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Global Research Trends in Genome-Based Aquafeed for Pacific White Shrimp (*Litopenaeus vannamei*): A Scientometrics Analysis (1976–2025)

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ABSTRACT

The integration of genomics and nutrigenomics has revolutionized aquafeed development, enabling the formulation of precision diets that optimize nutrient utilization, immune resilience, and growth in the Pacific white shrimp (*Litopenaeus vannamei*). This study provides the first comprehensive bibliometric and scientometric analysis of global research trends in genome based aquafeed from 1976 to 2025. Data were retrieved from the Scopus database and analyzed using Bibliometrix (RStudio) and VOSviewer to identify publication dynamics, thematic evolution, and emerging research frontiers. A total of 1,013 documents were analyzed, revealing a marked surge in publications after 2018 driven by the release of the *Litopenaeus vannamei* reference genome and the growing application of omics-based nutritional research. China, the United States, and Southeast Asia were identified as major contributors, forming dense international collaboration networks. Core journals such as Fish and Shellfish Immunology and Aquaculture dominated citation impact, with highly cited papers focusing on probiotics, immune gene expression, and host microbiome interactions. Keyword co-occurrence analysis indicated a thematic transition from conventional feed trials toward multi omics integration, oxidative stress modulation, and intestinal microbiota regulation, highlighting the emergence of precision immune nutrition and metabolomic guided feed design. Overall, this study delineates the intellectual structure, global landscape, and future directions of shrimp nutrigenomics, providing a strategic foundation for developing genome based, sustainable aquafeed technologies that align with the next generation of molecular aquaculture innovation.

INTRODUCTION

The application of genome-based and nutrigenomic approaches has emerged as a transformative trend in aquaculture nutrition science, reshaping how feed formulations

are developed and evaluated for commercial species such as the Pacific white shrimp (*Litopenaeus vannamei*). As one of the most economically important crustaceans worldwide, *Litopenaeus vannamei* accounts for nearly 60% of global shrimp aquaculture production and plays a pivotal role in food security and the blue economy **(de Souza *et al.*, 2021)**. The intensification of shrimp farming, however, has increased the demand for sustainable, cost-effective, and high-performance feeds. Conventional feed formulations largely dependent on fishmeal and unsustainable protein sources are now being replaced by genomically informed diets that integrate molecular-level insights to optimize nutrient utilization, immunity, and growth **(Aragão *et al.*, 2022; Akintan *et al.*, 2024)**.

Recent breakthroughs in omics technologies genomics, transcriptomics, proteomics, metabolomics, and nutrigenomics have revolutionized our understanding of diet–gene interactions in aquatic organisms. By decoding how nutrients influence gene expression and metabolic pathways, nutrigenomics enables the formulation of precision diets that enhance growth, immune resilience, and environmental adaptability **(Mondan & Panda, 2021; Agrawal *et al.*, 2024)**. For *Litopenaeus vannamei*, genomic resources such as the chromosome-level reference genome and transcriptomic libraries have accelerated the identification of key genes linked to feed efficiency, oxidative stress tolerance, and immune modulation **(Yuan *et al.*,, 2023; Liao *et al.*, 2025)**. Integrating these molecular datasets into feed design allows researchers to evaluate dietary performance not only through conventional metrics like feed conversion ratio (FCR) but also through molecular biomarkers reflecting cellular health and metabolic homeostasis **(Dai *et al.*, 2024)**. Consequently, genome-based aquafeed development has become a cornerstone of next-generation shrimp nutrition research, bridging molecular biology, aquaculture engineering, and environmental sustainability.

Despite these advancements, critical knowledge gaps persist. Most existing research remains fragmented across domains nutrition, physiology, and molecular genetics without a unified analytical framework to assess the evolution and interconnectivity of scientific progress. Furthermore, while specific genomic and metabolomic studies have expanded rapidly since 2018, comprehensive mapping of global research patterns, influential publications, and emerging themes in shrimp nutrigenomics remains limited. The absence of a consolidated scientometric perspective hinders the identification of leading contributors, collaboration networks, and high-impact journals that shape the trajectory of this rapidly expanding field.

This study addresses these gaps by presenting the first systematic bibliometric analysis of genome-based aquafeed research for *Litopenaeus vannamei* spanning 1976–2025, using data extracted from the Scopus database. Analytical tools including VOSviewer and Bibliometrix (RStudio) were employed to visualize publication trends, thematic evolution, and global collaboration networks. The objectives of this work were threefold: (i) to quantify the growth dynamics and geographical distribution of research outputs, (ii) identify leading journals, authors, and highly cited works that have shaped

the field, and (iii) uncover thematic transitions and future niches through keyword co-occurrence and overlay visualization. By bridging bibliometric evidence with domain-specific insight, this study not only delineates the intellectual structure of shrimp nutrigenomics but also outlines future research priorities toward sustainable, genome-guided feed innovation in aquaculture.

Furthermore, aligning shrimp nutrigenomics with global sustainability frameworks reinforces its strategic importance beyond feed innovation. The integration of molecular nutrition and genome-based aquafeed directly contributes to the achievement of Sustainable Development Goals (SDGs), particularly SDG 2 (Zero Hunger), SDG 12 (Responsible Consumption and Production), and SDG 14 (Life Below Water). By optimizing feed efficiency, reducing fishmeal dependency, and minimizing environmental discharge, nutrigenomic approaches support resilient and low-impact shrimp farming systems that are consistent with national and international policies on sustainable aquaculture development.

MATERIALS AND METHODS

Data source and search protocol

Bibliometric data were retrieved from the Scopus database (Elsevier, Netherlands), which provides comprehensive citation indexing for peer-reviewed scientific journals. The search was executed in March 2025 using a customized query string designed to capture genome-based and nutrigenomic studies related to Pacific white shrimp (*Litopenaeus vannamei*). The query used was: TITLE-ABS-KEY((("genome* based" OR genom* OR nutrigenom* OR transcriptom* OR metabolom* OR proteom* OR "gene expression" OR "molecular biology" OR "molecular nutrition" OR "genetic improvement" OR "genetic breeding" OR "molecular marker" OR "bioinformati*" OR "gene regulation" OR "functional genom*" OR "genetic diversity" OR "selective breeding") AND ("aquafeed" OR "aqua feed" OR "feed" OR "diet*" OR "feed formulation" OR "feed additive" OR "nutritional formulation" OR "functional feed" OR "feed development" OR "nutri*" OR "feed efficiency" OR "feed performance" OR "dietary supplementation") AND ("shrimp" OR "prawn" OR "*Litopenaeus vannamei*" OR "*Penaeus vannamei*" OR "whiteleg shrimp" OR "Pacific white shrimp" OR "marine shrimp" OR "shrimp aquaculture" OR "shrimp farming" OR "crustacean aquaculture"))).

The search was restricted to journal articles written in English, covering the 1976–2025 publication window and all subject areas. An initial 1,084 documents were retrieved. After filtering for journal articles and excluding non-article types (conference papers, reviews, book chapters), 1,014 documents remained. Duplicate removal and metadata standardization were performed in RStudio v2024.12.0-467, resulting in a final dataset of 1,013 unique records. The workflow of the data collection, screening, and analytical process is summarized in Fig. (1) **(**modified from **Al Zamzami *et al.*, 2025)**.

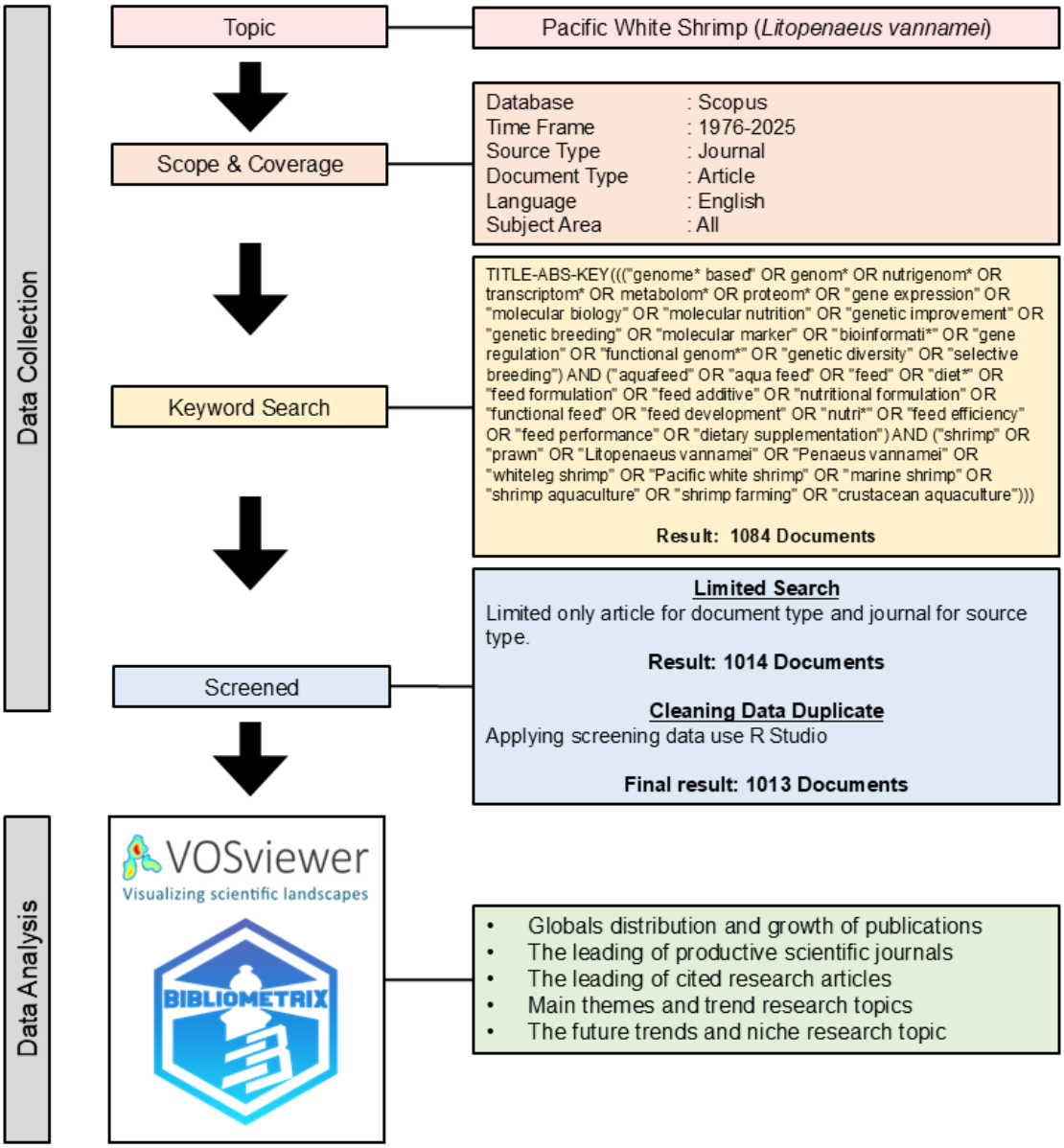


Fig. 1. Research framework

Data processing and analytical framework

Following data retrieval from the Scopus database, bibliographic metadata were exported in two complementary file formats to facilitate multidimensional analysis. The Comma-Separated Values (CSV) format was used for network visualization in VOSviewer, while the BibTeX (.bib) format was generated for statistical and performance analysis in RStudio using the Bibliometrix and Biblioshiny packages. Both formats contained essential bibliographic fields, including article titles, author names, affiliations, abstracts, author keywords, publication years, journals, citations, and digital object identifiers (DOIs). The integration of these formats enabled a comprehensive

workflow combining descriptive statistics, performance indicators, and visual network mapping.

Bibliometric and performance analysis

The BibTeX file was imported into RStudio v2024.12.0-467 and processed using the Bibliometrix package with its graphical interface Biblioshiny. This platform allowed for quantitative evaluation of publication performance and intellectual structure within the dataset. The analysis covered several key bibliometric indicators: (i) annual scientific articles production to assess temporal publication growth, (ii) countries' scientific production and collaboration networks to map international research dynamics, (iii) top relevant sources and their citation impacts to identify leading journals, and (iv) trends in publication across various subject areas to reveal interdisciplinary expansion. Additionally, (v) top globally cited documents were examined to highlight foundational studies, while (vi) keyword frequency analysis identified dominant research themes. Finally, (vii) trend research topics were generated through temporal keyword mapping, revealing shifts in thematic focus across decades. The results from Biblioshiny were visualized through bar graphs, line plots, and thematic trend maps, providing a clear representation of scientific productivity, collaboration intensity, and conceptual evolution in genome-based aquafeed research for *Litopenaeus vannamei*.

Science mapping and trend visualization

For network-based and trend visualization, the CSV dataset was analyzed using VOSviewer v1.6.18 (Leiden University, Netherlands). This software was employed to construct co-occurrence and co-authorship maps, focusing on the relationships among keywords, authors, and institutions. The keyword co-occurrence analysis used a minimum occurrence threshold of five terms to ensure statistical reliability, and synonymous keywords were manually merged to enhance data consistency. The resulting maps were generated in overlay visualization mode, allowing temporal interpretation of keyword emergence and decline.

The VOSviewer analysis specifically targeted the identification of future research trends and niche thematic areas. By examining term link strength and the average publication year, emerging topics in shrimp nutrigenomics and genome-based feed formulation could be detected. The color gradient in the overlay map reflected the chronological progression of themes older research appearing in blue tones and more recent or emerging topics appearing in yellow to red hues. This visual representation provided an empirical basis for predicting upcoming focal areas in the field, such as omics driven nutritional optimization, molecular pathway integration, and sustainable feed innovation.

Quality assurance and limitations

Collectively, the integration of Bibliometrix/Biblioshiny and VOSviewer ensured a robust analytical pipeline capable of describing both the structural evolution and future trajectory of scientific knowledge related to *Litopenaeus vannamei* nutrigenomics and aquafeed development. Data reliability was ensured by cross checking record counts across CSV and BibTeX exports, and by performing duplicate detection in RStudio prior to visualization. However, since the analysis relied exclusively on Scopus-indexed documents, relevant grey literature or non-indexed local journals may not be represented.

RESULTS AND DISCUSSION

Globals distribution and growth of publications

The temporal distribution of publications on genome-based aquafeed research for Pacific white shrimp (*Litopenaeus vannamei*) reveals a distinct three-phase trend characterized by a long latency, a transitional growth phase, and a subsequent period of exponential expansion (Fig. 2). From 1976 to 2009, research output remained minimal (<10 articles year^{-1}), reflecting the absence of genomic resources and the technological constraints of early aquaculture nutrition studies. The field began gaining momentum after 2010, coinciding with the advent of affordable next-generation sequencing and the emergence of functional genomics in aquaculture. Publication rates increased sharply after 2018, reaching over 100 articles year^{-1} by 2019 and approaching 170 articles year^{-1} in 2024–2025. The cumulative total exceeded 1,000 papers in 2025, signifying a consolidation of the field and its transition into a mature research domain.

This acceleration is strongly associated with two scientific milestones: the release of the chromosome-level reference genome of *Litopenaeus vannamei* in 2019 **(Zhang *et al.*, 2019)**, and the subsequent integration of multi-omics platforms transcriptomics, proteomics, metabolomics, and nutrigenomics into feed development and nutritional physiology research. The availability of genomic datasets has enabled the precise identification of diet–gene interactions and molecular pathways underlying feed conversion, stress tolerance, and immunity **(Tang *et al.*, 2020)**. Furthermore, the global shift toward sustainable aquaculture has catalyzed research on plant-based and microbial protein sources, pushing scientists to employ genomics-driven approaches to maintain shrimp performance under reduced fishmeal inclusion **(Moore *et al.*, 2021)**. These scientific and economic drivers jointly explain the exponential publication growth observed in the last decade.

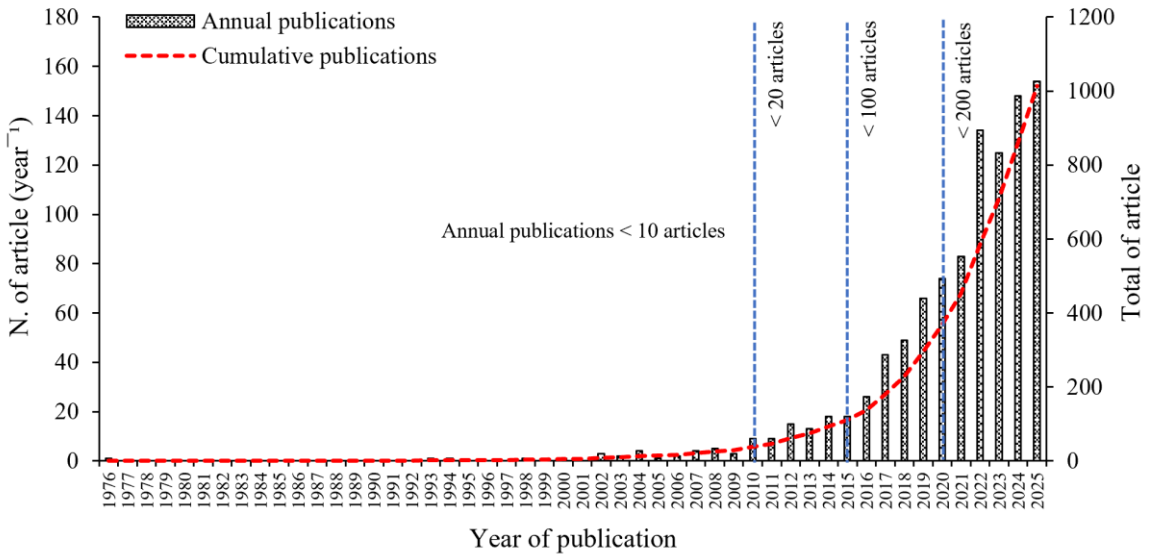


Fig. 2. Annual scientific articles production

Geographically, the global collaboration network (Fig. 3) demonstrates a highly centralized yet interconnected structure dominated by China, which functions as the principal hub of scientific production and international collaboration. Dense co-authorship links connect China to Southeast Asia, the United States, Europe, and Oceania, indicating both knowledge transfer and shared infrastructure across continents. This dominance corresponds with China's leadership in shrimp farming capacity and government-backed initiatives on aquatic genomics and sustainable feed innovation **(Huang *et al.*, 2025)**. The United States and European Union countries occupy secondary yet pivotal roles as analytical and biotechnological partners, particularly in studies involving high-throughput sequencing, metabolomic profiling, and feed additive validation. Meanwhile, emerging collaborations are evident in Brazil, Mexico, and India, reflecting the expansion of shrimp aquaculture research in the Global South and the growing accessibility of genomic technologies **(Mandal & Singh, 2025)**.

The observed pattern of global collaboration reflects a bi-directional exchange: Asian countries contribute large-scale experimental data from production systems, while Western partners provide expertise in molecular analysis, bioinformatics, and data modeling. Such complementarity has strengthened cross-disciplinary networks that underpin the "genome-to-feed" paradigm **(Mao *et al.*, 2021)**. Furthermore, bibliometric evidence suggests that publications involving multi-country collaborations tend to receive higher citation rates and broader thematic reach, confirming that international partnerships are essential to innovation in shrimp nutrigenomics **(Yossa, 2023)**.

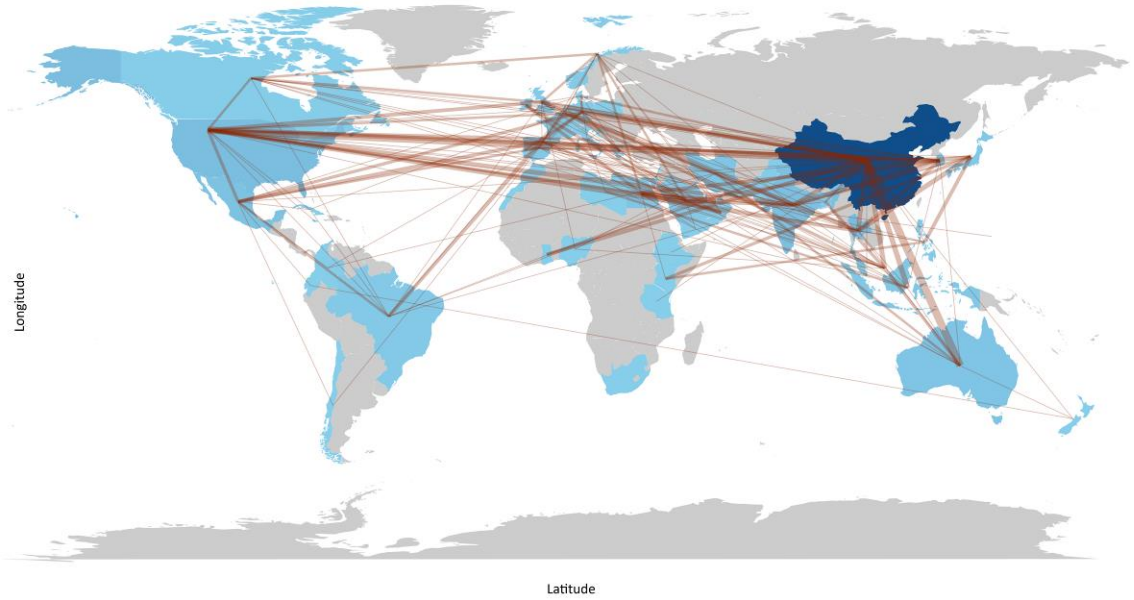


Fig. 3. Countries' scientific production and collaboration

The leading of productive scientific journals

Table (1) summarizes the top ten journals contributing to genome-based aquafeed research for *Litopenaeus vannamei*, highlighting both productivity and scientific influence. Fish and Shellfish Immunology ranked first, publishing 158 articles (15.6%) with the highest h-index = 43 and 6,090 total citations since its first related publication in 2006. Its dominance underscores the increasing intersection between nutrigenomics and immune modulation in shrimp nutrition studies. The journal Aquaculture followed with 129 publications (12.7%) and an h-index = 34, reflecting its established position as a core outlet for nutrition, feed formulation, and health-related aquaculture studies. Aquaculture Reports (52 articles; h-index = 12) and Aquaculture International (38 articles; h-index = 8) emerged as secondary yet rapidly expanding sources since 2011, emphasizing applied feed innovation and molecular approaches to shrimp performance.

Other journals such as Aquaculture Research, Animals, Aquaculture Nutrition, and Frontiers in Marine Science collectively contribute about 15% of total publications, with steady growth after 2016. Their thematic scope indicates the diversification of research toward animal physiology, environmental interactions, and systems biology. The presence of PLOS One and Comparative Biochemistry and Physiology among the top-ten journals suggests an expansion of shrimp nutrigenomics into multidisciplinary and biochemical domains, where comparative molecular mechanisms and metabolic biomarkers are increasingly examined. Overall, publication distribution shows a clear core periphery structure: a few leading aquaculture journals concentrate the majority of articles and citations, while emerging open access outlets are facilitating the dissemination of new omics-based methodologies and inter disciplinary feed studies. This pattern is typical of fields undergoing consolidation, where high-impact journals set

methodological standards and newer venues absorb specialized subtopics such as transcriptomic feed responses and microbiome-driven metabolism.

Table 1. Top relevant sources and impact

No	Source	No. of articles	h index	Total citation	First publication (year)	Percent of publication
1	Fish and Shellfish Immunology	158	43	6090	2006	15.6
2	Aquaculture	129	34	3361	2000	12.7
3	Aquaculture Reports	52	12	432	2016	5.1
4	Aquaculture International	38	8	204	2011	3.8
5	Aquaculture Research	32	11	571	2004	3.2
6	Animals	27	12	276	2020	2.7
7	Aquaculture Nutrition	23	11	326	2013	2.3
8	Frontiers in Marine Science	20	9	149	2020	2.0
9	Plos One	19	10	576	2012	1.9
10	Comparative Biochemistry and Physiology	16	8	215	2009	1.6

The evolution of subject categories, illustrated in Fig. (4), supports this structural shift toward biological and molecular integration. Prior to 2000, most studies were classified under Agricultural and Biological Sciences and Veterinary Science, reflecting a classical nutrition physiology focus. Beginning in the 2010s, research expanded markedly into Biochemistry, Genetics and Molecular Biology and Immunology and Microbiology, coinciding with the widespread adoption of sequencing and gene-expression platforms. By the 2020s, these categories together with Environmental Science and Chemical Engineering accounted for nearly 70 % of the total publication spectrum, demonstrating a move from applied feeding trials toward systems-level investigations of metabolic and immune pathways.

This disciplinary broadening mirrors broader trends in aquatic nutrition research, where integrative omics and environmental modeling increasingly intersect. In particular, studies now routinely link nutrient utilization to molecular markers of oxidative stress, epigenetic regulation, and microbiome composition **(Wikumpriya *et al.*, 2023; Kurniawan *et al.*, 2025)**. Consequently, the field has matured from descriptive feed evaluation to mechanistic nutrigenomics, aligning with global goals for precision aquaculture and sustainable feed innovation.

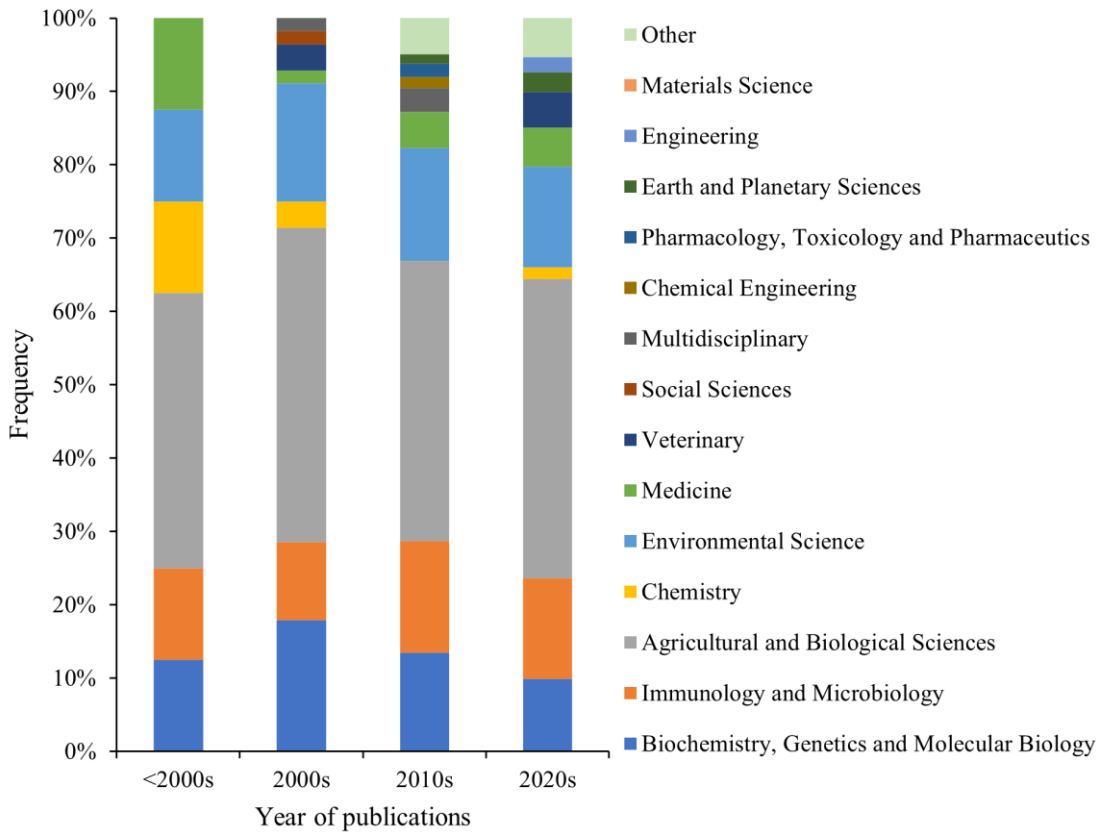


Fig. 4. Trends in publication across various subject areas

The leading of cited research articles

The citation structure of genome-based aquafeed research for *Litopenaeus vannamei* (Table 3) highlights several milestone studies that have shaped the scientific foundation of modern shrimp nutrigenomics and feed biotechnology. The citation pattern reveals that the most influential works in genome-based aquafeed research for *Litopenaeus vannamei* predominantly focus on microbial modulation, immune gene expression, and feed–host interaction. Highly cited studies such as those of **Chiu *et al.* (2007)** and **Zokaeifar *et al.* (2012)** established the foundation of shrimp nutrigenomics by integrating probiotics and lactic acid bacteria into feed trials while simultaneously quantifying molecular immune responses. These papers, published in Fish and Shellfish Immunology, marked the transition from conventional growth-based nutrition studies to mechanistic investigations connecting diet, microbiota, and immune regulation. Their consistent citation over more than a decade indicates that host–microbe–feed interactions remain a central research axis underpinning functional feed innovation and molecular shrimp health management.

Another striking finding from the citation landscape is the growing influence of studies linking functional feed bioactives and microbial ecology. For instance, the works of **Kim *et al.* (2014)**, **Duan *et al.* (2017)** and **He *et al.* (2017)** demonstrate how biofloc

systems, *Clostridium butyricum*, and organic acid essential oil blends not only improve growth and stress tolerance but also modulate intestinal microbiota and metabolic pathways. These findings laid the groundwork for multi-omics exploration of gut function, later expanded by **Huang *et al.* (2020)**, whose Microbiome paper reframed shrimp disease etiology through "microecological Koch's postulates." The shift toward microbiota-centered nutrigenomics suggests that feed research has evolved from nutrient formulation to ecological regulation of host microbe networks, reflecting a broader movement toward microbiome-based precision aquaculture.

Equally notable is the multidisciplinary expansion reflected in **Abdelrahman *et al.* (2017)**, which connected aquaculture genomics to national breeding and feed efficiency programs. This integration of genetic improvement with nutrigenomic insight underscores a transition toward systems-level aquaculture where genomic selection, nutrition, and environmental resilience converge. Collectively, the top-cited studies emphasize that scientific impact in shrimp nutrigenomics is strongly associated with methodological novelty and cross-domain integration. The convergence of immunology, microbiology, and molecular nutrition documented in these landmark papers illustrates how *Litopenaeus vannamei* has become a model species for linking genomic science to sustainable feed innovation.

Table 3. Top global cited documents

Author	Cited	Year	Title	Source title	DOI
Zokaeifar, Hadi	395	2012	Effects of *Bacillus subtilis* on the growth performance, digestive enzymes, immune gene expression and disease resistance of white shrimp, *Litopenaeus vannamei*	Fish and Shellfish Immunology	10.1016/j.fsi.2012.05.027
Chiu, Chiuhsia	362	2007	Immune responses and gene expression in white shrimp, *Litopenaeus vannamei*, induced by Lactobacillus plantarum	Fish and Shellfish Immunology	10.1016/j.fsi.2006.11.010
Kim, Sukyoung	211	2014	Effect of bioflocs on growth and immune activity of Pacific white shrimp, *Litopenaeus vannamei* postlarvae	Aquaculture Research	10.1111/are.12319
Liu, Xiaolong	199	2011	The effect of dietary Panax ginseng polysaccharide extract on the immune responses in white shrimp, *Litopenaeus vannamei*	Fish and Shellfish Immunology	10.1016/j.fsi.2010.11.018
Abdelrahman, Hisham A.	194	2017	Aquaculture genomics, genetics and breeding in the United States: Current status, challenges, and priorities for future research	BMC Genomics	10.1186/s12864-017-3557-1
Huang, Zhijian	187	2020	Microecological Koch's postulates reveal that intestinal microbiota	Microbiome	10.1186/s40168-020-

			dysbiosis contributes to shrimp white feces syndrome		00802-3
Kewcharoen, Werasan	178	2019	Probiotic effects of Bacillus spp. from Pacific white shrimp (*Litopenaeus vannamei*) on water quality and shrimp growth, immune responses, and resistance to Vibrio parahaemolyticus (AHPND strains)	Fish and Shellfish Immunology	10.1016/j.fsi.2019.09.013
Duan, Yafei	164	2017	Effect of dietary Clostridium butyricum on growth, intestine health status and resistance to ammonia stress in Pacific white shrimp *Litopenaeus vannamei*	Fish and Shellfish Immunology	10.1016/j.fsi.2017.03.048
Wang, Guoxia	155	2019	Evaluation of defatted black soldier fly (*Hermetia illucens* L.) larvae meal as an alternative protein ingredient for juvenile Japanese seabass (*Lateolabrax japonicus*) diets	Aquaculture	10.1016/j.aquaculture.2019.04.023
He, Wangquan	143	2017	Effects of organic acids and essential oils blend on growth, gut microbiota, immune response and disease resistance of Pacific white shrimp (*Litopenaeus vannamei*) against *Vibrio parahaemolyticus*	Fish and Shellfish Immunology	10.1016/j.fsi.2017.09.007

Main themes and trend research topics

Keyword co-occurrence analysis (Fig. 5) reveals that research on *Litopenaeus vannamei* nutrigenomics is dominated by biological and molecular terms such as “growth performance,” “gene expression,” “immunity,” “immune response,” “transcriptome,” and “intestinal microbiota.” This pattern indicates a consistent shift from conventional nutritional evaluation toward mechanistic studies exploring molecular pathways and host microbiome interactions. The prominence of gene expression and transcriptome suggests that transcriptomic profiling has become a standard analytical tool to assess diet induced physiological responses. Moreover, the frequent appearance of intestinal microbiota highlights the growing integration of microbiome science into feed optimization, confirming that gut microbial ecology now plays a pivotal role in defining nutrient utilization and immune modulation in shrimp **(Li *et al.*, 2018; Zhang & Sun, 2022)**.

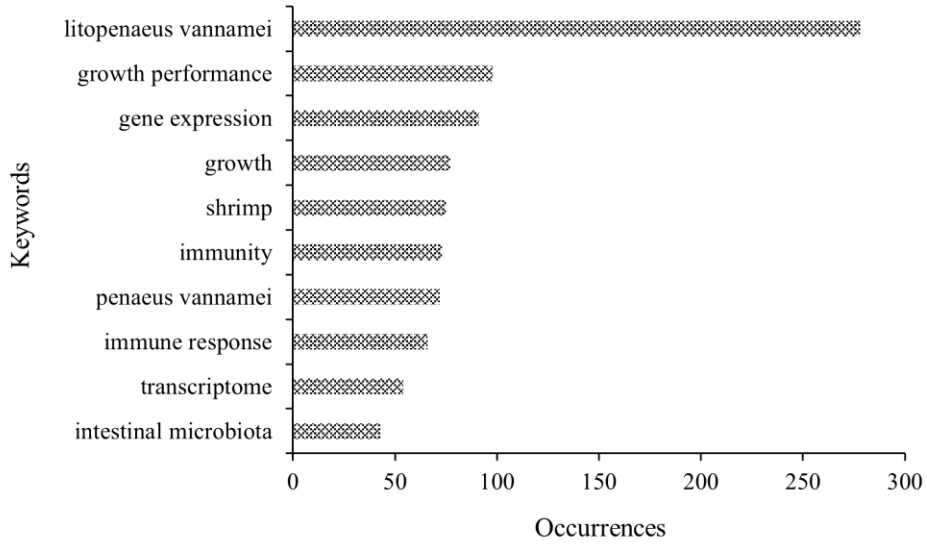


Fig. 5. Top frequent keywords

Temporal mapping of research topics (Fig. 6) demonstrates a clear chronological evolution of scientific focus. Early studies (2008–2014) centered around crustacea, fishmeal, and feed additives, emphasizing feed composition and nutrient substitution. Between 2015 and 2020, themes transitioned toward immunity, metabolism, and pathogen-related terms notably white spot syndrome virus (WSSV) and acute hepatopancreatic necrosis disease (AHPND) reflecting intensified research on molecular defense mechanisms and disease resilience. More recently (2021–2025), emerging keywords such as oxidative stress, antioxidant capacity, intestinal microbiota, and immune-related genes signify the dominance of nutrigenomic and metabolomic approaches focused on cellular stress regulation, antioxidant defense, and molecular immunity. These developments align with global trends in aquafeed innovation that leverage omics to enhance both performance and resilience.

Another noteworthy trend is the expansion from mono-species to comparative and ecosystem-level perspectives. Terms such as *Macrobrachium nipponense* and *Marsupenaeus japonicus* appear in recent years, suggesting cross-species analyses and the rise of multi-taxa nutrigenomic models for feed formulation. This diversification mirrors the application of biofloc and microbial-based feeding systems, where environmental management and diet microbiome synergies are studied as integrated components of shrimp health **(Deepti *et al.*, 2024; Mas'ud *et al.*, 2025)**. The data collectively illustrate that the research landscape has evolved toward a holistic systems biology framework, emphasizing molecular signaling, oxidative balance, and microbiota regulation as central levers for developing next-generation functional aquafeeds.

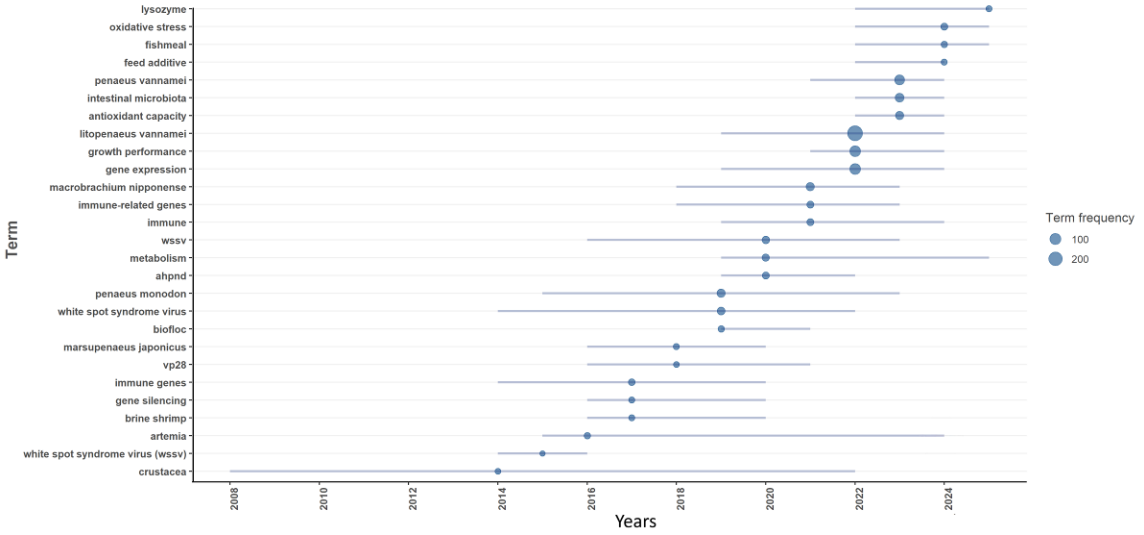


Fig. 6. Trend research topics

The future trends and niche research topic

The overlay visualization (Fig. 7A) illustrates a distinct trajectory in the evolution of *Litopenaeus vannamei* nutrigenomic research, where yellow to green nodes represent the most recent hotspots. A clear conceptual shift is evident from disease-centered studies (WSSV, AHPND) toward redox biology, immunity, and metabolic regulation as key leverage points for feed innovation. The network highlights strong linkages among oxidative stress, antioxidant capacity, lipid metabolism, apoptosis, and innate immunity, reflecting an integrative focus on cellular protection and performance resilience. This convergence suggests that future research will prioritize the development of multi-biomarker panels including antioxidant enzymes (SOD, CAT, GPx) **(Gusti *et al.*, 2021)**, immune markers (TLR, AMPs, lysozyme) **(Sangklai *et al.*, 2024)**, and lipid mediators (bile acids, cholesterol derivatives) **(Jiang *et al.*, 2025)** to evaluate dietary interventions at a mechanistic level. The emerging direction points toward precision immuno-nutrition, in which optimized combinations of bioactive peptides, polyphenols, minerals, and postbiotics are formulated to enhance immune readiness and oxidative balance without compromising growth efficiency.

When *Litopenaeus vannamei* is used as the central node (Fig. 7B), recent studies cluster along the growth, immunity, metabolomics axis, signaling a move from empirical feeding trials toward molecular dissection of adaptive growth pathways. Terms such as ammonia stress and stocking density appear in proximity to metabolomics and immune-related genes, indicating that experimental design is increasingly factorial testing the interaction of diet, environmental stress, and physiological response **(Sun *et al.*, 2024; Metwali *et al.*, 2025)**. These findings underscore the need for multi-omics integration (transcriptome, metabolome and microbiome) in evaluating resilience thresholds,

allowing for predictive modeling of how nutrient metabolism and immune modulation interact under intensive culture conditions.

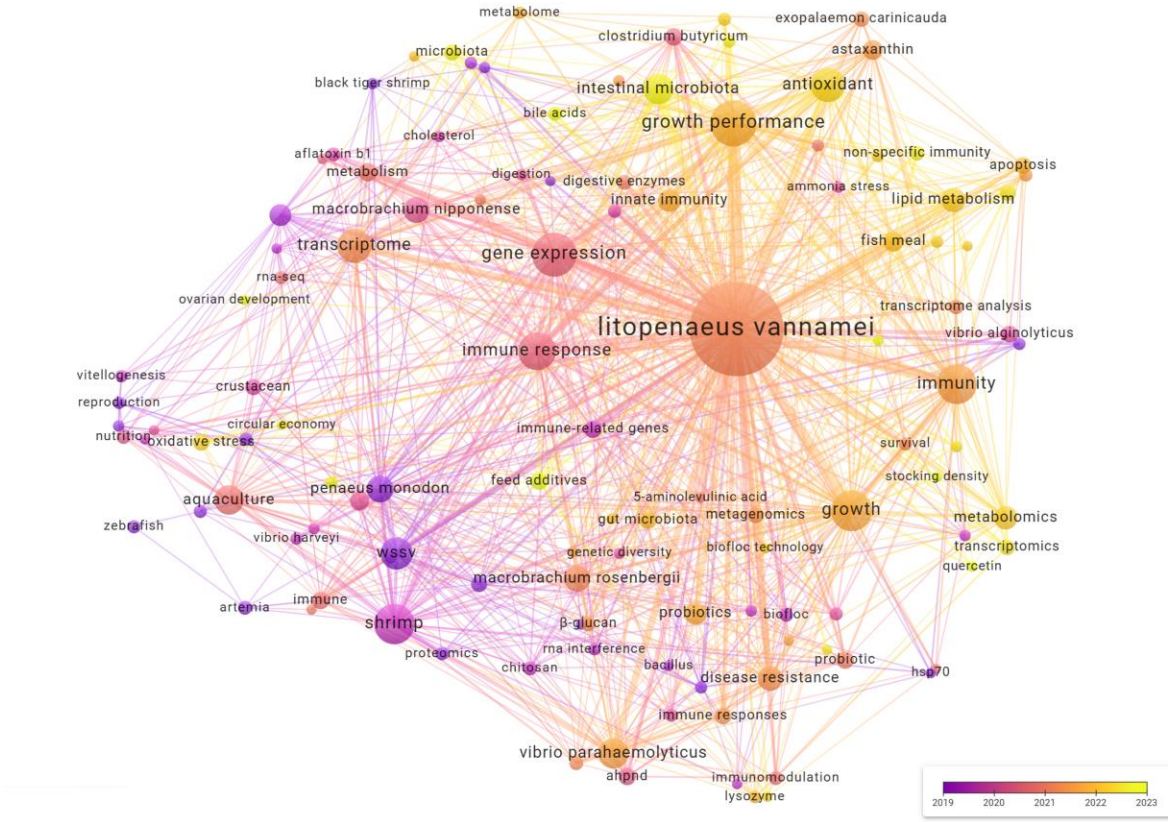
The overlay visualization focusing on intestinal microbiota (Fig. 7C) highlights this node as a recent and rapidly expanding research frontier within genome-based aquafeed studies for *Litopenaeus vannamei*, revealing strong co-occurrence with growth performance, digestive enzymes, innate immunity, bile acids, and metabolomics themes that signify a paradigm shift from descriptive microbial profiling toward functional microbiome engineering in shrimp nutrigenomics. The dominance of yellow-to-green nodes indicates that recent studies are increasingly investigating how gut microbial communities regulate host metabolism, immune signaling, and oxidative balance through bile acid modulation and microbial metabolite production. This emerging focus supports the view that microbiota-driven nutrient metabolism has become a determinant of feed efficiency and disease resistance **(Pewan *et al.*, 2025; Tardiolo *et al.*, 2025)**. Moreover, the clustering of terms such as antioxidant, bile acids, and innate immunity underscores the rising interest in synbiotic and postbiotic formulations capable of orchestrating digestive and immune processes via microbial functional pathways rather than taxonomic composition alone. These insights align with recent multi-omics research demonstrating that intestinal microbiota interacts dynamically with host transcriptomic and metabolomic responses to shape energy utilization, redox homeostasis, and resilience under environmental stress **(Prasad *et al.*, 2024; Jasbi *et al.*, 2025)**. Collectively, the network topology indicates that future innovations in genome-based aquafeed will prioritize precision modulation of the gut ecosystem through targeted feed additives, functional biofloc engineering, and metabolite-guided diet optimization to enhance both metabolic performance and immune robustness in sustainable shrimp aquaculture systems.

The visualization centered on feed additives (Fig. 7D) reveals their pivotal role as a converging hub linking immune response, probiotics, growth performance, antioxidant activity, and intestinal microbiota, with yellow nodes indicating the most recent studies. This configuration suggests that genome-based aquafeed research for *Litopenaeus vannamei* is moving toward a mechanistic understanding of additive functionality at molecular and microbial levels rather than merely evaluating growth outcomes. The clustering of keywords such as probiotic, astaxanthin, and lysozyme demonstrates that recent research increasingly explores bioactive feed components capable of enhancing immune gene expression, antioxidant defense, and metabolic efficiency under environmental stress conditions. The connectivity between feed additives and immune-related genes highlights the integration of nutrigenomic biomarkers including AMP, TLR, and NF-κB pathways to assess host responses to dietary interventions, confirming that molecular endpoints are now key indicators of feed performance **(Skenderidou *et al.*,, 2025)**. Furthermore, the proximity of intestinal microbiota and metagenomics nodes emphasizes the recognition of microbiome-mediated feed effects, where probiotics and postbiotics act not only as immune enhancers but also as modulators of digestive and

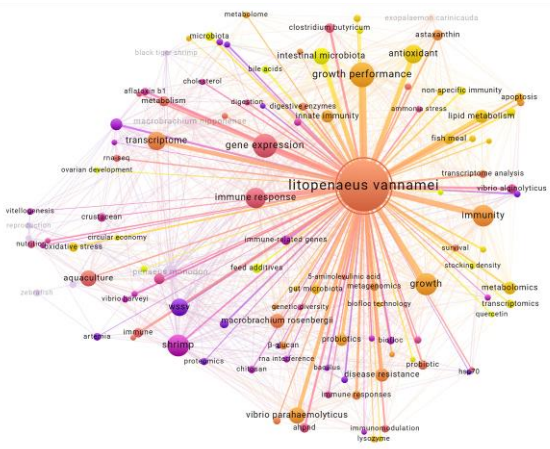
metabolic pathways **(Botta *et al.*, 2025)**. Collectively, these interactions reveal a major research trend toward precision functional feed development, integrating omics-based validation, microbial ecology, and antioxidant strategies to formulate additive combinations that simultaneously improve growth, immunity, and resilience representing a critical frontier in sustainable shrimp aquaculture.

The overlay visualization focusing on quercetin (Fig. 7E) highlights this flavonoid as an increasingly prominent node in shrimp nutrigenomics research, especially in relation to metabolomics, immunity, growth, and immunomodulation. The co-occurrence of quercetin with terms such as "antioxidant enzyme activity", "immune gene expression", and "metabolome" suggests that researchers are exploring its multiple modulatory pathways. For example, a transcriptomic–metabolomic study found that dietary quercetin supplementation in *L. vannamei* enhanced expression of genes in the NF-κB pathway while improving disease resistance **(Zhai *et al.*, 2022; Jin *et al.*, 2024)**. In addition, enrichment of quercetin in biofloc systems improved antioxidant status and growth performance in *L. vannamei* **(Leon *et al.*, 2028)**. Together, these findings support quercetin as a promising functional feed additive in shrimp culture provided that more mechanistic work (dose response, multi-omics integration, microbiome shifts) is conducted. Accordingly, while we refer to quercetin as a potential next-generation biomolecular regulator, we temper the claim by framing it as a high-potential candidate, pending further confirmatory research.

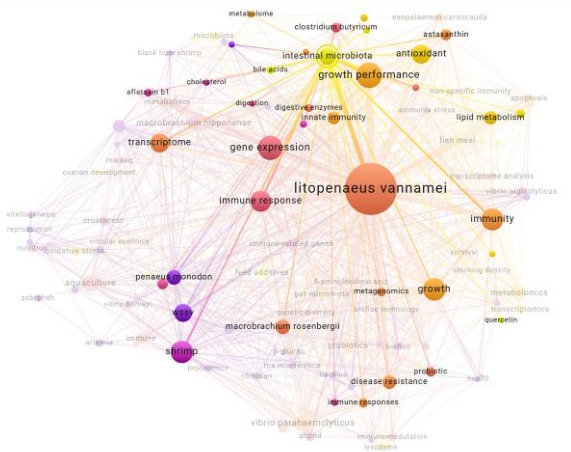
Collectively, the trajectories in Fig. (7A–7E) outline three strategic frontiers shaping the future of genome-based aquafeed research: (1) Precision redox-immunonutrition, combining multi-omics biomarker panels (enzyme activities, immune transcripts, lipid mediators) to validate next-generation feed additives. (2) Integrated diet–microbiota–environment modeling, employing factorial biofloc and aerofloc systems with performance and biomarker endpoints such as feed conversion ratio (FCR), Integrated Biomarker Response (IBR), microbial diversity, and bile-acid metabolite flux. (3) Predictive metabolomic dosing, using metabolite signatures to define the "sweet-spot" concentrations of key bioactives (quercetin, astaxanthin) that maximize resilience while minimizing metabolic cost. In essence, the green-yellow gradients across all maps signify the consolidation of a next-generation, omics-driven smart-feed paradigm one that integrates antioxidant regulation, immune conditioning, and gut-microbiome engineering as the triad of innovation for sustainable and precision shrimp aquaculture.


metabolome
exopalaemon carinicauda
clostridium butyricum
microbiota
astaxanthin
black tiger shrimp
intestinal microbiota
antioxidant
bile acids
growth performance
cholesterol
aflatoxin b1
non-specific immunity
apoptosis
metabolism
digestion
digestive enzymes
ammonia stress
innate immunity
lipid metabolism
macrobrachium nipponense
transcriptome
gene expression
fish meal
rna-seq
ovarian development
transcriptome analysis
litopenaeus vannamei
vibrio alginolyticus
immune response
vitellogenesis
immunity
crustacean
reproduction
circular economy
immune-related genes
nutrition
oxidative stress
survival
stocking density
feed additives
penaeus monodon
aquaculture
5-aminolevulinic acid
gut microbiota
metagenomics
growth
metabolomics
zebrafish
vibrio harveyi
biofloc technology
transcriptomics
wssv
genetic diversity
quercetin
macrobrachium rosenbergii
artemia
immune
probiotics
biofloc
shrimp
β-glucan
rna interference
proteomics
probiotic
chitosan
bacillus
hsp70
disease resistance
immune responses
vibrio parahaemolyticus
ahpnd
immunomodulation
lysozyme
2019
2020
2021
2022
2023

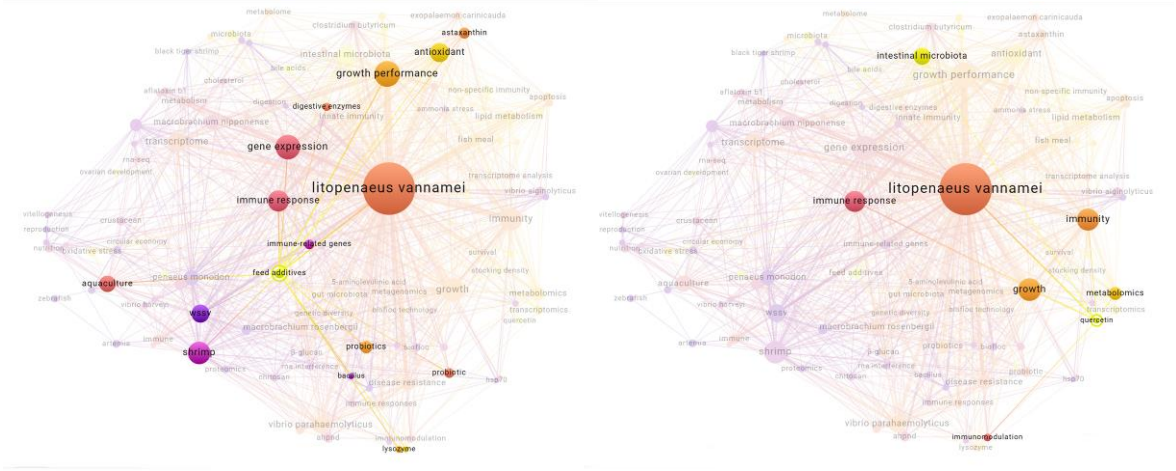
(A)



(B)



(C)



(D) (E)

Fig. 7. All co-occurrences (A); Focus co-occurrences on *Litopenaeus vannamei* (B); Focus co-occurrences on intestinal microbiota (C); Focus co-occurrences on feed additives (D); Focus co-occurrences on quercetin (E)

CONCLUSION

This study presents the first comprehensive bibliometric analysis of global research on genome-based aquafeed and nutrigenomics in *Litopenaeus vannamei* from 1976 to 2025, revealing an exponential growth of publications after 2018 driven by advances in omics technologies and genomic resources. The findings indicate a paradigm shift from conventional feed evaluation toward molecular and integrative approaches focusing on gene expression, oxidative stress regulation, immune response, and intestinal microbiota modulation. China and Southeast Asia emerged as major research hubs, with Fish and Shellfish Immunology, Aquaculture, and Aquaculture Reports identified as the most influential journals. The evolution of thematic clusters highlights the rise of precision immuno-nutrition, metabolomic-guided feed formulation, and microbiome engineering as central future directions. In practical terms, the bibliometric insights provide a roadmap for formulating next-generation feeds that integrate molecular biomarkers and microbiome regulation to enhance shrimp health and sustainability. Moreover, these findings can inform policymakers and funding agencies to prioritize nutrigenomic-based feed innovation under sustainable aquaculture programs aligned with SDGs 2, 12, and 14. Collectively, these trends demonstrate that genome-based aquafeed research is advancing toward a data-driven, sustainable, and biologically informed framework that integrates molecular nutrition, host resilience, and environmental performance to shape the next generation of shrimp aquaculture systems.

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