

Review

Adaptive Evolution of Marine Organisms: A Bibliometric Analysis Based on CiteSpace

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Abstract: (1) Background: The increasing complexity of marine organism habitats and the impact of climate change on the marine environment have garnered global attention towards the adaptive evolution of marine organisms. However, there still remains a lack of understanding regarding the historical development and research trends of adaptive evolution in marine organisms. (2) Methods: We conducted an analysis on the adaptive evolution of marine organisms published in the Web of Science (WOS) over the past two decades. Through a visualization of publications, authors, institutional affiliations, and keywords based on CiteSpace, this review examines research contributions, identifies research hotspots, and outlines future development trends in this field. (3) Results: The findings indicate a surge in the advancement of the adaptive evolution of marine organisms, particularly since 2017, with tight collaboration among European nations. Additionally, Chinese research institutions and scholars have emerged as some of the most significant contributors in this field. (4) Conclusions: This review provides an overview of the main research hotspots and frontiers in the field pertaining to adaptive evolution of marine organisms, as well as the historical timeline of research and development. This review has offered scientific guidance to scholars and institutions concerned with conducting research on marine organisms and adaptive evolution.



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1. Introduction

Adaptive evolution is a process that results in alterations to the phenotypic characteristics of a population, allowing for local adaptation within a given environment over an extended period of evolutionary time. When the genetic phenotype of organisms undergoes modifications in response to a specific environment, thereby improving the survival and reproductive success of the species within that environment, the resulting phenotype is considered to be adaptable [1]. This adaptive relationship between gene mutations and the environment reflects the adaptability of biological functional traits. The heritable variations observed among marine organisms can ultimately be attributed to evolutionary occurrences. However, the absence of suitable adaptive genetic variation has the potential to impact the population's evolutionary pattern and rate [2]. Additionally, the systematic distribution and hereditary characteristics of marine organisms may be influenced by factors such as depth, sea water pressure, food availability, trench and ridge morphology, larval development duration, and other pertinent variables [3–5]. Consequently, studying the adaptive evolutionary traits of marine organisms within a specific ecological setting is instrumental in elucidating the mechanisms by which these organisms adapt to their environment through natural selection. Comprehending and investigating the evolutionary lineage of the origin and the adaptability in marine species assumes paramount significance.

Due to their sessile or benthic nature and limited mobility, marine organisms are highly sensitive to the alterations in environmental conditions such as seawater composition and temperature. The advent of high-throughput sequencing technology has facilitated the investigation of marine organisms at the molecular level, which aids in the analysis and prediction of gene expression patterns in marine organisms as they adapt to their surroundings [6]. Numerous studies on the adaptability of marine organisms to environment have been conducted by scholars across the world, leading to its emergence as a popular research area. Several scholars have conducted research on the evolutionary relationship of marine organisms across different sea depths, documented the evolutionary diversity of these species [7], and employed specific genetic variation in nucleotide positions in the mitochondrial genome to monitor the adaptation of local populations [8,9]. Additionally, researchers have investigated sexual differences and explored the mechanisms of environmental adaptation in marine organisms, particularly in high salinity and high temperature conditions [10–15]. Additional research have expanded upon the diverse adaptations exhibited by related species inhabiting deep seas and shallow seas, encompassing their characteristics and molecular adaptation mechanisms [16–18]. Nevertheless, contemporary scholars predominantly focused on specific topics within this domain, thereby lacking a comprehensive understanding of the prominent research areas, cutting-edge advancements, developmental trajectories, and prevailing challenges within this field. This review work seeks to answer the following questions: What are the primary potential trends for the advancement of research on the adaptive evolution of marine organisms? What are the prominent research areas and hotspots? In order to investigate the focal areas and emerging patterns in the study of adaptive evolution among marine organisms, it is imperative to meticulously categorize the existing scholarly literature in this domain, perform bibliometric and knowledge graph analyses, and elucidate the quantitative characteristics and developmental trend of the research literature.

Therefore, this review employed a bibliometric analysis and knowledge mapping analysis, with the core collection database of Web of Science (WOS) serving as the primary data source, from which works in the literature pertaining to the adaptive evolution of marine organisms were selected as samples, by utilizing clustering knowledge mapping based on keyword co-occurrence and mutation detection in the CiteSpace 6.2.R4 visualization software. This review aims to objectively uncover the research hotspots and development trends in the field of adaptive evolution of marine organisms, thereby shedding light on its research foundation.

2. Materials and Methods

2.1. Data Source

Since WOS currently serves as the primary English-language database compatible with CiteSpace, it was employed to perform a search for the keywords [“marine organism” or “ocean organism” or “ocean species” or “marine species” and “adaptive evolution”] on 24 October 2023. The retrieved publications from the WOS core collection encompass the period from 2003 to 2023 and specifically focus on the topic of adaptive evolution in marine organisms. To ensure the relevance of the gathered information, only research papers and reviews were included, while any research directions unrelated to the adaptive evolution of marine organisms were manually excluded. A total of 659 articles were screened and subsequently exported in plain text format, comprising complete records and cited references. Citespecies 6.2.R4 software was used to conduct a bibliometric analysis on the adaptive evolution of marine organisms research.

2.2. Data Analysis

This review has employed bibliometric techniques to quantify the pertinent documents, authors, institutions, countries, journal distribution, keyword co-occurrences, references, and other data, and conducted a thorough analysis. The bibliometric tool, CiteSpace, was utilized for visualization purposes, leveraging its knowledge graph analysis approach to

examine author collaboration, national collaboration networks, research progress, and areas of focus, while visually presenting the statistical outcomes of the academic literature [19]. To ascertain the prominent areas of research within the domain of adaptive evolution of marine organisms and the interconnections among countries where the relevant literature has been published, we constructed a keyword co-occurrence network and a transnational cooperation network map. This was achieved by employing keyword clustering and time trend analysis, along with the visualization of national cooperation networks (Figure 1). The outlined procedure can be summarized as follows: Initially, the literature plain text file that has been downloaded is imported into the CiteSpace software for the purpose of conducting the literature deduplication and format conversion process, resulting in the acquisition of the processed data file. Subsequently, the software's pertinent parameters were set and the desired modules (e.g., authors, institutions, country (first author), journal, keywords, references) were selected for analysis, followed by the execution of the software to generate visual outcomes. Finally, the parameters were fine-tuned to enhance the reliability and clarity of the visual graphics [20,21]. Betweenness centrality (BC) serves as an indicator of the potential for any shortest path through a node within a network [22]. The BC of node directly correlates with the significance of a node within the network. Particularly in networks with weak connections, nodes exhibiting higher BC may assume pivotal roles as connectors. The quantities of nodes (N) and edges (E) represent crucial metrics that reflect the scale of the network [20]. Modularity (Q) serves as an indicator for assessing the internal structure of the network. A higher Q value indicates a more pronounced clustering effect within the network. Notably, a Q value exceeding 0.3 signifies a significant clustering structure within the network [23]. Similarly, the weighted mean silhouette (S) is employed as an indicator to ascertain the homogeneity of network clustering. A proximity to 1 on the S value denotes a high level of homogeneity within the network, clustering outcomes are deemed persuasive when the S value surpasses 0.7 [24].

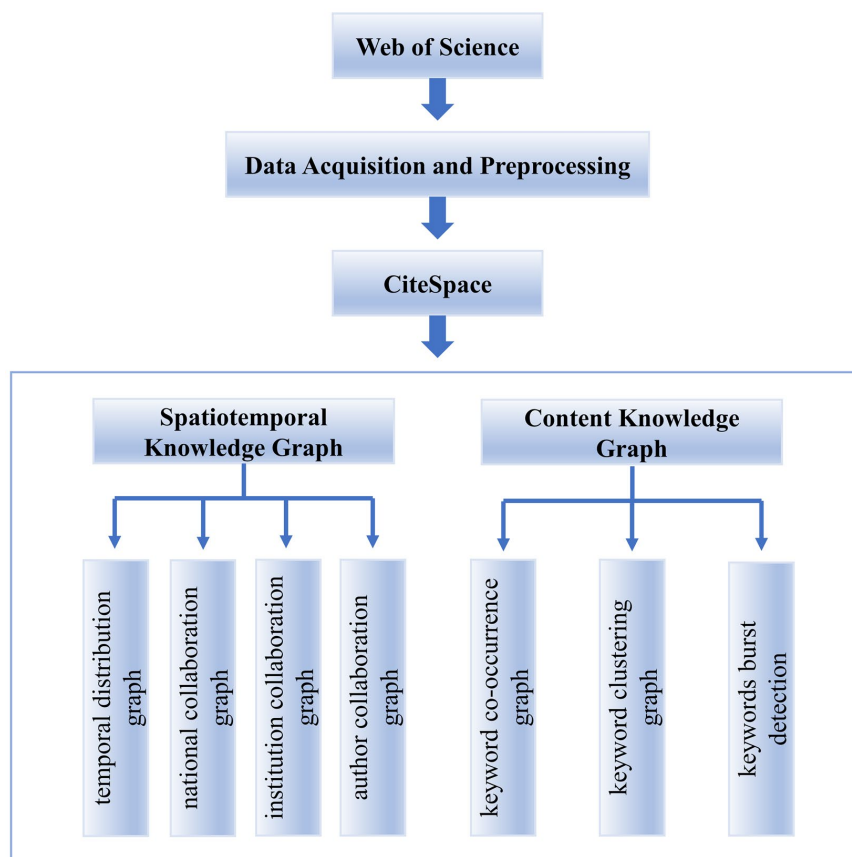


Figure 1. Flow diagram of the method.

3. Results

3.1. Overall Research Overview

The quantification of publications can serve as a rough indicator for estimating the popularity and development of a certain research domain within a given historical period. As depicted in Figure 2, the annual and cumulative publication number of publications pertaining to the adaptive evolution of marine organisms are presented. Over the past two decades, there has been an increase in annual publications. Notably, between 2003 and 2016, the annual publication counts experienced a slow rise, ranging from 13 to approximately 30 publications, but the average annual publication count did not surpass 18 publications. Since 2017, the field has experienced a period of rapid development, evidenced by an annual publication count exceeding 45 publications, peaking at 69 publications in 2022. Despite a temporary increase followed by a decline between 2019 and 2020, the overarching trend in the number of publications has exhibited a rapid growth. This trend displays the heightened interest among researchers in the adaptive evolution of marine organisms, which has progressively emerged as a popular area of investigation. Notably, the most frequently cited documents within this domain include “Microplastic in marine organism: Environmental and toxicological effects” (372 citations) [25] and “Genomic signatures of local directional selection in a high gene flow marine organism; the Atlantic cod (*Gadus morhua*)” (185 citations) [26].

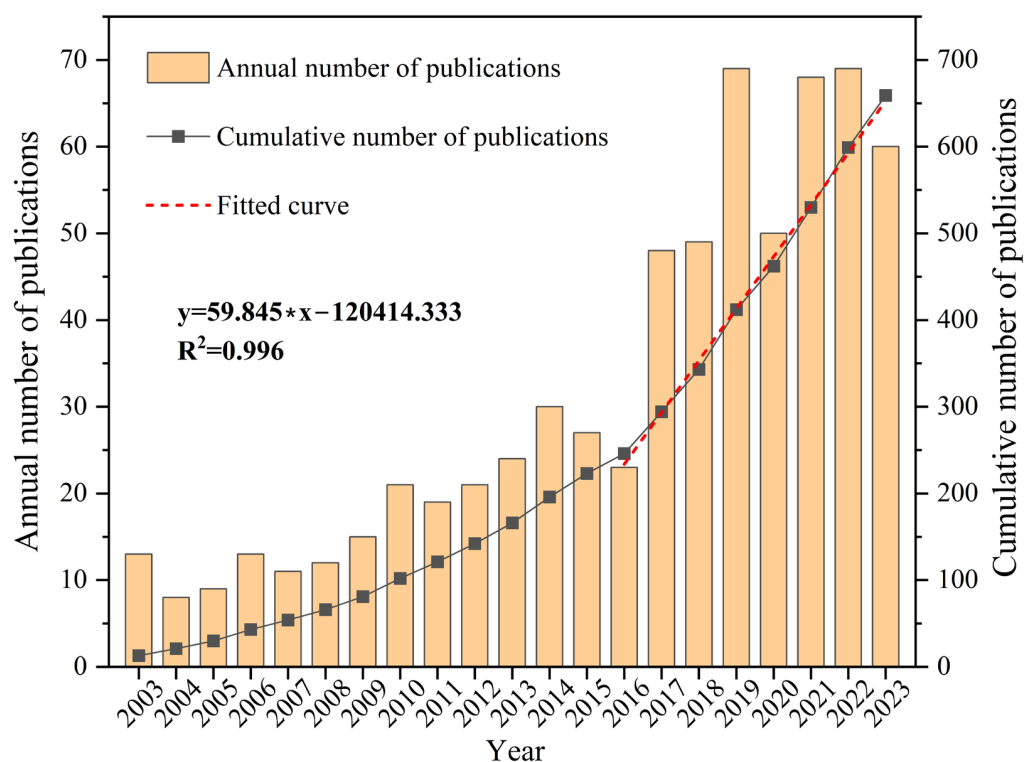


Figure 2. Trends in the number of publications on adaptive evolution of marine organisms from 2003 to 2023.

Based on a comprehensive survey examining the global distribution of publications, China has emerged as the leading country in terms of the quantity of publications pertaining to the adaptive evolution of marine life, with a total of 272 publications, constituting 41.27% of the overall publications. Following China is the USA, which has contributed 120 publications, accounting for 18.21% of the total. Germany secures the third position with 55 articles published. The top 10 countries actively engaged in publishing articles within this domain are presented in Table 1.

Table 1. National publication volume statistics (top 10).

Number	Country	Document Quantity	Percentage (%)
1	China	272	41.3
2	USA	120	18.2
3	Germany	55	8.3
4	Ireland	53	8.0
5	Australia	52	7.9
6	England	40	6.1
7	Italy	39	5.9
8	France	39	5.9
9	Japan	35	5.3
10	Lithuania	30	4.6

A comprehensive examination of the literature sources reveals that research pertaining to the adaptive evolution of marine organisms is published across a wide range of 238 scholarly journals, including journals such as *Frontiers in Marine Science*, *Zootaxa*, *Marine Pollution Bulletin* and *Journal of Oceanology and Limnology*. Notably, Table 2 provides an enumeration of the ten most prolific journals in terms of research output within this domain. Specifically, a cumulative number of 205 publications, constituting 31.11% of the overall literature, are published in these ten journals. Among the journals in Table 2 (namely *Frontiers in Marine Science*, *Marine Pollution Bulletin*, and *Molecular Phylogenetics and Evolution*), they are categorized into Q1 JCR quartile, exhibiting comparatively higher impact factors. In *Frontiers in Marine Science*, 43 articles have been published, meaning it is the journal with the most articles published. A small number of professional core journals publish most of the professional literature, while some studies are often scattered across journals of different disciplines.

Table 2. The statistics of journals in adaptive evolution of marine organisms (top 10).

Publication Name	Document Quantity	Impact Factor	JCR Quartile
<i>Frontiers in Marine Science</i>	43	3.7	Q1
<i>Zootaxa</i>	40	0.9	Q3
<i>Marine Pollution Bulletin</i>	32	5.8	Q1
<i>Journal of Oceanology and Limnology</i>	23	1.6	Q3
<i>Mitochondrial DNA part B Resources</i>	20	0.5	Q4
<i>Chinese Journal of Oceanology and Limnology</i>	12	/	/
<i>Zookeys</i>	11	1.3	Q2
<i>Bioinvasions Records</i>	8	1.4	Q3
<i>Journal of Experimental Marine Biology and Ecology</i>	8	2.0	Q2
<i>Molecular Phylogenetics and Evolution</i>	8	4.1	Q1

3.2. Cooperation Network Analysis

3.2.1. Country Cooperation Network

The distribution of the literature output and cooperation relationships between countries is visually represented by the national cooperation network. Figure 3 illustrates the national cooperation network pertaining to research on the adaptive evolution of marine organisms. The size of each node corresponds to the quantity of relevant documents originating from a particular country, while the thickness of the lines connecting countries indicates the level of collaboration between them. Additionally, the darkness of the color signifies the earliness of the publications. The analysis presented in Figure 3 reveals a notable level of proximity in the cooperation among countries, particularly among European nations like Spain, Russia, and France ($BC > 0.1$), which have conducted early engagement in research pertaining to the adaptive evolution of marine organisms. Despite China's prolific publication output in this domain, its involvement commenced at a later stage, resulting in a more autonomous research approach with limited international collaboration.



Figure 3. The country collaboration network. The size of each node represents the quantity of relevant publications, the thickness of lines represents the level of collaboration between countries, and the darkness of the color represents the earliness of publications.

3.2.2. Research Institution Cooperation Network

Figure 4 illustrates the cooperation network among international research institutions. The network density is 0.0191, including 260 nodes and 644 edges. The network exhibits a density of 0.0191, comprising 260 nodes and 644 edges. Notably, four institutions, namely the Chinese Academy of Sciences (208 articles, $BC = 0.1$), Institute of Oceanology (194 articles, $BC = 0.1$), University of Chinese Academy of Sciences (130 articles, $BC = 0$), and Laoshan Laboratory (103 articles, $BC = 0.09$), have contributed significantly to the study of adaptive evolution in marine organisms, with a minimum of 100 publications each. These four institutions collectively accounted for the highest number of publications in this field, surpassing 70% of the total publications worldwide by all institutions. However, the level of cooperation network among these four institutions is relatively low, with a BC value not exceeding 0.1. On the contrary, despite the limited number of publications from institutions such as UDICE-French Research Universities (17 articles, $BC = 0.17$), Center National de la Recherche Science (18 articles, $BC = 0.17$), and University of California System (5 articles, $BC = 0.11$), their collaborative network exhibits a higher degree of connectivity. This observation highlights the significant role played by these institutions in fostering international cooperation within this field.

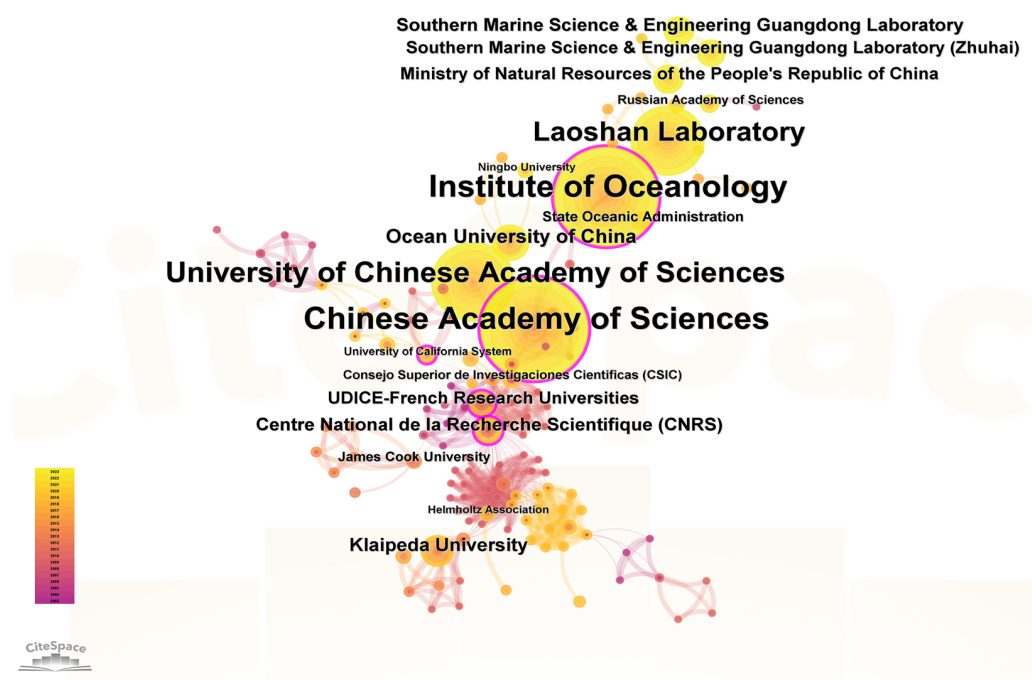


Figure 4. The institution collaboration network. The size of each node represents the quantity of relevant publications, the thickness of lines represents the level of collaboration between institutions, and the darkness of the color represents the earliness of publications.

3.2.3. Author Cooperation Network

The utilization of author collaboration network analysis can serve as a valuable tool for visualizing prominent research teams and scholars within a certain academic field. As depicted in Figure 5, the collaboration network of authors specializing in the adaptive evolution of marine organisms exemplifies a cooperative structure. A series of investigations conducted by researchers in this field has contributed to the establishment of a relatively distinct author collaboration network. However, it is worth noting that the level of collaboration among authors remains modest ($N = 291$, $E = 281$, density = 0.0067), necessitating the enhancement of international cooperation among authors. Among the authors, a mere eight scholars have published a minimum of 10 articles in this particular field. Specifically, Xu Kuidong (Chinese Academy of Sciences Inst Oceanol, 37 articles) and Li Xinzheng (Chinese Academy of Sciences Inst Oceanol, 25 articles) stand out with their publication of 37 and 25 articles, respectively, surpassing the threshold of 20 articles. This evidence suggests their active involvement in this field, positioning them at the forefront globally in terms of publication volume. Additionally, our analysis reveals that the nodes of these two authors are interconnected with four other authors Zhan Zifeng (Chinese Academy of Sciences Inst Oceanol, 10 articles), Dong Dong (Chinese Academy of Sciences Inst Oceanol, 5 articles), Sui Jixing (Chinese Academy of Sciences Inst Oceanol, 5 articles), and Kou Qi (Chinese Academy of Sciences Inst Oceanol, 4 articles). Moreover, there exist more node connections among them, which signify a significant level of collaboration among these six authors. Based on a comparative analysis of the institutions of the authors and their published articles, it can be deduced that six scholars, under the leadership of Xu Kuidong and Li Xinzheng, have established two research teams that hold significant global influence in the domain of adaptive evolution of marine organisms. Their primary focus lay in investigating marine biodiversity and biological adaptability across diverse habitats. Despite a delayed initiation, Chinese scholars have progressively attained substantial outcomes in this research domain, culminating in the formation of specific research teams. This development signified the gradual emergence of Chinese scholars as frontrunners in this field.



Figure 5. The author cooperation network. The size of each node represents the quantity of relevant publications, the thickness of lines represents the level of collaboration between authors, and the darkness of the color represents the earliness of publications.

3.3. Keyword Analysis Cooperation Network

Keywords are concise words that effectively represent the subject and substance of an article. The utilization of keyword co-occurrence and cluster analysis aids in the swift identification of prominent subjects within a specific research domain. Figures 6 and 7 display the outcomes of keyword co-occurrence and clustering analysis within the field of adaptive evolution in marine organisms. The resulting keyword co-occurrence and clustering network exhibit a relatively sparse structure ($N = 286$, $E = 363$, density = 0.0089). To ensure conciseness and clarity, only keywords with frequencies equal to or exceeding 5 are highlighted in Figure 6. Among the 287 identified keywords, 28 keywords exhibit a frequency equal to or exceeding 10, while 21 keywords display a frequency ranging between 10 and 20. Additionally, 7 keywords demonstrate a frequency surpassing 20. Collectively, these keywords manifest conspicuous nodes and exhibit dense line connections. Notably, 12 keywords possess a BC value equal to or exceeding 0.1, including diversity (36 times, BC = 0.21), fish (26 times, BC = 0.27), sea (24 times, BC = 0.18), patterns (18 times, BC = 0.14), growth (17 times, BC = 0.13), adaptive evolution (14 times, BC = 0.13), marine (14 times, BC = 0.17), abundance (12 times, BC = 0.14), biological invasions (11 times, BC = 0.14), and bay (11 times, BC = 0.16). These keywords exhibit both high frequency and connectivity, and they also align well with the research topic of “adaptive evolution of marine organisms”. Furthermore, in addition to the aforementioned 10 high-frequency keywords, the remaining two keywords, namely dispersal (BC = 0.15) and gulf (BC = 0.10), are identified.

The utilization of cluster analysis based on a keyword co-occurrence network reveals the keyword clustering within the research field of marine organism adaptive evolution, as depicted in Figure 7. The observed keyword clustering structure exhibits statistical significance ($Q = 0.8317 > 0.3$), and the obtained clustering outcomes are highly persuasive ($S = 0.9381 > 0.7$). Figure 7 illustrates a total of 10 cluster labels, arranged in ascending order of cluster numbers, which are as follows: adaptive evolution (cluster #0), species richness (cluster #1), phylogenetic analysis (cluster #2), ocean acidification (cluster #3), health risk (cluster #4), DNA barcoding (cluster #5), differential gene expression (cluster #6), *Crassostrea gigas* (cluster #7), biological invasions (cluster #8), and marine organisms (cluster #9).

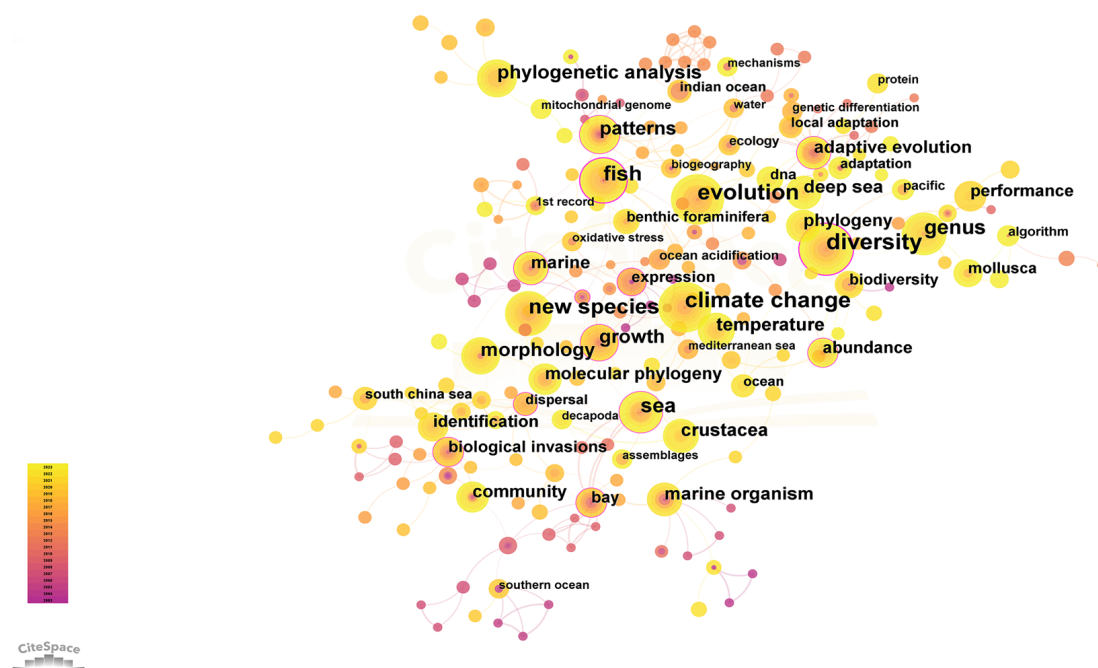


Figure 6. The keyword cooperation network. The size of each node represents the frequency of relevant keywords, the lines represent the collaboration between keywords, and the darkness of the color represents the earliness of keywords.

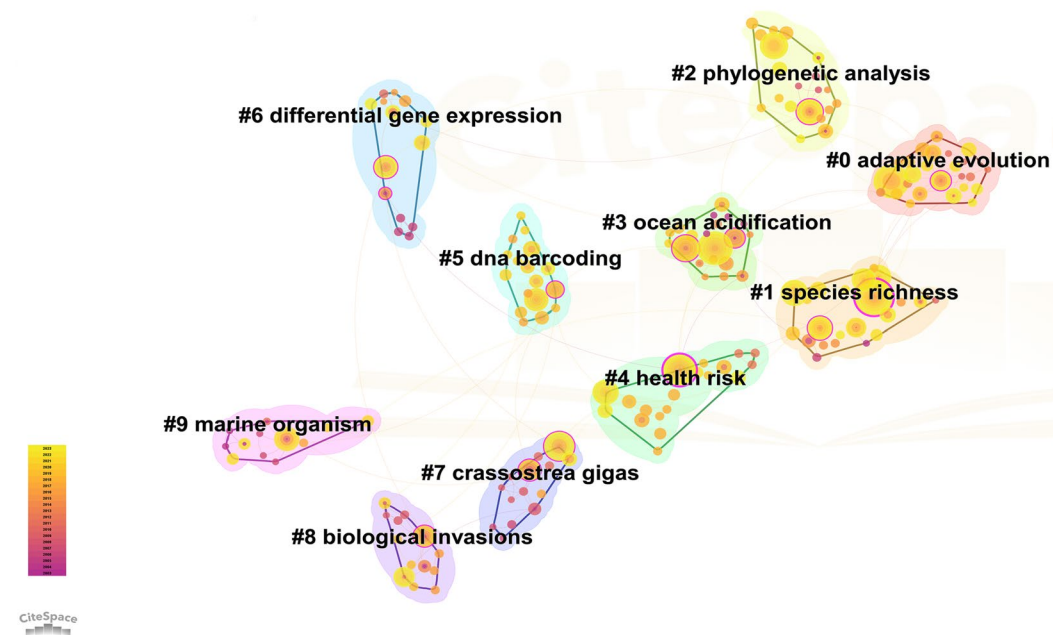


Figure 7. The clustered keywords cooperation network. The size of each node represents the frequency of relevant clustered keywords, the lines represent the collaboration between clustered keywords, and the darkness of the node color represents the earliness of keywords.

3.4. Keyword Timeline Network Analysis

The utilization of the keyword timeline facilitates a deeper comprehension of the chronological progression and advancement of distinct keyword clusters within the realm of adaptive evolution in marine organisms. In order to illustrate this, a keyword timeline network analysis was undertaken on clustered keywords spanning from 2003 to 2023, as depicted in Figure 8. The outcome of this analysis reveals the existence of 10 keyword clusters, wherein keywords belonging to the same cluster are presented on a shared timeline

based on their respective time of occurrence. Cluster#5 had the shortest duration, while Cluster#1 exhibits the longest duration, thereby suggesting that the investigation of species richness had consistently been a prominent research direction in the field of adaptive evolution of marine organisms; Cluster#8 garners considerable attention in initial stages, but this trend had stagnated before 2020; despite commencing later, Cluster#0 remains an active and significant research topic within the field of adaptive evolution of marine organisms.

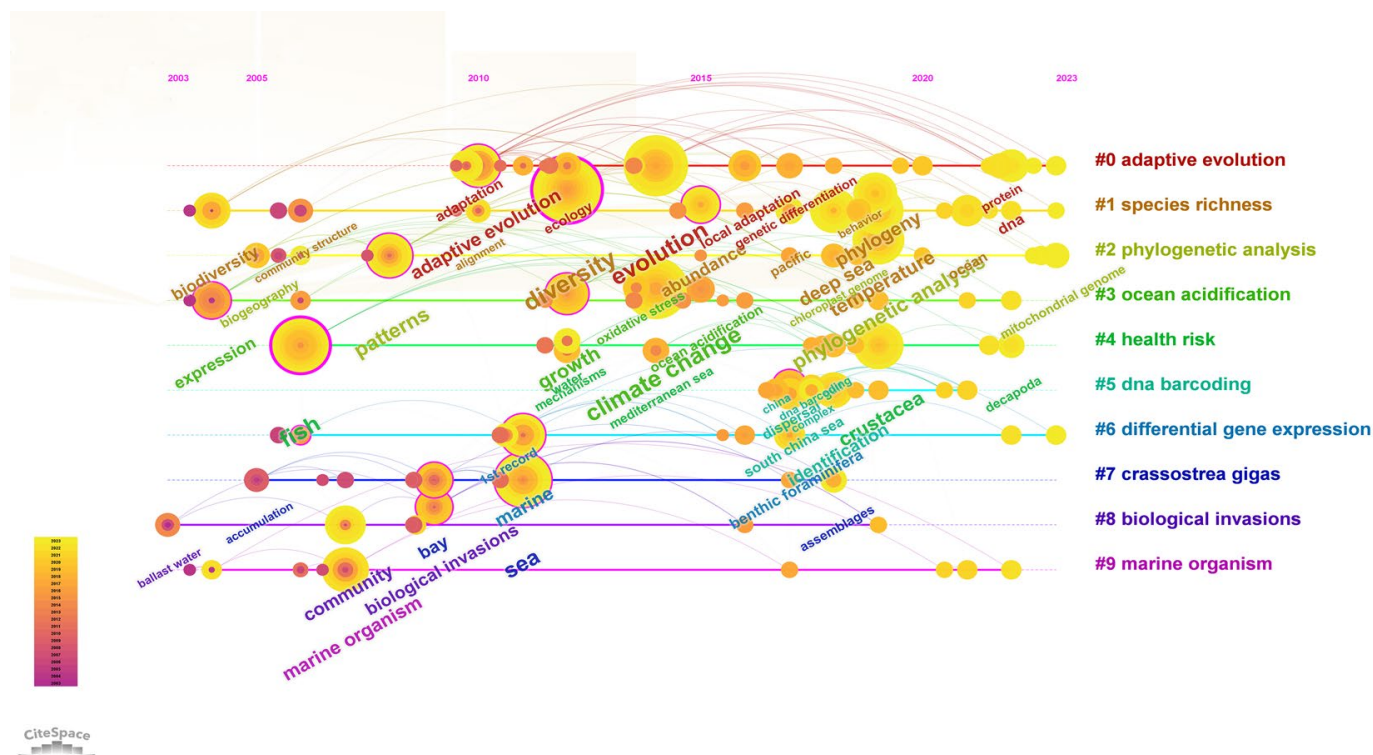


Figure 8. The keyword timeline network. The vertical axis represents the cluster labels, the horizontal axis represents the time, the size of each node represents the frequency of relevant keywords, the lines represent the collaboration between keywords, and the darkness of the color represents the early keywords.

3.5. Keywords Burst Citation

The abrupt surge and burst of a specific keyword within a short timeframe can serve as an indicator of a frontier hot spot within the realm of research. Through the identification of keywords that experience rapid proliferation, we can effectively observe and comprehend the alterations in research topics that have transpired in recent years, employing the analysis of keyword burst detection. In our study on the adaptive evolution of marine organisms spanning from 2003 to 2023, we constructed a network of keyword co-occurrence and successfully detected the top 25 keywords exhibiting the strongest citation burst, as depicted in Table 3. The keyword “performance” exhibits the strongest burst citation strength (strength = 6.21) and is characterized by a relatively brief duration (2020–2021). “Accumulation” is the keyword with the earliest outbreak time (strength = 2.43). The majority of keywords experience a gradual burst after 2016, while only seven keywords (accumulation, adaptive evolution, new species, expression, mediterranean sea, ocean acidification and bay) exhibit burst patterns prior to 2016, aligning with the trend of a limited number of publications during that period.

Table 3. Top 25 keywords with the strongest citation bursts.

Keywords	Strength	Begin	End	2003–2023
accumulation	2.43	2005	2009	
bay	2.19	2009	2017	
adaptive evolution	2.67	2010	2016	
new species	2.23	2013	2014	
expression	3.7	2014	2017	
mediterranean sea	2.16	2014	2018	
ocean acidification	3.32	2015	2017	
local adaptation	2.42	2016	2020	
dispersal	3.2	2017	2019	
genetic differentiation	2.72	2017	2018	
molecular phylogeny	2.22	2017	2018	
evolution	2.15	2017	2018	
fish	2.8	2018	2019	
identification	2.74	2018	2023	
gulf	2.13	2018	2019	
chloroplast genome	2.13	2018	2019	
temperature	2.95	2019	2020	
behavior	2.12	2019	2020	
performance	6.21	2020	2021	
genus	4.58	2020	2023	
crustacea	2.81	2020	2023	
morphology	2.57	2020	2023	
deep sea	3.73	2021	2023	
ocean	3.28	2021	2023	
phylogeny	2.67	2021	2023	

Note: The blue and red represent the duration of the keywords, and the red represents the years of burst keywords.

4. Discussion

4.1. Trends in the Number of Publications

The ocean harbors abundant biological resources and holds a significant role in global biodiversity. Marine organisms undergo diverse adaptations through the interplay of genetic variation, drift, and natural selection. Adaptive evolution refers to the dynamic process by which organisms respond to external environmental pressures [27]. Despite the ocean's unique and intricate environment serving as a crucial catalyst for the adaptive evolution of marine organisms [28], the underlying mechanisms governing this process remain unclear. In recent years, the advancement of high-throughput sequencing technology and gene editing technology has facilitated extensive investigations in the domain of adaptive evolution, thereby significantly propelling forward the progress of adaptive evolution research on marine organisms [29,30]. The research on adaptive evolution in marine organisms can be categorized into two distinct phases: the initial stage spanning from 2003 to 2016, and the stage of rapid development spanning from 2017 to 2023. Despite a delayed initiation in 2016, the research in this field has witnessed exponential growth in publications owing to the remarkable expansion of research resources, funding opportunities, scholarly engagement, extensive scientific collaboration, and the emergence of diverse disciplines such as biogeography, phylogeny, and population genetics [31–33]. This trend underscores the increasing significance and widespread interest in investigating the adaptive evolution of marine organisms, which has emerged as a prominent research hotspot.

4.2. Scientific Contributions

Through the utilization of cooperative network analysis encompassing countries, institutions, and authors, it becomes possible to summarize the worldwide research prowess pertaining to the adaptive evolution of marine organisms. Moreover, this approach facilitates understanding of the institutions and research groups with academic influence, as well as the collaborative relationships among them. Notably, China has emerged at a dominant position in terms of research output and publication count within this domain, while also exhibiting distinct research directions. Zhang et al. (2023) [34] have examined the adaptation of two closely related oysters inhabiting distinct areas (intertidal and estuarine) to varying salinity environments. The research has elucidated the adaptive mechanisms employed by these marine mollusks, while also evaluating their capacity for

adaptive evolution under climate change. Zhao et al. (2018) [35] and Li et al. (2020) [36] have conducted research on the population genetic differentiation and adaptive evolution of Chinese Sea Bass (*Lateolabrax maculatus*) and Pacific Oyster (*Crassostrea gigas*), respectively, shedding light on the population differentiation and local adaptation of these two organisms. Concerns have been raised by scholars regarding the ocean environment, as their research has revealed the presence of microplastics, nanoparticles, heavy metals, and pesticides that remain in marine organisms [37–40]. These residues have the potential to induce toxicity in marine organisms and elicit adaptive stress responses. Nonetheless, the realm of domestic research exhibits relative independence with limited engagement in international collaboration. Nevertheless, certain European nations have demonstrated a greater inclination towards cooperation in this domain. Scholars hailing from France and Spain have examined the adaptive evolutionary traits of *Corallium rubrum* amidst climate change, encompassing pivotal genes such as heat shock protein70 and genetic selection, which significantly influenced individual adaptation [41]. In addition, as a result of the diverse hydrological conditions present in the Baltic Sea, researchers have identified various mechanisms through which invasive species and new cryptic species were introduced and adapted to the local environment. The research was collaboratively initiated and conducted by research institutions in Estonia, Lithuania, Sweden, and Russia [42]. Notably, Chinese research institutions, including Chinese Academy of Sciences and Ocean University of China, have made significant contributions to the field of adaptive evolution of marine organisms, constituting a substantial proportion of the overall research efforts. Similarly, the author's collaborative network analysis can be employed to visually represent prominent research teams and scholars within a specific academic domain. The two teams, under the leadership of Li Xinzheng and Xu Kuidong, are affiliated with the Chinese Academy of Sciences Institute of Oceanology, exhibiting a high level of cooperation and concentrating their efforts on the exploration of marine biodiversity and biological adaptability across diverse habitats [43,44]. Chinese scholars have increasingly garnered contributions in the domain of adaptive evolution of marine organisms, despite their relatively delayed entry into the field. Their fruitful results and the establishment of robust research teams have positioned Chinese scholars as emerging leaders in this area.

4.3. Research Hotspots

Keywords serve as highly condensed words of the paper, effectively conveying its theme and content. Employing keyword co-occurrence and clustering analysis facilitates the rapid identification of prominent hotspots within a research domain. In the realm of adaptive evolution of marine organisms, the prevailing research interests revolve around adaptive evolution, species richness, phylogenetic analysis, and health risk. Notably, “adaptive evolution” stood as the most pertinent keyword. *Provanna glabra*, as a dominant species inhabiting hydrothermal vents and cold seeps in the deep sea, exhibited significant genetic variations local adaptability. These findings are likely attributed to geographic barriers, constrained diffusion capacity and diverse pressures imposed by deep-sea environments [45]. Similarly, Perez et al. (2023) [46] discovered that gene methylation in deep-sea polychaetes contributes to the expression of housekeeping gene, thereby facilitating their adaptation to the deep-sea environment. Notably, DNA methylation played a significant role in this adaptive process. “Species richness” is the most frequently keyword. It is widely acknowledged that coral serve as vital ecosystems, providing habitat for many marine organisms, and exhibiting a high level of species richness. However, there is limited knowledge regarding the factors influencing the diversity and abundance of coral symbionts. In their study, Britayev et al. (2023) [47] discovered that the size and density of colony had an impact on the diversity and abundance of coral symbionts, and that species competitiveness escalated with the increasing of abundance. Since 2004, the utilization of phylogenetic analysis has been an essential analytical approach for marine biodiversity and classification research. Asahida et al. (2004) [48] employed microsatellite locus to determine the base substitution rate of rockfishes from various geographical regions. The

findings from the phylogenetic tree analysis revealed notable variations in DNA sequences, indicating a distinct evolutionary history compared to North American species. In a recent investigation, the rearrangement and phylogenetic analysis of Ophiuroidea species' mitogenomes unveiled the differentiation of ophiuroids during the Permian-Triassic mass extinction event with deep-sea lineages differentiating in the Cretaceous period [49]. The immune response and adaptive evolution of numerous marine organisms occur within harsh habitats. In the research conducted by Saidani et al. (2019) [50], clams were subjected to photocatalyst nanocomposites (TiO₂NPs and AuTiO₂NPs) to simulate the impact on marine ecology. The researchers observed the accumulation of Au and Ti in the gill and digestive glands of the clams, which subsequently led to a reduction in their filtration and respiration rates. Consequently, the clams exhibited alterations in their adaptive behavior towards the environment. In general, the investigation of phylogeny, biodiversity, and adaptive immunity in marine organisms represent prominent research hotspots within the field of marine organism adaptive evolution.

4.4. Hotspots Evolution and Research Frontiers

The utilization of a keyword timeline proves advantageous in gaining a deeper comprehension of the evolution and development process of diverse keywords within the realm of adaptive evolution pertaining to marine organisms. The cluster "species richness" emerges as the most extensive, encompassing the time period spanning from 2003 to 2023. It represents the earliest and most enduring direction of investigation within the field of marine biological research and development. Initially, scholars focused their research on the recognition and identification of novel species [51,52]. However, as a consequence of potential anthropogenic pressure and climate change within marine ecosystems, an increasing number of researchers have directed their attention towards the issue of invasive species [53]. In a rapid assessment survey, Minchin et al. (2017) [54] employed the abundance and distribution range approach to revealed a potential correlation between the intrusion of Asian kelp *Undaria pinnatifida* and seawater salinity. Due to the growing demand for seafood and the extensive utilization of molecular technology and DNA barcoding, researchers primarily focused on examining the genetic diversity and population structure of economically significant marine species. Additionally, they aimed to forecast the interaction between system geography history and population history through the identification of haplotype diversity within biological populations [55]. Furthermore, several researchers have conducted inquiries into the impact of geomorphological characteristics on marine biodiversity, revealing that sediment depth, temperature, and nutrient levels played a crucial role in shaping gene flow and population differentiation [56]. Nevertheless, the short application period of DNA barcoding technology could be attributed to the limitation posed by a single gene fragment and the low mutation frequency [57].

Several keywords experience burst during a specific historical period, such as "adaptive evolution" and "ocean acidification", suggesting that these keywords garner significant interest during the year of burst. However, with the continuous update and iteration of the research, the attention towards these keywords gradually diminished, ultimately leading to the ending of their burst. The discussion surrounding the population structure and adaptive evolution of marine organisms had garnered significant attention from scholars due to the escalating impact on the marine environment, including ocean acidification [58]. Consequently, the keywords "phylogeny" and "identification" have emerged as new frontier hotspots within this domain. The sudden burst in the frequency of the keyword "deep sea" within a brief timeframe indicates that the field of deep-sea biology has become a prominent frontier hotspot, likely attributable to the rapid advancements in submersible [59].

5. Conclusions

This review conducts a bibliometric analysis of the literatures pertaining to the adaptive evolution of marine organisms from 2003 to 2023, utilizing CiteSpace. The analysis focuses on the fundamental characteristics and sources of the retrieved literature from the

aspects of annual publications and journals. Notably, there has been a significant increase in the number of publications within this domain over the past two decades. Subsequently, through the establishment of a collaborative network involving countries, institutions, and authors of the publications, it became evident that domestic research is more independent and some European countries cooperate more tightly. Ultimately, the utilization of keyword co-occurrence, time evolution, and burst detection analysis enable the comprehensive synthesis of the impacts pertaining to adaptive evolution, species richness, systematic evolution analysis and toxicity immunity of marine organisms. This analysis has served to elucidate the research frontiers, offering novel perspectives on the frontier hotspots and trends within this domain. Therefore, it is recommended that future research should be carried out from the following aspects: (1) Despite the significant contributions made by domestic research in the realm of adaptive evolution of marine organisms, it remains largely independent and lacks global collaboration. Domestic scholars should enhance cooperation and collaboration among institutions to further investigate the mechanism of adaptive evolution; Simultaneously, foreign scholars are encouraged to seize the opportunity of rapid changes in the marine environment, thereby expanding research outcomes and making substantial contributions to the global of marine biological adaptability. (2) The research on DNA barcoding commences belatedly and exhibits inadequate persistence, thereby enabling researchers to develop conserved DNA barcoding applications in marine biological adaptability. (3) In recent times, studies pertaining to “biological invasion” have become infrequent, while the exploration of the deep sea and phylogeny has emerged as novel frontier hotspots. Researchers can intensify their exploration of marine organism resources, encompassing remote sensing and in situ investigation, to unveil additional mechanisms of invasive alien species. Given the ongoing discovery of novel species, it is imperative to promptly update phylogenetic research on marine organisms. However, the research resources available for deep-sea organisms remain constrained. Consequently, it is crucial to actively advance the development of deep-sea equipment and technology to safeguard the in situ data of deep-sea samples, thereby enabling more precise analyses of biological research. This will facilitate the examination in adaptive characteristics, distribution patterns and evolution pathways of marine organisms, further investigating the molecular basis underlying character diversity and elucidating the biological endogenous mechanism.

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