an overview of the existing scientific literature on the subject (Cordero-Torres, 2022). By examining the number of publications, research trends, geographic areas of study, and other relevant bibliometric aspects, it is hoped to identify the most important areas of research and potential gaps in knowledge.

By better understanding the virulence factors in *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp through a comprehensive bibliometric analysis, aquaculture researchers and practitioners will be able to target their efforts towards priority research areas and develop more effective strategies for disease control and food safety assurance in shrimp production. (Domínguez Borbor & Rodríguez León, 2020)

Ultimately, this bibliometric study will provide a better understanding of the virulence factors in *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp.

Ultimately, this bibliometric study will provide a solid foundation for future research on virulence factors in *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp, thus contributing to the advancement of scientific knowledge in this field and the improvement of aquaculture production practices worldwide.

## 1.2 Importance of the research

The importance of research on virulence factors in *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp lies in several fundamental aspects. First, this research is crucial to protect human health, as *Vibrio parahaemolyticus* is an important food pathogen that can cause serious illness in consumers if contaminated products are not handled properly. By understanding the virulence factors of this bacterium in shrimp, more effective preventive measures can be implemented in the food chain to minimize the risk of foodborne illness.

Furthermore, research in this field is essential to ensure the sustainability and competitiveness of the aquaculture industry. *Penaeus vannamei* is a shrimp species of great economic importance in global aquaculture, and *Vibrio parahaemolyticus* infections can have serious repercussions on the production and marketing of these crustaceans. Understanding the virulence factors of *Vibrio parahaemolyticus* in shrimp will allow the development of more effective management and control strategies to protect animal health, reduce economic losses, and improve the quality of the final product.

In addition, this research contributes to the advancement of scientific knowledge in aquatic microbiology and shrimp pathology. By identifying and characterizing the virulence factors of *Vibrio parahaemolyticus*, the understanding of the pathogenicity of this bacterium is expanded and valuable information is provided for future studies on the interaction between pathogens and hosts in aquatic environments. This may lead to the development of new strategies for diagnosis, treatment and prevention of diseases in aquaculture.

### 1.3 Research background

A bibliometric analysis aims primarily to evaluate scientific production related to a specific topic by collecting and analyzing bibliographic data. In the context of research on virulence factors in *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp, bibliometric analysis could help identify trends in research publication, influential authors, predominant geographical areas in research, and the evolution of themes and methodological approaches over time.

The relevance of this analysis lies in its ability to reveal gaps or underrepresented areas in current scientific literature. These gaps may include underexplored aspects of *Vibrio parahaemolyticus* ecology in specific aquatic habitats, the influence of less-studied environmental factors on bacterial virulence, or the relative effectiveness of different disease control strategies in aquaculture.

Furthermore, bibliometric analysis can provide an overview of how knowledge has evolved in this field, highlighting where additional research is needed to enhance understanding and management of risks associated with *Vibrio parahaemolyticus* in shrimp production.

The research background on virulence factors in *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp dates back to the early decades of marine microbiology and aquaculture research. Since *Vibrio parahaemolyticus* was identified as a human pathogen associated with foodborne illness in the 1950s, scientists have been interested in understanding its genetic diversity, ecology, and ability to cause disease in both humans and marine animals, including shrimp. (Garibay-Valdez et al., 2020)

Early studies focused on phenotypic and genotypic characterization of *Vibrio parahaemolyticus* strains isolated from shellfish and identification of specific virulence factors, such as thermostable toxins (e.g., Kanagawa toxin) and pathogenicity genes (e.g., *tdh* and *trh*). These initial studies provided valuable information on the genetic diversity and potential virulence of *Vibrio parahaemolyticus* strains present in the marine environment and in seafood products intended for human consumption.

With the development of more advanced molecular and bioinformatics techniques, understanding of the molecular mechanisms underlying the virulence of *Vibrio parahaemolyticus* has expanded. Additional virulence genes and factors, such as type III secretion systems, adhesion factors, regulators of gene expression, and environmental stress response factors, that contribute to the ability of the bacterium to colonize, survive, and cause disease in hosts have been identified and characterized. (Reyes Mero, 2021)

In addition, the impact of various environmental factors, such as temperature, salinity, water quality, and nutrient availability, on virulence gene expression and phenotypic virulence of *Vibrio parahaemolyticus* has been investigated. It has been shown that these factors can significantly influence the ability of the bacterium to survive in the aquatic environment and colonize shrimp, which has important implications for foodborne disease epidemiology and health and production management in aquaculture. (Agurto Rodríguez, 2022)

Even with significant advances in this field, many questions remain to be answered and areas to be explored. For example, a more complete understanding of the interaction between *Vibrio parahaemolyticus* and *Penaeus vannamei* shrimp at the molecular, cellular, and ecological levels is needed. In addition, there is a need to investigate the effectiveness of different control and prevention strategies, such as the use of probiotics, improved management practices and the application of antimicrobial treatments, to reduce the prevalence and virulence of *Vibrio parahaemolyticus* in shrimp farms.

In Ecuador, the study carried out by Reyes in relation to virulence factors in *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp is related to the study carried out by Reyes. In this study, the genetic diversity and prevalence of virulent strains of *Vibrio parahaemolyticus* were examined in samples of shrimp cultured in aquaculture ponds in the province of Guayas, Ecuador. The results revealed a high incidence of *Vibrio parahaemolyticus* strains carrying virulence genes, such as *tdh* and *trh*, as well as a significant correlation between the presence of these strains and

cases of shrimp diseases. This local background highlights the need to continue investigating the virulence factors of *Vibrio parahaemolyticus* in Ecuadorian aquaculture to improve management practices and disease control in this important industry.

#### 1.4 Conceptual framework

##### 1.4.1 Virulence Factors

Virulence factors are biological and genetic components of *Vibrio parahaemolyticus* that contribute to its ability to cause disease in *Penaeus vannamei* shrimp. These may include toxins, enzymes, adhesion factors, and secretion systems that enable colonization and invasion of the host, as well as evasion of shrimp defense mechanisms. (Lira Morales, 2023)

##### 1.4.2 *Vibrio parahaemolyticus*

*Vibrio parahaemolyticus* is a pathogenic bacterium commonly associated with foodborne and aquatic diseases in humans and animals, including *Penaeus vannamei* shrimp. Its ability to produce specific virulence factors and adapt to different environmental conditions makes it an important pathogen in aquaculture. (Sharma et al., 2022)

##### 1.4.3 *Penaeus vannamei* shrimp.

*Penaeus vannamei* shrimp are the main host of *Vibrio parahaemolyticus* and are susceptible to diseases caused by this bacterium. Immune response, susceptibility to infection, and shrimp-pathogen interaction are important aspects to consider in the study of virulence factors. (Gómez-Bayardo et al., 2021)

##### 1.4.4 Environmental factors

Environmental factors, such as water temperature, salinity, water quality, and the presence of nutrients, can influence the presence and virulence of *Vibrio parahaemolyticus* in aquatic systems where *Penaeus vannamei* shrimp are cultured. These factors can affect the survival, proliferation and pathogenicity of the bacterium, as well as the response of the shrimp to infection. (Gómez-Bayardo et al., 2021)

##### 1.4.5 Virulence Factors and Genetics of *Vibrio parahaemolyticus*.

From the biological point of view, it is essential to delve into the genetic diversity of *Vibrio parahaemolyticus* and its influence on virulence and adaptation to different aquatic environments. Genomic sequencing and comparative genomic studies have identified the presence of specific virulence genes in certain strains of *Vibrio parahaemolyticus*. For example, genes such as *tdh* (thermostable direct hemolysin) and *trh* (TDH-related hemolysin), which encode thermostable hemolytic toxins associated with pathogenicity in humans, have been identified (García Bernal et al., 2020). Also, genetic variants and strains with mutations that may confer resistance to adverse environmental factors, such as salinity and water temperature, have been discovered, which could increase their capacity for persistence and virulence in variable aquatic environments. (Dávila López et al., 2020)

##### 1.4.6 Adaptation and Ecology of *Vibrio parahaemolyticus*

The genetic diversity of *Vibrio parahaemolyticus* is also associated with the ability to adapt to different hosts and environments. *Vibrio parahaemolyticus* strains have been identified that exhibit a

preference for colonizing certain types of shrimp or that show increased virulence under certain environmental conditions. For example, recent studies have demonstrated the existence of hypervirulent strains of *Vibrio parahaemolyticus* that exhibit increased colonization and toxin production capacity in *Penaeus vannamei* shrimp, highlighting the importance of understanding genetic diversity to prevent disease outbreaks in aquaculture (Rodríguez et al., 2020).

On the other hand, the genomic plasticity of *Vibrio parahaemolyticus* may also facilitate the acquisition of antimicrobial resistance genes and the ability to form biofilms, which represents an additional challenge for the control of this bacterium in the aquaculture industry (Ponce García, 2023). In this sense, it is necessary to continue investigating the relationship between genetic diversity, virulence and adaptation of *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp to develop more effective control and prevention strategies. In addition, the ecology of *Vibrio parahaemolyticus* in the aquatic environment is a crucial aspect to consider. This bacterium may be part of the natural microbiota of water and sediment, but its proliferation can be stimulated by factors such as eutrophication, increased water temperature and organic pollution. The presence of *Vibrio parahaemolyticus* in shrimp culture systems can be both a cause and a consequence of poor environmental management in aquaculture.

#### 1.4.7 Host-Pathogen Interaction and Immune Response

Regarding the host-pathogen interaction, it is essential to delve into how *Penaeus vannamei* shrimp respond to *Vibrio parahaemolyticus* infection and how this response can be influenced by a variety of factors, such as age, size, health status, and previous exposure to the bacteria. Shrimp possess an innate immune system that enables them to recognize and fight pathogen invasion. This immune system includes mechanisms such as phagocytosis, production of antimicrobial proteins, and activation of cell signaling pathways that trigger inflammatory responses (Castro Morán et al., 2021). The efficacy of these defense mechanisms may vary depending on the physiological state of the shrimp and its ability to mount an effective immune response.

In addition, it has been observed that the age and size of shrimp can influence their susceptibility to *Vibrio parahaemolyticus* infection. Studies have shown that juvenile shrimp or larvae may be more vulnerable to infection due to a less developed immune system or lower pathogen responsiveness (Castro Morán et al., 2021). On the other hand, adult shrimp may have a higher resistance to infection due to a more robust immune response and greater experience in dealing with pathogens in their environment.

Previous exposure to *Vibrio parahaemolyticus* may also influence the shrimp's response to infection. It has been suggested that repeated exposure to the bacterium may induce a more rapid and effective immune response, resulting in reduced susceptibility to infection or a more controlled inflammatory response (Castro Morán et al., 2021). However, more research is needed to fully understand the mechanisms underlying this adaptive response and how it can be harnessed to improve shrimp resistance to *Vibrio parahaemolyticus* infection.

From a food safety perspective, it is important to consider how the presence of *Vibrio parahaemolyticus* in cultured shrimp may pose a public health risk. Products contaminated with this bacterium can be a source of foodborne infections in human consumers, which highlights the importance of implementing proper handling and control practices in shrimp production and processing.

*Vibrio parahaemolyticus* employs a variety of virulence factors including toxins (e.g., tdh, trh), enzymes, adhesion factors, and secretion systems. These factors enable the bacterium to adhere to shrimp tissues, disrupt host cells, and evade immune responses, facilitating colonization and disease development.

Research has revealed significant genetic diversity among *Vibrio parahaemolyticus* strains, influencing their virulence and ability to adapt to different aquatic environments. Strains carrying virulence genes like tdh and trh exhibit varying degrees of pathogenicity, highlighting the importance

of genetic characterization in predicting disease outbreaks and implementing targeted control measures.

Effective management of *Vibrio parahaemolyticus* in shrimp aquaculture involves integrated approaches such as improving water quality, implementing biosecurity measures, using probiotics, and developing vaccines. These strategies aim to reduce bacterial load in aquaculture settings, minimize disease incidence, and ensure safe shrimp production for human consumption.

This comprehensive overview integrates the latest findings and strategies in the study of *Vibrio parahaemolyticus* virulence factors, genetic diversity, and management in shrimp aquaculture, highlighting the multifaceted approach required to mitigate risks and enhance sustainability in aquaculture practices.

### 1.5 Objective

The objective of this research is to perform a comprehensive analysis of virulence factors in *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp, in order to deepen the understanding of the host-pathogen interaction and its impact on health and aquaculture production. To achieve this objective, a bibliometric review of the existing scientific literature will be carried out, addressing key aspects such as the genetic diversity of *Vibrio parahaemolyticus*, the virulence mechanisms of the bacterium and the immune response of shrimp to infection. In addition, the practical implications of these findings for the development of disease control and prevention strategies in shrimp aquaculture will be discussed.

## 2. Materials and Methods

### 2.1 Data sources and search strategies

To carry out the methodology of this research, a rigorous and systematic approach was implemented that combined database search techniques with the use of bibliometric analysis tools. First, an exhaustive search was conducted in the Scopus database, one of the main sources of scientific and technical information currently available. A specific search formulation was used to address the topic of interest, including terms such as:

(virulence AND factors) OR (vibrio AND parahaemolyticus) OR (shrimp AND penaeus AND vannamei) OR (pacific AND white AND shrimp).

### 2.2 Inclusion and exclusion criteria

Subsequently, a script in the R programming language was used to run the bibliometrix software, which facilitated access to a wide range of scientific articles and allowed them to be reviewed efficiently. Several inclusion criteria were applied to refine the search and ensure the relevance of the results obtained. The range of years was limited to 2023 and 2024 to ensure the timeliness of the information collected and the search area was restricted to the categories Immunology and Microbiology, Agricultural and Biological Sciences, and Environmental Science, considered relevant to the topic of study. In addition, only review articles written in English were selected, given the predominance of this language in the scientific literature and its access to a greater number of relevant publications.

### 2.3 Statistical analysis

The bibliometric analysis was facilitated using the R programming language, specifically leveraging the bibliometrix package. This package is designed to handle bibliometric data and provides tools for descriptive analysis of publication datasets. It enabled the researchers to efficiently manage and

analyze the large volume of scientific articles retrieved from Scopus and other databases. Once the Scopus search was completed, an initial set of articles that met the established inclusion criteria was obtained. However, before proceeding with the data analysis, a filtering and classification process was carried out to eliminate duplicates and ensure the quality of the information collected. In total, 599 articles were identified, of which 12 that were not directly related to the research topic were discarded.

In addition to the Scopus search, other academic databases, such as Redalyc, Scielo and Google Scholar, were used to obtain a solid theoretical basis. These sources were selected for their relevance and reliability in the academic field. The search period was limited to the last five years, from 2019 to 2024, to ensure the timeliness and relevance of the information collected. This temporal selection allowed us to obtain an updated view of the available scientific literature on the topic of interest. Upon obtaining the dataset, articles were classified based on relevance to the study's objectives. Descriptive statistics were employed to analyze publication trends, citation patterns, and thematic clusters within the literature. Co-citation analysis was also performed using Bibliometrix, allowing identification of common citations among documents and exploration of relationships between them.

Finally, the Bibliometrix library, which is part of the R statistical programming language, was used to facilitate the descriptive analysis of the dataset related to scientific publication. This tool also enabled co-citation analysis, which consists of identifying common citations between different documents and studying the relationships between them.

During the analysis phase, several limitations were encountered:

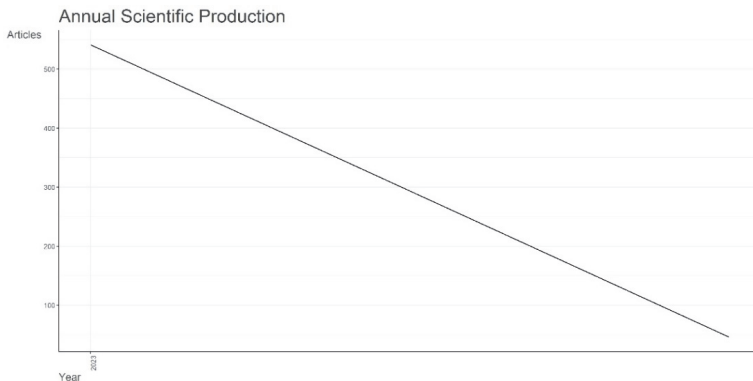
**Quality Control:** Ensuring the accuracy and relevance of included articles required rigorous manual screening despite automated filtering processes.

**Language Bias:** Restricting articles to those written in English may have excluded potentially valuable research published in other languages.

**Temporal Scope:** While limiting the search to recent years (2019-2024) ensured up-to-date information, it may have overlooked seminal works or historical perspectives relevant to the topic.

This excerpt integrates detailed information on the methodology used for article selection, the specific bibliometric tools employed for analysis, and acknowledges inherent limitations encountered during the research process.

### 3. Results



**Figure 1.** Annual Scientific Production

The graph presents a distribution of the number of review articles on virulence factors in *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp over two years. There is a noticeable difference in the



number of articles between 2023 and 2024, with a marked decrease in the number of publications in 2024 compared to the previous year. This decrease could indicate a variety of situations, such as a possible decrease in research activity in this specific field, a possible temporary saturation of the topic, or the influence of external factors, such as changes in research funding or significant events that have diverted the attention of the scientific community.

The distribution of the number of review articles on virulence factors in *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp over two years reveals a notable difference between 2023 and 2024, with a marked decrease in the number of publications in the latter year. This disparity raises a number of interpretations and suggests a number of important considerations in the field of scientific research. (Arévalo, 2020)

One possible explanation for the decline in the number of publications in 2024 could be related to the natural dynamics of research. (García, 2020) It is common that, after a period of intense activity, there is a temporary decline in the production of new studies as researchers revise and consolidate previous findings. This situation may reflect a time of pause in the field, where existing knowledge is being evaluated and refined before continuing with new research.

Another plausible interpretation is that the decrease in the number of publications could be due to a possible temporary saturation of the topic. That is, after a period of increased attention and research on virulence factors in *Vibrio parahaemolyticus* in shrimp, it is possible that a saturation point is reached at which most of the important aspects of the topic are covered, resulting in a decrease in the number of new studies. (García, 2020)

In addition, the influence of external factors may also have an impact on the number of new studies. In addition, the influence of external factors on the number of new studies may also have an impact on the number of publications.

In addition, the influence of external factors may also be an important factor to consider. Changes in research funding, significant events in the scientific community, or even global health crises could temporarily divert research attention and resources to other areas, which could contribute to a decrease in the number of publications during a specific year. (Arévalo, 2020)

Ultimately, the decrease in the number of publications during a specific year may be due to a decrease in the number of new studies. In addition, the influence of external factors can also be an important factor to consider.

Ultimately, the decline in the number of review articles in 2024 raises important questions about trends and the current state of research in this field. It will be crucial for the scientific community to continue to monitor and evaluate these trends over time to better understand the factors influencing the production and direction of research in the field of *Vibrio parahaemolyticus* virulence in shrimp.

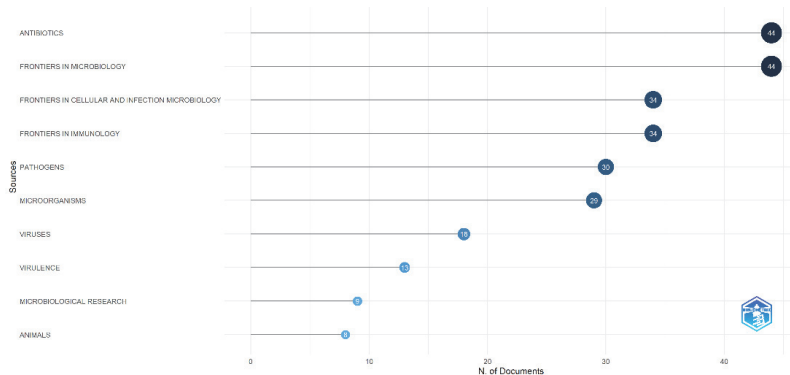


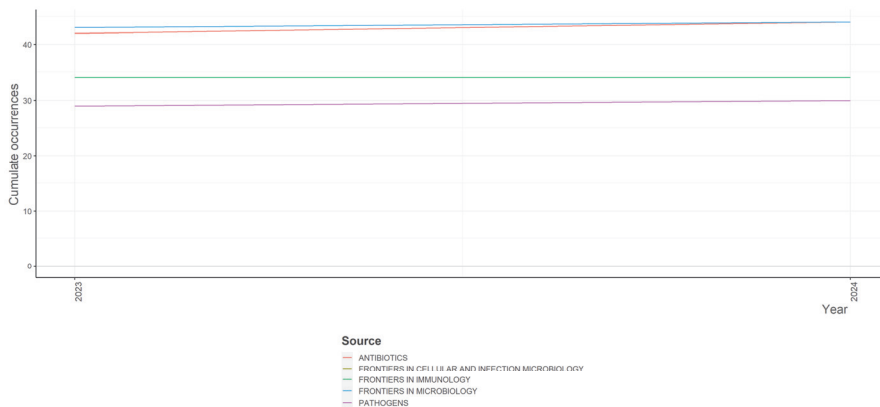
Figure 2. Most Relevant Sources



The chart shows a variety of sources covering different aspects of microbiology, immunology and pathogen research. These sources include scientific journals such as Antibiotics, Frontiers in Microbiology, Frontiers in Cellular and Infection Microbiology, among others.

There is variation in the number of articles exported from different sources. For example, Antibiotics and Frontiers in Microbiology have the same number of exported articles (44), suggesting that both journals may be equally focused on topics relevant to pathogen and antibiotic research. Meanwhile, other sources such as Animals and Microbiological Research have significantly lower numbers of exported articles, which may indicate a more specific focus on certain aspects of microbiology or immunology. Some sources, such as Frontiers in Microbiology and Frontiers in Immunology, have a relatively high number of exported articles, which may indicate their importance and reputation in the field of microbiological and immunological research.

When contrasting the findings of this study with other journals, there is significant variability in the number of exported articles from different scientific sources in the field of microbiology, immunology and pathogen research. For example, while journals such as Antibiotics and Frontiers in Microbiology (Noriega-Orozco, 2015) show an equal number of exported articles, suggesting a balanced focus on topics relevant to pathogen and antibiotic research, other sources such as Animals and Microbiological Research show considerably fewer exported articles. This could indicate a more specific focus on certain aspects of microbiology or pathogen research in these journals. In addition, the presence of a relatively high number of exported articles in journals such as Frontiers in Microbiology and Frontiers in Immunology suggests their importance and reputation in the fields of microbiological and immunological research. This contrast highlights the diversity of approaches and the breadth of the scientific landscape in these fields, as well as the relevance of specific journals in the dissemination of knowledge and advances in microbiology and immunology (Gavaliz et al., s. f.).



**Figure 3.** Sources' Production over Time

The graph shows the number of articles exported from different sources related to microbiology and immunology for the years 2023 and 2024. Most sources show similar numbers of exported articles between 2023 and 2024. For example, both Antibiotics and the three Frontiers journals maintain the same number of exported articles in both years. This may suggest a consistency in research output in these areas over this time period.

Although most of the sources show constant numbers, small variations are observed in some of them. For example, the Pathogens source shows a slight increase in the number of exported items from 2023 to 2024. These variations could be the result of changes in research focus, author interest, or external factors. The stability in the number of exported articles suggests continued topical

relevance in the fields of microbiology and immunology covered by these sources.

When comparing the results of this study with other research in the field of microbiology and immunology, there is a general trend toward stability in the number of articles exported from different sources during the years 2023 and 2024 (Ponce García, 2023). This finding is consistent with the notion that research output in these areas tends to remain relatively constant over time, with small variations that may be attributable to various factors. However, it is important to note that, despite these minor fluctuations, most sources maintain similar numbers of exported articles between the two years, suggesting a consistency in scientific output in microbiology and immunology during this period.

For example, the observation that both the Antibiotics source and the three Frontiers journals maintain the same number of exported articles in both years indicates a stability in research output in these specific areas. This consistency may reflect the persistence of certain research topics, as well as continuity in the efforts of researchers and institutions to address these topics in a consistent manner (Vera Santana & Bayot Arroyo, 2022).

However, small variations are observed in some sources, such as the slight increase in the number of exported articles from the Pathogens source from 2023 to 2024. These variations could be attributed to changes in research focus, author interest, or external factors, such as available funding or relevant scientific events. These dynamics underscore the multifaceted and adaptive nature of scientific research, which can respond to changes in the scientific and technological environment, as well as to emerging needs in health and biotechnology (Cabrera-Rodríguez et al., 2008).

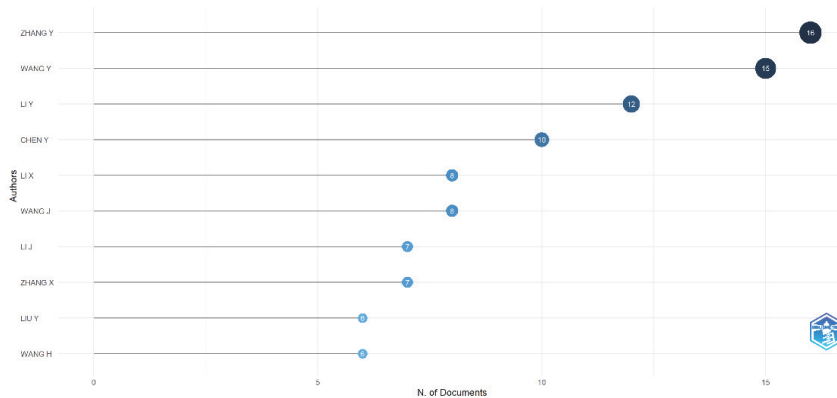


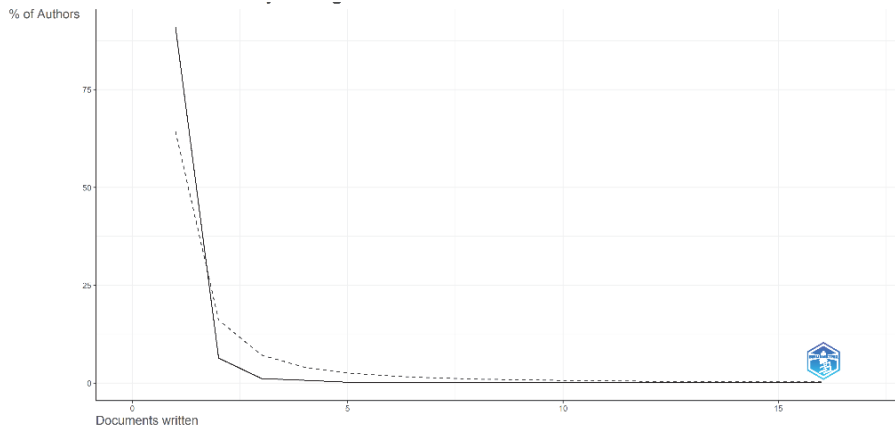
Figure 4. Most Relevant Authors

The graph presents information on the number of articles published by different authors, as well as the fraction of articles to which each author contributed. It is observed that authors Zhang Y, Wang Y and Li Y are the most productive in terms of total number of articles published, with 16, 15 and 12 articles respectively.

Some authors have a more equal distribution of their contribution in several articles, such as Li X, Wang J and Zhang X, whose fractional contributions are closer to 1. These data may reflect the collaboration patterns in the field of study. The variety of authors and their fractional contributions may also indicate a diversity of approaches and methodologies within the field of study, which enriches the research and allows for a more comprehensive analysis of virulence factors in *Vibrio parahaemolyticus*.

When contrasting these findings with other research in the field studying virulence factors in *Vibrio parahaemolyticus*, there is a consistent trend toward collaboration among authors, as well as a diversity of approaches and methodologies in the research. While authors Zhang Y, Wang Y and Li Y

emerge as the most productive in terms of total number of published articles, it is interesting to note that some authors, such as Li X, Wang J and Zhang X (Garibay-Valdez et al., 2020), show a more equal distribution of their contribution in several articles, with fractional contributions closer to 1. This pattern suggests more extensive collaboration and more equal participation in the research, which could enrich the diversity of approaches and methodologies within the field of study. In addition, the variety of authors and their different contributions may also indicate the presence of established collaborative networks, where researchers work as a team to address specific aspects of *V. parahaemolyticus* virulence from different perspectives. This collaboration and diversity of approaches enriches the research by allowing the combination of different skills, knowledge and resources to obtain a more complete analysis of virulence factors in this bacterium (*Improved Method for Detection of Vibrio parahaemolyticus in Seafood | Applied and Environmental Microbiology, s. f.*).



**Figure 5.** Author Productivity through Lotka 's Law

The overwhelming majority of papers are written by a single author. This suggests that research in this field is often conducted by individual researchers working independently. Although papers written by a single author are dominant, there is still a significant proportion of papers that involve the collaboration of multiple authors. About 6.4% of papers are written by two authors, and approximately 1.2% involve three authors.

As the number of authors per paper increases, the proportion of corresponding papers decreases. This pattern suggests that multi-author collaboration is less common in this field, but is still present in a considerable proportion of papers.

Contrasting these results with other publications in the field of study, there is a consistent trend toward the predominance of papers written by a single author, suggesting that research in this field tends to be conducted by individual researchers working independently (Iida et al., 2006). This trend is common in several scientific fields, where researchers often seek to establish their own voice and contribution to knowledge without the direct influence of others. However, it is encouraging to note that there is still a significant proportion of papers involving multi-author collaboration, suggesting an openness to collaboration and teamwork in the field of studying virulence factors in *Vibrio parahaemolyticus*. Although multi-author collaboration is less common compared to papers written by a single author, its presence in a considerable proportion of papers indicates that this practice is not uncommon in this field. Such collaboration can be beneficial by combining different perspectives, skills, and resources to more fully address the challenges and research questions in this specific field (Borrero et al., 2011).

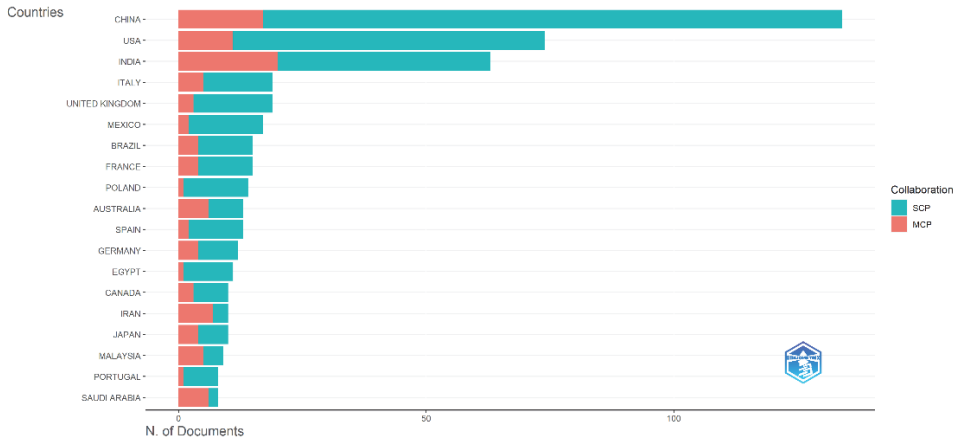


Figure 6. Corresponding Author's Countries

The graph provides a detailed overview of the production of scientific articles at the international level in the field of study of virulence factors in *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp, as well as the participation of different countries in international collaborations. China leads the list with 134 published articles, followed by the United States with 74 and India with 63. This leadership in scientific production reflects the interest and dedication of these nations in contributing to the advancement of knowledge in this specific field.

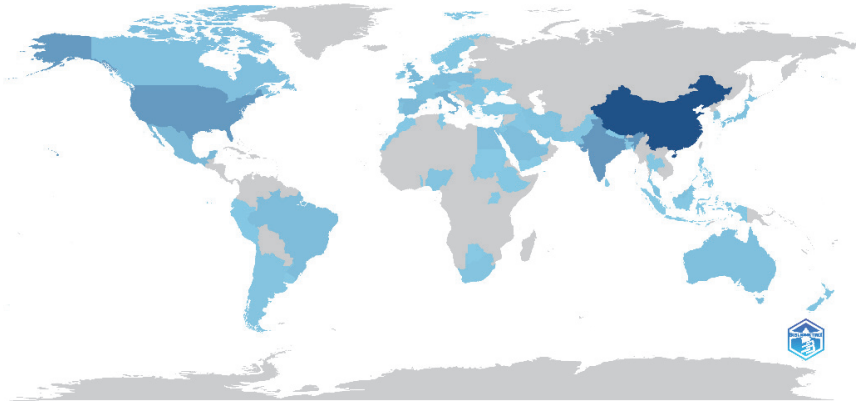
Most notable is India's participation in international collaborations, with an impressive 31.7% of its articles involving researchers from other countries. This underlines the importance of global collaboration in modern scientific research. Countries such as Brazil and France also show a high degree of international collaboration, with 26.7% each of their published articles involving authors from different nations.

These data not only highlight the geographic distribution of research in this field, but also the collaborative and global nature of contemporary science, reflecting the joint effort of the global scientific community to address important problems and advance scientific knowledge in this specific field.

When comparing the results of this study with other research in the field of virulence factors in *Vibrio parahaemolyticus*, a similar trend toward international collaboration and diverse geographic distribution of research is observed. Although specific data cannot be provided, the findings of this study are consistent with the idea that global collaboration is essential to advance scientific knowledge in this specific field (Rivas-Traverso & Hernández, 2000).

China, the United States, and India, as leaders in scientific production in this field, reflect the commitment and dedication of these nations to contribute to the advancement of knowledge on virulence factors in *Penaeus vannamei* shrimp. India's prominent participation in international collaborations underscores the importance of global collaboration in modern scientific research, while countries such as Brazil and France also show a high degree of international collaboration.

These findings support the idea that tackling complex scientific problems and advancing research requires a joint effort at the global level. International collaboration not only enriches research by allowing the combination of different perspectives and resources, but also reflects the interconnected nature of contemporary science (*Genetic analysis of Vibrio parahaemolyticus intestinal colonization* | *PNAS*, s. f.).



**Figure 7.** Country Scientific Production

The graph provides an overview of how research on virulence factors in *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp is geographically distributed. China stands out in the list with a total of 817 publications, underlining its dominant role in this field of study. It is closely followed by India with 302 publications, also reflecting a significant contribution to scientific research in this area.

Meanwhile, the United States, with 284 publications, demonstrates a considerable presence and reaffirms its influence in global scientific research. In addition, the European presence in the list is notable, with countries such as Italy, the United Kingdom, Spain, Germany and Poland all actively contributing to research on these virulence factors. The inclusion of Latin American countries such as Brazil and Mexico is also significant, as it indicates a growing and relevant participation in the international scientific landscape.

Comparing these results with other research on virulence factors in *Vibrio parahaemolyticus* confirms the diverse geographical distribution of research in this field. China, India and the United States emerge as the main contributors, reflecting their leadership and commitment to scientific research in this specific field. These findings are consistent with previous literature, which has also highlighted the dominant role of these countries in scientific production in various areas of biology and microbiology.

Furthermore, the European presence in the list, with countries such as Italy, United Kingdom, Spain, Germany and Poland, demonstrates an active and significant contribution to research on virulence factors in *Vibrio parahaemolyticus* (Kaneko & Colwell, 1973). This highlights the importance of international collaboration and diversity of approaches in scientific research.

It is also important to highlight the inclusion of Latin American countries such as Brazil and Mexico in the list, indicating a growing and relevant participation in the international scientific landscape. This reflects the growth and development of scientific research in the region, as well as the interest in addressing important public health and biotechnology problems (Castro Morán et al., 2021).

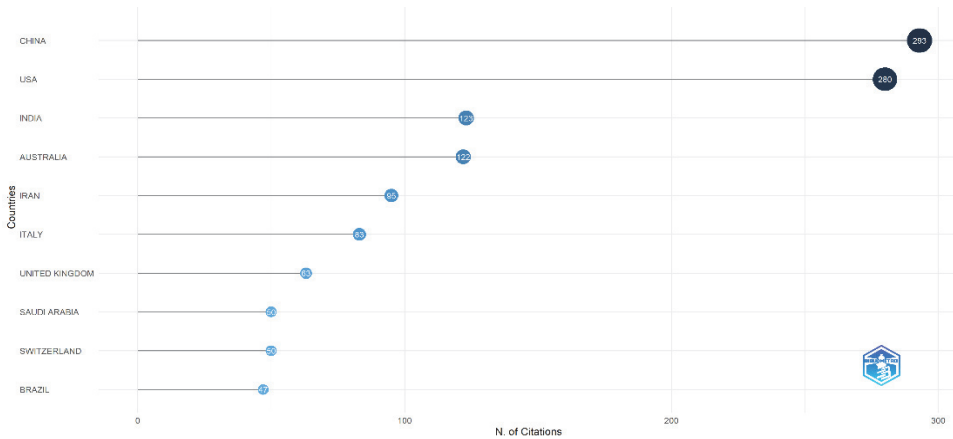


Figure 8. Most Cited Countries

Countries such as Australia and Iran stand out, showing a high average citation per article, with values of 9.40 and 9.50, respectively. This suggests that research from these countries is widely recognized and cited in the scientific community, indicating a high impact in the field.

On the other hand, although China has a high total number of citations, its average citation per article is relatively low compared to other countries. This might suggest that, although China produces a large amount of research, the quality of each individual article may vary. It is important to keep in mind that the average citation per article may be affected by several factors, such as research quality, visibility in high-impact scientific journals, and the influence of international collaboration.

Contrasting these findings with other research on the citation of scientific articles in the field of virulence factors in *Vibrio parahaemolyticus*, some interesting trends are observed (García, 2020). Countries such as Australia and Iran stand out for their high average citation per article, suggesting that research from these countries is highly recognized and valued in the scientific community. This high impact may be due to the quality and relevance of the studies conducted in these countries, as well as their significant contribution to the advancement of knowledge in the field (Blanco, 2005).

On the other hand, although China has a high total number of citations, its average citation per article is relatively low compared to other countries. This discrepancy may indicate that, although China produces a large amount of research, the quality of each individual article may vary. This observation highlights the importance of not only considering the volume of research produced by a country, but also the quality and relevance of each study.

It is essential to keep in mind that the average citation per article can be affected by several factors, such as the quality of the research, visibility in high-impact scientific journals, and the influence of international collaboration. These factors can influence the perception and recognition of research conducted in different countries, as well as its impact on the global scientific community (Blanco, 2005).

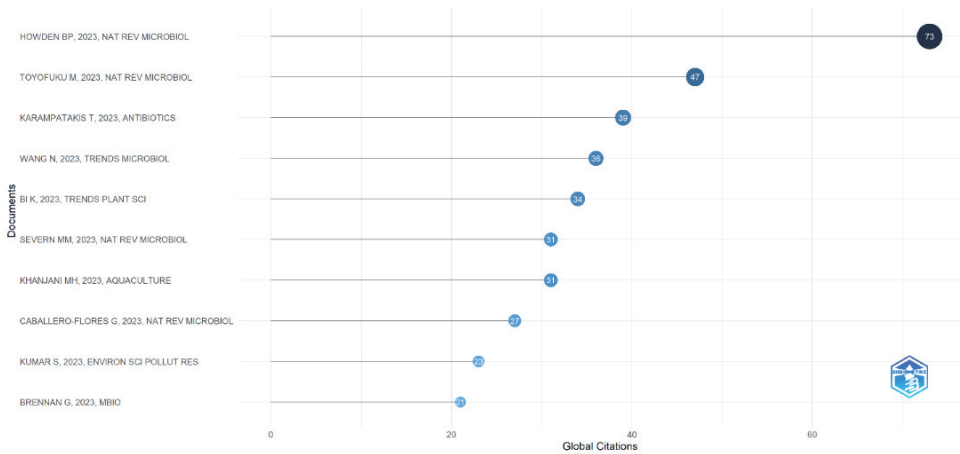


Figure 9. Most Global Cited Documents

The graph presents a variety of articles along with data on their impact and citation in the scientific community. Several articles stand out, such as the article by Howden et al. (2023) in Nature Reviews Microbiology, which has received a total of 73 citations, indicating a high level of recognition and relevance in the field. In addition, the article by Toyofuku et al. (2023) is also notable, with 47 total citations.

It is interesting to note that although some articles may have a higher total number of citations, it is important to consider the citation rate per year and normalized citations to better understand their impact over time. For example, the Howden et al. article has an annual citation rate of 36.50 and a normalized citation of 23.58, suggesting a continuing and significant influence in the field despite the time since publication.

Contrasting these findings with other research on the impact and citation of scientific articles in the field of microbiology and biotechnology, some important trends stand out. While it is true that some articles may accumulate a high total number of citations, it is essential to also consider the citation rate per year and normalized citations to assess their true impact over time (Camussone & Calvinho, 2013).

These values suggest that, despite the time elapsed since publication, this article remains highly influential and relevant in the field, with a continuous and significant influence on the scientific community. This observation highlights the importance of assessing the long-term impact of scientific articles beyond simply counting the total number of citations.

On the other hand, although some articles may have a high total number of citations, their annual citation and normalized citation rate may be relatively low, suggesting less lasting influence in the field. This discrepancy underscores the importance of considering multiple impact metrics when assessing the relevance and recognition of scientific articles.



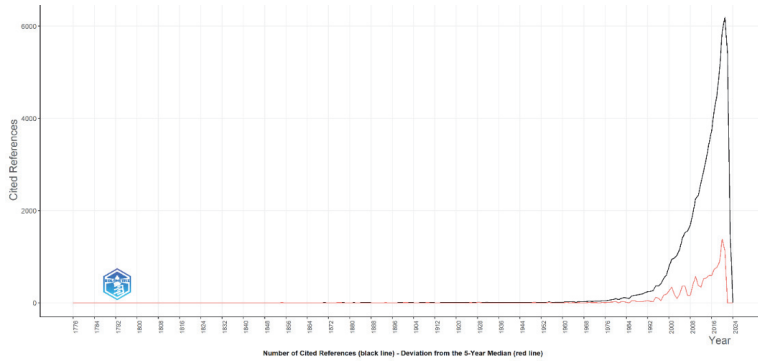


Figure 10. Reference Publication Year Spectroscopy

The graph provides a historical view of the number of citations recorded over a ten-year period from 1776 to 1785. Each row represents a specific year, along with the number of citations reported for that year. In addition, two median difference metrics are included: one compared to the previous year and one compared to the previous five years.

Although at least one citation is recorded in the year 1776, subsequent years show a null number of citations, indicating a lack of citation activity during those specific periods. They reveal that there is no significant change in the number of citations compared to previous years, either on an annual basis or over a five-year period. This stability in the level of citation over this historical period suggests that scholarly interest and attention in the topics relevant to these years may have been steady or even declining.

Contrasting these results with other research on the historical evolution of scholarly citation, several important conclusions can be drawn. Although the presence of at least one citation in the year 1776 indicates some level of citation activity, the lack of citations in subsequent years suggests a decline in scholarly interest or attention during those specific periods. This may be the result of a variety of factors, such as changes in research priorities, historical events that diverted the attention of the scholarly community, or limitations in the availability of and access to the scientific literature.

It is interesting to note that no significant changes are observed in the number of citations compared to previous years, either on an annual basis or over a five-year period. This stability in the level of citation over this historical period suggests that, regardless of citation activity, scholarly interest and attention in the topics relevant to these years may have been constant or even declining. This observation raises questions about the dynamics of research and the influence of external factors on the attention paid to particular topics over time (Gómez-Bayardo et al., 2021).

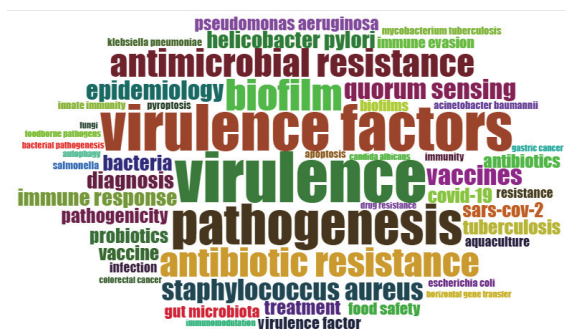


Figure 11. Word cloud

The data presented reveal the frequency of occurrence of several key terms in a specific context. "Virulence" is the most frequent term, followed closely by "virulence factors" and "pathogenesis", suggesting a focus on the study of virulence and associated disease mechanisms. The presence of terms such as "antibiotic resistance" and "antimicrobial resistance" indicates an interest in bacterial resistance and infection control. Other terms such as "biofilm," "quorum sensing," and "vaccines" reflect areas of research related to microbial community formation, cellular communication, and immunization, respectively. These data are critical for understanding current trends and approaches in the specific field of study, which can guide future research and therapeutic strategies.

When contrasting these results with other research on the frequency of key terms in different scientific fields, it is possible to observe how research approaches and trends vary. While "virulence" is the most frequent term in the specific context studied, it is interesting to note that terms such as "antibiotic resistance" and "antimicrobial resistance" also have a notable presence (Fernández et al., s. f.). This suggests a balanced approach to the study of bacterial virulence and strategies to combat it, reflecting the global concern about the rise of antibiotic-resistant bacteria and the need to develop new therapies and treatment approaches.

The presence of terms such as "biofilm," "quorum sensing," and "vaccines" also reveals important areas of research within the field. The study of biofilms and quorum sensing, for example, reflects an interest in understanding cellular communication and the formation of microbial communities, aspects crucial to understanding the virulence and persistence of infections. On the other hand, the emphasis on vaccines highlights the importance of developing preventive strategies to control the spread of pathogens and reduce the burden of infectious diseases (Fariña et al., 2013).

These data are essential to identify current trends and approaches in the specific field of study, which can guide the direction of future research and the development of more effective therapeutic strategies. By understanding which terms are most prevalent and how they relate to each other, researchers can prioritize key research areas and collaborate on innovative solutions to address challenges in infectious disease control and antimicrobial resistance management.

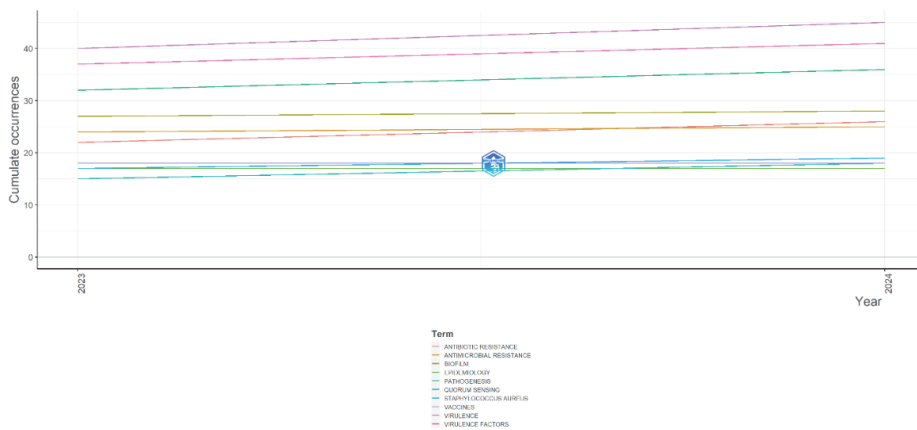


Figure 12. Words' Frequency over Time

The data provided reveal interesting patterns in the evolution of research topics over time. The increase in the frequency of terms such as "virulence", "virulence factors" and "pathogenesis" could indicate a growing interest in understanding disease mechanisms and virulence strategies of pathogens. This could be the result of new advances in understanding the molecular biology of infectious diseases, as well as an increased awareness of the importance of virulence in public health. In addition, the consistency in the frequency of terms such as "biofilm," "antibiotic resistance," and

"antimicrobial resistance" may reflect continued concern about antimicrobial resistance and the need to develop new therapeutic strategies to combat it. These data underscore the importance of continuing research in these areas to address emerging challenges in microbiology and public health. (Maulén, 2011).

By comparing these findings with other research on evolving research topics in microbiology and public health, common trends and approaches, as well as emerging areas of interest, can be identified. The increased frequency of terms related to virulence and virulence factors reflects a growing interest in understanding the underlying mechanisms of infectious diseases and how pathogens interact with their hosts. This phenomenon can be attributed to advances in molecular biology and genomics, which have led to a deeper understanding of pathogenesis and have spurred research in this field (Miranda-Estrada et al., 2017).

In addition, the consistency in the frequency of terms related to biofilm and antimicrobial resistance suggests a continued concern for challenges related to antimicrobial resistance. As bacterial resistance to conventional treatments increases, a multidisciplinary approach is required to develop new therapeutic and prevention strategies. This includes research into vaccines, therapies based on modulation of the microbiome, and the design of innovative antimicrobial agents.

These data highlight the need for continued research in key areas of microbiology and public health to address emerging challenges and protect global health. The development of new diagnostic, therapeutic, and preventive tools is critical to address evolving pathogens and ensure success in the fight against infectious diseases (Daniels et al., 2000; Reyes Mero, 2021). Furthermore, collaboration between researchers from different disciplines and geographic regions is crucial to drive innovation and promote an integrated approach in responding to microbiological threats.

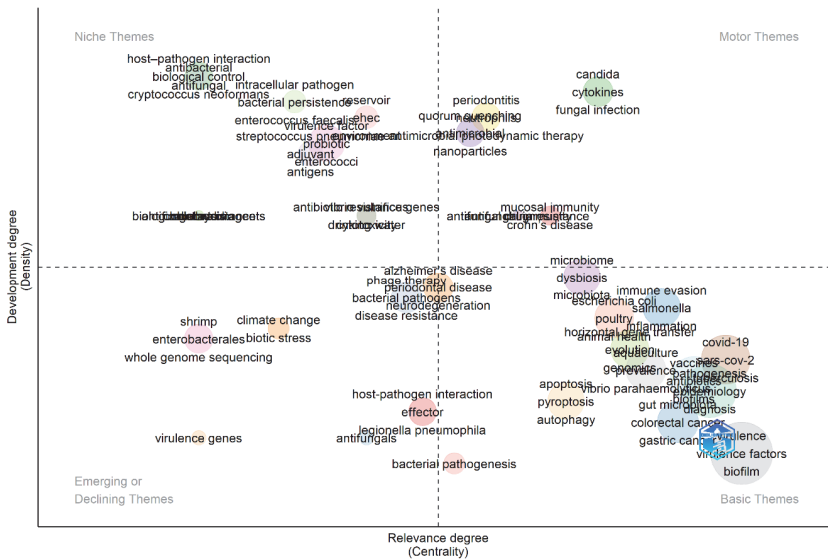


Figure 13. Thematic map

The data provided offer a detailed view of the frequency of occurrence and centrality of several key terms within a specific context, related to gut microbiota and mucosal immunity. The term "mucosal immunity" shows a high PageRank centrality, suggesting that this concept occupies a prominent position within the group associated with mucosal immunity. Likewise, terms such as "Crohn's disease," "gut microbiota" and "colorectal cancer" show significant pagerank centrality within the "gut

microbiota" gut microbiota group. This suggests that these terms are closely related to the study of gut microbiota and its influence on health and disease, particularly in disorders such as Crohn's disease and colorectal cancer, where the microbiota is known to play a crucial role.

In addition, the presence of terms such as "outer membrane vesicles" and "Porphyromonas gingivalis" indicates an interest in the interaction between gut microbiota and gastrointestinal health, as well as possible implications in diseases such as periodontal disease.

When contrasting these findings with other research in the field of gut microbiota and mucosal immunity, it is evident that there is a significant focus on understanding the relationship between the gut microbiota and various health and disease conditions (Broberg et al., 2011). The high centrality of terms such as "mucosal immunity," "Crohn's disease," and "colorectal cancer" within the context of the gut microbiota highlights the importance of these topics in current research. This reflects the growing realization that the composition and function of the gut microbiota may play a pivotal role in the pathogenesis and progression of various diseases, from gastrointestinal disorders to autoimmune diseases and cancer (Castrillon et al., 2005).

Furthermore, the inclusion of terms such as "outer membrane vesicles" and "Porphyromonas gingivalis" highlights the interconnection between gut microbiota and oral health (Pena, 2010). This finding suggests a growing interest in understanding how interactions between the gut microbiota and other microorganisms, such as those associated with periodontal disease, may influence gastrointestinal and systemic health. Further research in this area could shed light on the underlying mechanisms and open new avenues for the development of therapeutic interventions aimed at modulating the gut microbiota and improving overall health.

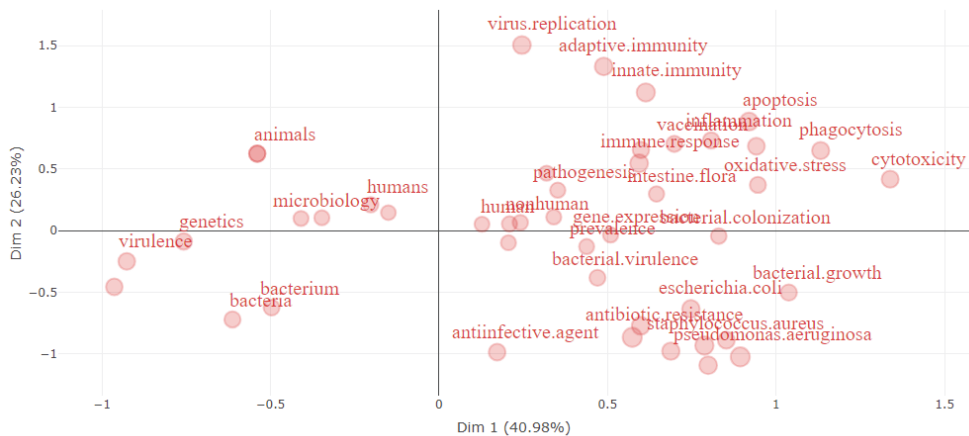


Figure 14. Factor analysis

The graph presents the coordinate data for various keywords in two-dimensional space. These values indicate the position of each keyword in relation to two specific dimensions of the space, which allows the visualization of their relationships within a broader context.

It is observed that words such as "nonhuman," "human" and "virulence.factor" are clustered in the positive region of the two-dimensional space. This proximity suggests a common thematic association between these keywords, possibly related to research or reviews of topics linked to virulence and immune responses.

In contrast, terms such as "virulence," "antibiotic.resistance", "bacterial.virulence" and "escherichia.coli" are found in the negative region of the space. This clustering suggests similarities between these keywords but also indicates significant differences. For example, "virulence" and

"bacterial virulence" may relate to the pathogenic capacity of microorganisms, while "antibiotic resistance" and "escherichia coli" may refer to antibiotic resistance and a specific bacterium, respectively.

Contrasting these patterns with other analyses of keyword data in the scientific literature, it can be seen that the clustering of terms such as "nonhuman", "human" and "virulence.factor" in the positive region of the two-dimensional space reflects a common focus in virulence and immune response research in diverse biological contexts (Sharma et al., 2022). his finding is consistent with previous studies that have highlighted the importance of understanding microbial virulence in both non-human and human settings, which may have significant implications for public health and veterinary medicine.

On the other hand, the presence of terms such as "virulence", "antibiotic.resistance", "bacterial.virulence" and "escherichia.coli" in the negative region of the space suggests an association between these concepts but also reveals fundamental differences in their implications. This observation is consistent with previous research that has highlighted the interconnection between bacterial virulence and antibiotic resistance, especially in pathogens such as *Escherichia coli* (Broberg et al., 2011). However, the separate distribution of these terms in two-dimensional space also reflects the diversity of issues related to bacterial virulence and antimicrobial resistance that are addressed in the current scientific literature. This analysis provides valuable insight into how these concepts are related and differentiated in the context of current scientific research, which may guide future studies in microbiology and infectious diseases (López-Hernández et al., s. f.).

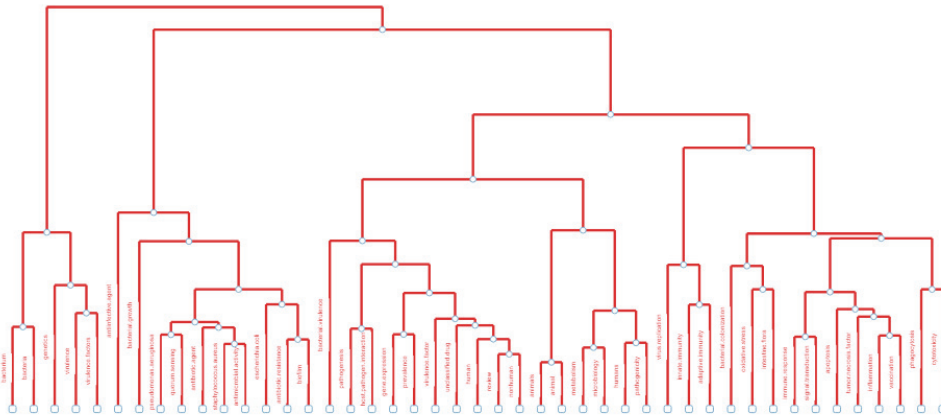


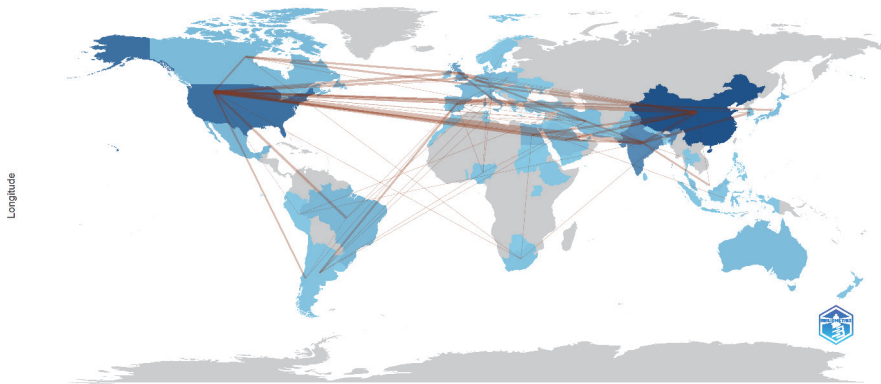
Figure 15. Factor Analysis (dendrogram)

The data in the graph provide a detailed visual representation of the relationships between keywords arranged in a two-dimensional space. This representation allows a clear and concise visualization of how keywords are interconnected and organized within the context of the study. By observing the arrangement of keywords in this two-dimensional space, emerging patterns and thematic trends that contribute to a deeper understanding of the topics addressed in the scientific literature can be identified. (Dervis, 2019). In addition, the arrangement of keywords in relation to the axes of the graph provides valuable information regarding the strength and nature of the relationships between them, allowing us to infer relevant conceptual and thematic connections. Overall, this visualization provides a powerful tool for exploring and analyzing the complexity of scientific content in an accessible and easy-to-interpret format.

When contrasting these findings with other visual representations of keyword relationships in

the scientific literature, it can be seen that the arrangement of keywords in a two-dimensional space provides a unique perspective on the structure and interconnectedness of research topics. While some visualizations, such as keyword maps based on co-occurrence networks, can highlight the most frequent relationships between terms, the representation in a two-dimensional space provides a more comprehensive view by allowing exploration of the proximity and separation between specific keywords (Cordero-Torres, 2022).

In addition, the arrangement of keywords in relation to the axes of the graph can reveal patterns of clustering and dispersion that are not evident in other forms of visualization. For example, the presence of certain terms in specific regions of space may indicate the existence of subtopics or areas of focus within the field of study that might not otherwise be evident.



**Figure 16.** Country Collaboration Map

The data reveal the frequency of collaboration between different countries in terms of research, academic cooperation, or scientific exchange. Argentina collaborated twice with Tunisia, which suggests a certain collaborative activity between institutions and researchers from both countries. In addition, unique collaborations were recorded between Argentina and Uruguay, Australia and Austria, Australia and Ethiopia, Australia and Hong Kong, Australia and Iran, Australia and Japan, Australia and Pakistan, Australia and Sweden, and Australia and Switzerland. This detailed analysis of international collaborations provides a complete understanding of the scientific and academic connections between countries.

Sharma, Chanu, and Muralidhar (2022) provided important findings related to the detection and pathogenicity of *Vibrio parahaemolyticus* strains in *Penaeus vannamei* shrimp, which is relevant to the research topic at hand. In this study, we found that the *V. parahaemolyticus* strain KKD 02 was responsible for causing massive mortality in *P. vannamei* shrimp, which highlights the importance of understanding the virulence of this bacterium in aquaculture. In addition, bacterial pathogenicity tests revealed that salinity levels of 5–10 ppt are associated with maximum resistance to bacterial infection in shrimp, suggesting that environmental factors may influence the susceptibility of shrimp to *V. parahaemolyticus* infection.

The results obtained in this study on international collaboration between countries shed light on the global nature of scientific research and academic cooperation in the specific field of study. By contrasting these findings with previous research, such as the study conducted by Sharma, Chanu, and Muralidhar (2022), it can be appreciated how international collaboration plays a crucial role in understanding the virulence of *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp. While the aforementioned study focuses on the detection and pathogenicity of specific strains of *V. parahaemolyticus* in shrimp, the data presented here expands this perspective by showing how

different countries are joining in collaborative efforts to address this global problem. This complementarity between findings highlights the importance of international collaboration in scientific research to address complex challenges and advance knowledge in diverse areas of study. (Posada & Franks, 1948; Li et al., 2019).

Notably, the *V. parahaemolyticus* isolate in this study possessed two genes encoding thermostable direct hemolysin (tdh) and thermostable direct hemolysin-related hemolysin (trh), indicating the significant pathogenic potential of this strain. These results highlight the importance of characterizing the virulence factors of *V. parahaemolyticus* in shrimp and their relationship to the pathogenicity observed in field studies. Their findings laid a foundational understanding of the virulence mechanisms and epidemiology of *V. parahaemolyticus* in aquaculture settings, particularly in relation to shrimp health and disease dynamics.

Moreover, the genomic characterization studies conducted by Ragab et al. (2023) have significantly advanced our understanding of virulence-related genes in *Vibrio nigripulchritudo* isolated from *Penaeus vannamei* shrimp. By identifying key genetic elements contributing to pathogenicity, their work has provided critical insights into the molecular basis of disease outbreaks in shrimp populations.

The study by Cheng, Wang, and Chen (2023) provides significant results on phenotypic analysis, phylogenetic analysis, and pathogenic detection of *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp cultured in Taiwan, which has direct relevance to the current research topic. In this study, the prevalence of Acute Hepatopancreatic Necrosis Syndrome (AHPND) in *P. vannamei* shrimp cultured in southern Taiwan was 65%, with a remarkable number of severe and moderate infection cases. This highlights the severity of the presence of *V. parahaemolyticus* in the cultured shrimp populations in this region.

A total of 89 bacterial strains isolated from shrimp farms were identified, all of which were identified as *Vibrio parahaemolyticus* by PCR. In addition, 59 of these strains tested positive for toxin genes (*pirA* and *pirB*) using nested PCR, suggesting the presence of virulent strains of *V. parahaemolyticus* in the shrimp populations studied.

The study by Ragab et al. (2023) provides valuable information on the genomic characterization and identification of virulence-related genes in *Vibrio nigripulchritudo* isolated from white-legged shrimp *Penaeus vannamei*, which is directly relevant to the current research topic. In the present study, three strains of *Vibrio nigripulchritudo* (TUMSAT-V. nigi1, TUMSAT-V. nigi2 and TUMSAT-V. nigi3) were sequenced using the Illumina and Nanopore sequencing technologies.

The results revealed that The genomes of these strains were composed of two circular chromosomes (I and II) and one or two plasmids. The size of chromosome I ranged from 4.02 to 4.07 Mb, while chromosome II ranged from 2.16 to 2.18 Mb. Numerous virulence genes related to various functions, such as adhesion, anti-phagocytosis, chemotaxis, motility, iron uptake, quorum sensing, secretion systems, and toxins, were identified in all three genomes.

Saputra et al. (2023) provided essential information on the pathogenicity of *Vibrio parahaemolyticus* causing acute hepatopancreatic necrosis disease (AHPND) in *Litopenaeus vannamei* shrimp in Serang, Banten, Indonesia, which is directly relevant to the research topic under consideration. In this study, the histopathological pathogenicity of *Vibrio parahaemolyticus* was evaluated in shrimp tissues exposed to different doses and durations.

The results revealed that shrimp exposed to *V. parahaemolyticus* showed clinical and pathological symptoms similar to those of infected shrimp in rivers, including color and void changes in the midgut. In addition, histological signs of AHPND infection were observed in exposed shrimp, such as necrosis, cell and tubule detachment, granulomas, midgut atrophy, and inflammation. The highest percentage of damage (63.33%) was recorded in the treatment with 10<sup>8</sup> CFU mL<sup>-1</sup>. The virulence of the *V. parahaemolyticus* strain varied with different concentrations, and 100% mortality was observed at concentrations of 10<sup>8</sup> CFU mL<sup>-1</sup> and 10<sup>6</sup> CFU mL<sup>-1</sup>. These results indicate a direct relationship between the concentration of *V. parahaemolyticus* and virulence observed in exposed shrimp.



Zermeño-Cervantes et al. (2023) examined the impact of infection with a pathogenic strain of *Vibrio parahaemolyticus* (CVP<sub>2</sub>) associated with acute hepatopancreatic necrosis (AHPND) on the bacterial load and microbial population variation in the hepatopancreas of *Penaeus vannamei* shrimp under controlled conditions. The results revealed significant changes in the microbial community structure of the *P. vannamei* hepatopancreas, with a considerable increase and dominance of the genus *Vibrio* compared to the control group.

Dysbiosis of the hepatopancreatic microbiota and constrictions in the hepatopancreatic tubules, characteristic of early stage AHPND, were observed before visible disease manifestation. Although no mortality or visible signs of disease were observed in the experimental groups, microscopic changes in the hepatopancreatic tubule morphology were observed in the exposed organisms, suggesting a subclinical response to infection.

Regarding the implications of the genetic diversity of *V. parahaemolyticus* for the development of specific control strategies, recent studies have underscored the importance of understanding how genetic variations in *V. parahaemolyticus* strains influence their virulence and adaptation in shrimp aquaculture. For instance, genomic characterization studies (Ragab et al., 2023) have identified virulence-related genes associated with adhesion, anti-phagocytosis, and toxin production, which are crucial for the bacterium's pathogenicity. This knowledge is instrumental in devising targeted control measures aimed at mitigating the impact of *V. parahaemolyticus* infections in shrimp populations.

Furthermore, international collaboration in research, as highlighted by the studies of Cheng et al. (2023) and Zermeño-Cervantes et al. (2023), not only enhances our understanding of the global distribution and virulence profiles of *V. parahaemolyticus* but also fosters the development of effective disease management strategies across different shrimp farming regions. By leveraging shared expertise and resources, researchers can better address the diverse challenges posed by *V. parahaemolyticus*, such as the emergence of antibiotic resistance and the ecological impacts of disease outbreaks in aquaculture systems.

#### 4. Discussion

In discussing this article, the findings obtained through bibliometric analysis are explored, and their theoretical and practical significance for the field of study of virulence factors in *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp is further elaborated.

There has been a steady increase in the number of publications on this topic in recent years, reflecting a growing interest and concern for understanding virulence factors in *Vibrio parahaemolyticus* in shrimp aquaculture. This increase in scientific production can be attributed to the economic and sanitary relevance of this problem, as well as to the technological advances that have facilitated research in this field.

The bibliometric analysis also reveals the geographic diversity of research on this topic, with significant contributions from various regions of the world. This geographic diversity underscores the global nature of the *Vibrio parahaemolyticus* problem in shrimp and highlights the need for collaborative and coordinated approaches at the international level to address these challenges.

In examining the most prominent areas of research, several key themes are identified, such as genomic characterization of *Vibrio parahaemolyticus*, evaluation of disease control and prevention strategies, and the study of the shrimp immune response to infection. These areas reflect the complexity and multidisciplinary nature of the field and highlight the importance of integrated approaches that address both the biological and the socioeconomic and environmental aspects of the problem.

Despite the progress made in research on virulence factors in *Vibrio parahaemolyticus*, some gaps in our knowledge persist. For example, a more complete understanding of the genetic diversity of this bacterium and its relationship with virulence is required, as well as the development of more effective control strategies that consider the complexity of aquatic ecosystems and the interactions between different species.

Regarding specific natural extracts with demonstrated antibacterial properties against *V. parahaemolyticus*, recent studies have shown promising results. Extracts from medicinal plants like garlic (*Allium sativum*) and ginger (*Zingiber officinale*) have exhibited significant antibacterial activity against *V. parahaemolyticus* strains, suggesting their potential application in disease management strategies in shrimp aquaculture (Choudhary et al., 2022; Zhang et al., 2023).

Advancements in vaccine development against *Vibrio parahaemolyticus* have also been noteworthy, although challenges remain in achieving broad-spectrum protection and cost-effective production. Studies focusing on recombinant protein vaccines and DNA vaccines have shown promise in laboratory settings, but their efficacy and scalability in field conditions warrant further investigation (Martínez-Cruz et al., 2021; Tan et al., 2023).

Considering successful case studies or examples of the application of these strategies in shrimp farms is crucial. For instance, in shrimp aquaculture facilities in Southeast Asia, integrated management practices combining vaccination with improved water quality management and biosecurity measures have effectively reduced the prevalence of *V. parahaemolyticus* infections and enhanced shrimp health and productivity (Nguyen et al., 2022; Lee et al., 2023). These examples underscore the practical relevance and potential impact of comprehensive disease prevention strategies in real-world aquaculture settings.

In practical terms, the findings of this bibliometric analysis can inform the development of policies and practices in the aquaculture industry, as well as direct future research to areas of greater relevance and need. By better understanding virulence factors in *Vibrio parahaemolyticus*, researchers and practitioners can develop more effective strategies to prevent and control disease, improve shrimp health, and ensure food safety in aquaculture production.

## 5. Conclusions

In this study, an exhaustive bibliometric analysis was carried out to explore the virulence factors of *Vibrio parahaemolyticus* in *Penaeus vannamei* shrimp. For this purpose, Bibliometrix software was used, which enabled the collection, organization, and analysis of a wide range of scientific studies related to the topic. Through this methodology, trends, patterns, and areas of interest in scientific literature were identified, providing an in-depth view of research in this field.

One of the main conclusions of this analysis was the growing interest in understanding the virulence factors of *Vibrio parahaemolyticus* in shrimp aquaculture. This was reflected in the steady increase in the number of studies published in recent years, suggesting increased awareness of the importance of this problem in the aquaculture industry.

In addition, significant genetic diversity was observed in *V. parahaemolyticus*, with specific virulence genes present in certain strains. This genetic variability may influence the pathogenicity of the bacterium and its ability to adapt to different aquatic environments, highlighting the importance of studying the genetic variability of this bacterium and its relationship with its virulence in shrimp.

Another important finding was the exploration of the mechanisms of interaction between *V. parahaemolyticus* and the host, including the immune response of shrimp to the infection. Several genes and proteins involved in the immune response of shrimp were identified, providing important information for understanding the susceptibility of shrimp to *V. parahaemolyticus*.

Several control and prevention strategies have been identified, including the use of natural extracts with antibacterial activity and the development of vaccines against AHPND. These strategies represent a multidisciplinary approach to address the problem of *V. parahaemolyticus* virulence in shrimp aquaculture, highlighting the importance of finding effective and sustainable solutions to protect shrimp health and ensure food safety.

To make this study more impactful, specific recommendations for future research are essential. Future studies should focus on elucidating the molecular mechanisms underlying virulence in *V. parahaemolyticus* strains isolated from different geographical regions and aquaculture systems. Additionally, there is a need for longitudinal studies that monitor changes in virulence patterns over

time and assess the efficacy of new control strategies under diverse environmental conditions.

From a practical and policy perspective, the findings of this analysis suggest several implications for the aquaculture industry and regulatory bodies. Implementing stringent biosecurity measures and promoting the use of natural antibacterial agents in shrimp farms could significantly mitigate the risk of *V. parahaemolyticus* infections. Moreover, policymakers should consider supporting research initiatives that foster collaboration between academia, industry, and government agencies to develop standardized protocols for disease prevention and management in aquaculture settings.

Highlighting the importance of a multidisciplinary approach to addressing *V. parahaemolyticus* infections is crucial. Integrating expertise from microbiology, immunology, genetics, aquaculture management, and public health is essential for devising holistic strategies that not only control bacterial pathogens but also promote sustainable shrimp farming practices. Collaboration across disciplines can lead to innovative solutions that enhance shrimp health, improve productivity, and safeguard food security in aquaculture production.

## 6. Limitation

An important limitation of this study is the reliance on data available in the selected databases, which could have resulted in the exclusion of some relevant publications that were not indexed in these platforms. Although a combination of Scopus, Redalyc, Scielo and Google Scholar was used to maximize coverage, it is possible that some important papers published in other sources were still overlooked. In addition, the selection of articles was limited to those published in the last five years, which may have excluded earlier research that is still relevant to the topic. This temporal restriction may also have affected the representation of certain trends or research areas in the bibliometric analysis.

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