

EXPLORING THE IMPACT OF HYBRIDIZATION ON BIODIVERSITY: A BIBLIOMETRIC ANALYSIS AND VISUALIZATION OF RESEARCH TRENDS

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Abstract. Hybridization plays a crucial role in shaping biodiversity by influencing genetic diversity, species adaptation, and ecosystem stability, with both beneficial and detrimental effects. This bibliometric analysis examines the impact of hybridization on biodiversity using Scopus data covering the period from 1993 to 2024, with Biblioshiny, VOSviewer, and CiteSpace used for data processing and visualization. The study analyzes annual scientific production trends, identifying key contributors, most relevant authors, and the most cited documents globally in this research domain. The network visualization of co-citation of cited authors and cited journals provides insights into influential research clusters and interdisciplinary connections. A timeline network visualization of country collaborations highlights the global distribution of hybridization research and key contributing nations. The study also explores trend topics and thematic maps, revealing emerging research themes such as climate change, conservation genomics, and microbial hybridization. The co-occurrence analysis of author keywords identifies core research foci and evolving areas of interest. The findings reveal significant research gaps, particularly in long-term ecological consequences, hybrid species management, and integration with conservation policies. The study's practical implications emphasize the need for policy-driven biodiversity management, enhanced interdisciplinary collaboration, and genomic tools for conservation strategies.

Keywords: *genetic introgression, species adaptation, scientometric analysis, Biblioshiny, VOSviewer, CiteSpace*

Introduction

Hybridization, the process of interbreeding between two different species or genetically distinct populations within a species, has long been a topic of interest in evolutionary biology and conservation science (Fitzpatrick et al., 2015; Quilodr n et al., 2020; Shang and Yan, 2017). It can occur naturally in ecosystems where species distributions overlap, or it is facilitated by human activities such as habitat modification, climate change, and species introductions (Draper et al., 2021; van Wyk et al., 2017a). While hybridization has historically been recognized as a driver of genetic diversity and speciation, it also poses significant threats to biodiversity, particularly when it leads to genetic homogenization, the loss of unique species, or the disruption of ecosystem

stability (Vedder et al., 2022). The impact of hybridization on biodiversity is therefore complex, with both beneficial and detrimental consequences (Chan et al., 2019).

Hybridization has a positive effect on genetic diversity and adaptability. Hybrid organisms are likely to express heterosis, or hybrid vigor, inheriting desirable traits that will further promote their survival and fertility (Heil et al., 2016; Ri, 2020). Under changing environments, such hybrid organisms are likely to adapt to new environments more effectively, thus improving the robustness of the population during climate change, habitat fragmentation, and the challenges of diseases (Bautista et al., 2020; Samarasinghe et al., 2020). Also, hybridization plays an essential role in the formation of new species, a process referred to as hybrid speciation, documented both in plant and animal life (Cuevas et al., 2019; Nelson et al., 2017).

However, hybridization can be extremely detrimental to biodiversity if it occurs between native and invasive species (Dormontt, 2008; van Wyk et al., 2017b). The hybrid offspring will then supplant native species, reducing them to lower population sizes that will eventually be extinct (Kovach et al., 2015). This is especially harmful if the hybrid possesses greater aggression, higher fertility, or other characteristics that enable them to be superior to native purebreds (Zuber et al., 2012). Also, through the process of introgressive hybridization, where hybrid offspring backcross to parent species, genetic purity of native species will be eroded through the dissolution of specific genetic lineages and evolutionary characteristics (Johnson et al., 2016; Moy et al., 2019).

Anthropogenic hybridization has accelerated over the past few decades as a result of habitat disturbance, altered migration routes, and intentional or accidental introduction of alien species (Benjamin-Fink and Reilly, 2018; Ottenburghs, 2021). Hybridization of wild and domestic species, for example, wolves and domestic dogs or wild and farmed fish, has raised concerns over genetic pollution and the ultimate loss of wild-type characteristics (Nussberger et al., 2023; van Wyk et al., 2017b). Conservationists routinely face ethical and practical difficulties in managing hybrid populations because eliminating hybrids would be necessary in order to protect genetic purity, but hybrid individuals would also belong to the evolving ecosystem (Donfrancesco and Luque-Lora, 2021).

Understanding hybridization's impact on biodiversity requires a balanced viewpoint that balances conservation interests with evolutionary potential (Chan et al., 2019; Seehausen et al., 2008). While hybridization can enhance genetic diversity and adaptability under some conditions, it can also cause species depletion and ecosystem discord (Brennan et al., 2014; Stelkens et al., 2014). Conservation responses must therefore be case-specific, welcoming genetic monitoring, habitat management, and policy intervention to ensure that hybridization enhances biodiversity rather than threatening it (Fitzpatrick et al., 2015). As science continues to develop, a greater appreciation of hybridization's role in ecosystem formation will be central to effective biodiversity conservation during an era of heightened environmental change (Hirashiki et al., 2021; Yan et al., 2017).

Due to the expanding literature within this theme, systematic analysis of research trends, influential researchers, landmark papers, and emerging themes is crucial (Agac et al., 2023; Alavi et al., 2024). Bibliometric analysis offers an efficient method to understand the evolution of research on hybridization and the implications to biodiversity (Simion et al., 2023). This study employs three advanced bibliometric tools—Biblioshiny, VOSviewer, and CiteSpace—to investigate the research landscape of hybridization research on biodiversity (John et al., 2024; Lukose et al., 2025). The online

tool Biblioshiny offers extensive analysis functions to determine publication trends, citation networks, and theme trends (Komperda, 2017; Souza de Cursi, 2023; Thangavel and Chandra, 2023; Waghmare, 2021). VOSviewer offers the ability to visualize complex bibliometric networks such as co-authorship, co-citation, and keyword co-occurrence that support the identification of influential research groups and collaborations (Abbas et al., 2021; Jose et al., 2024; Joseph et al., 2024; Van Eck and Waltman, 2010). CiteSpace, employed to identify emerging trends and seminal shifts within the literature, offers an understanding of the dynamic evolution within the theme. The tools collectively offer an overarching view of the research landscape (Mathew et al., 2024; Ye, 2018; Zhang, 2023).

This bibliometric analysis presents an organized view of hybridization and biodiversity publications over the period 1993–2024, providing insights into research trends, key contributors, and thematic evolution. The analysis measures vital indicators like publication growth, citation impact, top journals, and the geographical distribution of the research (Thangavel and Chandra, 2023). The study also identifies research clusters, intellectual structures, and the evolution of the topic (Alfouzan et al., 2023; Babu and Thomas, 2022; Thomas et al., 2023). The analysis discusses both the scientific and the conservational sides of hybridization to emphasize the interdisciplinary nature of the topic and the diversified views that enrich our understanding about the outcomes of hybridization to biodiversity.

One of the principal purposes of this research is to find the most influential authors, institutions, and countries contributing to hybridization research. This involves mapping collaborative networks and the evolution of research collaborations over time (Adobes Martin et al., 2020; Agbo et al., 2021). The analysis also investigates the theme areas that are gaining the highest interest, such as hybrid speciation, genetic introgression, and the role of hybridization to invasive species dynamics. Uncovering bursts of citations and keyword trends, the study determines emerging hotspots and research lacunas to offer future research directions to this rapidly expanding research field (Chen et al., 2023).

Through the use of advanced bibliometric tools, this study provides a comprehensive analysis of the bibliographic landscape of research on hybridization and biodiversity. The research findings are pertinent to researchers, policymakers, and conservations alike, underscoring the necessity to integrate bibliometric methodologies within ecological research. With hybridization having a continuous effect on the pattern of biodiversity within the context of global environmental change, information regarding the research track within this field is vital to the development of evidence-based conservation measures and the facilitation of international collaboration. This bibliometric analysis does not merely synthesize the existing information but also sets the stage for future multidisciplinary research that will further elucidate the complex role played by hybridization to preserve biodiversity.

Materials and methods

The bibliometric data for this study was sourced from Scopus, a widely recognized database that offers a broad collection of peer-reviewed scientific literature, ensuring high-quality research inclusion (Archambault et al., 2009; Harzing and Alakangas, 2016; Mongeon and Paul-Hus, 2016). The search query used was TITLE-ABS-KEY (hybridization) AND TITLE-ABS-KEY (biodiversity), allowing us to capture publications where hybridization and biodiversity were central themes. The search was not restricted by language, and the dataset included articles from peer-reviewed journals,

book chapters, and conference papers. A total of 2269 articles from 743 different sources were retrieved, covering the period from 1993 to 2024. Although the search query was not restricted by language, the results predominantly consisted of publications in English, which aligns with Scopus's indexing practices for high-impact scientific literature. To refine the dataset, all records were carefully screened for duplicates, and non-relevant document types, such as reviews, editorials, books, short notes, letters, and short surveys, were excluded. Only articles, conference papers, and book chapters were retained for analysis. The Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) approach was used to systematically filter the records, ensuring that only relevant studies were included for bibliometric analysis (Wang et al., 2014) (*Fig. 1*). To perform the bibliometric analysis, the final dataset was saved in CSV and RIS formats and processed using CiteSpace version 6.2.R3 (Advanced), VOSviewer, and Biblioshiny (Bibliometrix R package).

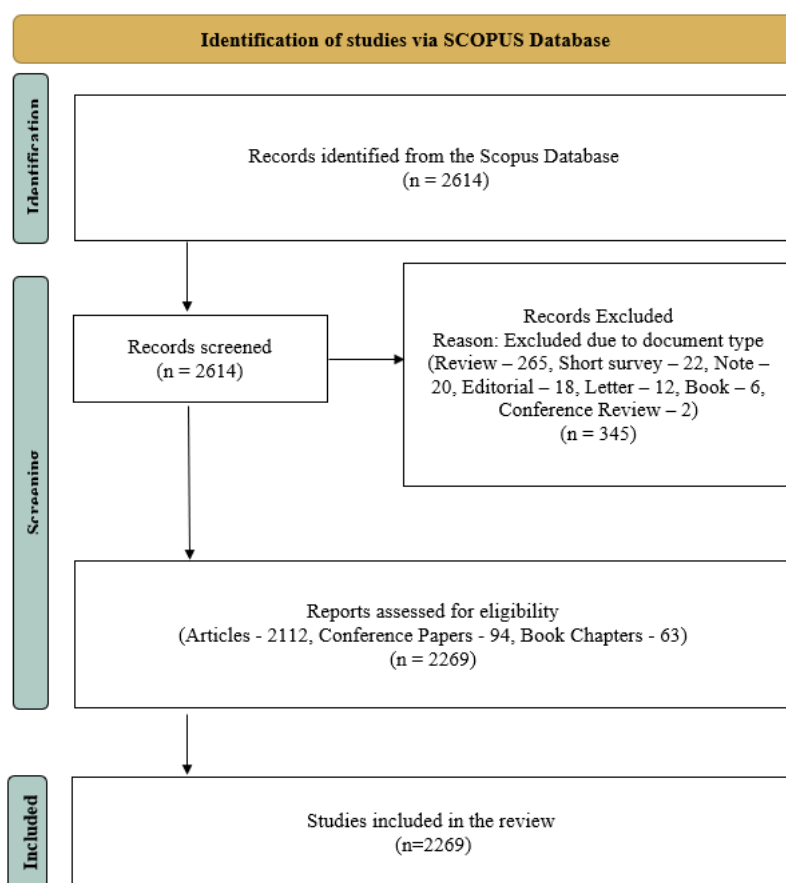


Figure 1. PRISMA flow diagram used to identify, screen, and include papers in the bibliometric analysis

Findings

Main information of the investigation

The bibliometric analysis covers publications on hybridization and biodiversity from 1993 to 2024, drawing from 743 different sources, including journals, books, and conference proceedings. A total of 2269 documents were analyzed, with an annual growth

rate of 6.71%, indicating a steady increase in research output. The average age of the documents is 12.7 years, reflecting a mix of both historical and recent contributions. Each document, on average, received 57.81 citations, highlighting the relevance and impact of the topic. The dataset includes 120,708 references, demonstrating extensive interconnections within the research field. In terms of content, 13,799 Keywords Plus (ID) and 5597 Author's Keywords (DE) were identified, suggesting a diverse range of research themes. The study involved 10,883 authors, with 127 single-authored contributions and 132 single-authored documents. The average number of co-authors per document is 5.57, indicating a high level of collaboration, and 38.4% of publications involved international co-authorships, emphasizing the global nature of hybridization research. Among the document types, 2112 are journal articles, 63 are book chapters, and 94 are conference papers, confirming that peer-reviewed journal articles dominate the field. This data provides a comprehensive overview of the research landscape, illustrating the significance, collaboration patterns, and evolution of the study of hybridization's impact on biodiversity.

Annual scientific productions

Figure 2 presents the scientific production of hybridization and biodiversity from 1993 to 2024, which exhibits a general upward trend, though with notable fluctuations and no consistent growth in recent years. The early phase (1993–2000) shows a gradual increase in publications, reflecting an emerging interest in the topic. The number of articles rose from 2 in 1993 to 24 in 2000, suggesting steady growth in research activities. A significant jump is observed in 2001 (63 articles) and 2002 (68 articles), indicating increasing recognition of hybridization's impact on biodiversity within the scientific community.

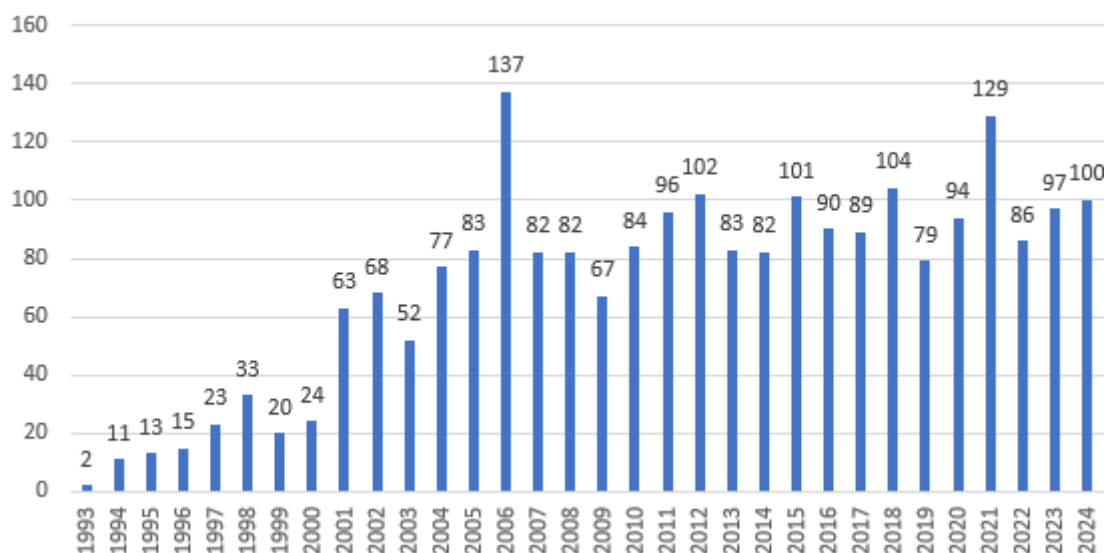


Figure 2. Significant growth trajectory from 1993 to 2024

The mid-2000s experienced a growth surge, culminating in 2006 (137 articles), the highest publication rate during this period. This surge was connected to international debate about biodiversity preservation, advances in genetic analysis techniques, and growing awareness of hybridization as both a natural and anthropogenic process. A

decline followed in 2007 and 2008 (82 articles each), possibly due to a shift in research priorities or reallocation of funding. It is important to note that the observed increase in publications during this period may not solely reflect a rise in research activity on hybridization and biodiversity. The growth is also influenced by the enhanced availability and accessibility of online journals and digital databases, which facilitated broader dissemination and indexing of scientific work. This shift in publishing infrastructure likely contributed to the apparent surge in topic-oriented publications, especially from the early 2000s onward.

From 2010 to 2020, the number of publications stabilized rather than increased significantly, ranging between 84 and 104 articles annually. Peaks in 2012 (102 articles) and 2018 (104 articles) reflect renewed interest, likely driven by developments in molecular biology and conservation genomics. However, this period does not reflect a continuously rising trend, supporting the reviewer's observation. A decrease in 2019 (79 articles) may have resulted from changing funding landscapes or strategic research shifts.

A resurgence is noted in 2021 (129 articles), possibly spurred by heightened global attention to biodiversity in the context of climate change and habitat fragmentation. A dip in 2022 (86 articles) likely reflects pandemic-related disruptions. Publication counts rebounded in 2023 (97 articles) and 2024 (100 articles), indicating ongoing interest, though still within a fluctuating range.

Overall, while there is a long-term upward trend from 1993 onwards, the pattern post-2010 is better described as stabilized with periodic peaks, rather than a consistent increase. These variations are likely influenced by shifts in funding, methodological developments, and changing global research priorities.

Most relevant authors

Figure 3 presents the most relevant authors based on the number of publications, highlighting the contributions of individual researchers and their affiliated institutions. The chart reveals distinct variations in publication volume, with Rudolf Amann from the Max Planck Institute for Marine Microbiology, Bremen, Germany emerging as the most prolific researcher, having authored over 20 publications. His significant output suggests a leading role in advancing knowledge on hybridization and biodiversity, supported by a strong institutional foundation.

Following Amann, J. S. Heslop-Harrison from the University of Leicester, United Kingdom, and Per H. Nielsen from Aalborg University, Denmark, also stand out as highly active contributors, each with a substantial number of publications, though fewer than Amann. Other noteworthy contributors include Simona Rossetti from the Istituto di Ricerca sulle Acque, Monterotondo, Italy; Thomas G. Whitham from Northern Arizona University, United States; Ricardo Amils from the Universidad Autónoma de Madrid, Spain; Cleusa Yoshiko Nagamachi and Julio Cesar Pieczarka from the Universidade Federal do Pará, Brazil—all of whom have made valuable contributions to the field.

Bernhard M. Fuchs, also from the Max Planck Institute for Marine Microbiology, has the fewest publications among the listed researchers, yet remains a significant contributor, reinforcing the institute's central role in this domain. Lastly, Michael Wagner from the University of Vienna, Austria, also adds to the list of impactful scholars with a strong academic footprint.

Overall, the distribution of authorship illustrates a blend of highly prolific individuals and a broader base of researchers contributing fewer but meaningful works. This dynamic underscores both individual leadership and the collaborative, interdisciplinary nature of

research in hybridization and biodiversity. Future analyses of co-authorship networks could further illuminate collaboration patterns and institutional linkages among these key contributors.

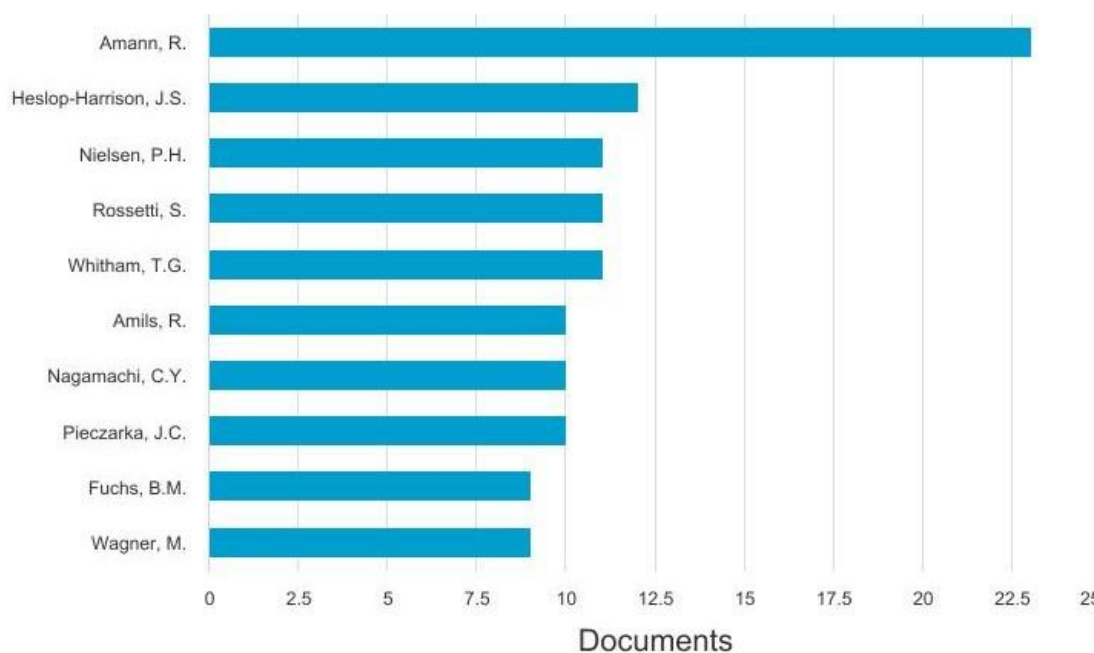


Figure 3. Most relevant authors

Network visualization of co-citation of cited authors

Figure 4 illustrates the network visualization of the co-citation of cited authors in bibliometric analysis, highlighting the structure and evolution of hybridization research within biodiversity studies. The network consists of 18 distinct clusters, each representing a major thematic area. The largest cluster (#0), Situ Hybridization, with 263 members, reflects the dominance of molecular techniques in studying microbial communities and genetic interactions. Key cited authors in this cluster, such as Amann RI, Manz W, and Altschul SF, have significantly contributed to the development of situ hybridization and microbial ecology methodologies. The presence of such a large cluster suggests that molecular approaches remain central to hybridization research, particularly in analyzing microbial diversity and genetic exchange mechanisms.

The next two largest clusters, Genetic Diversity (#1) and Cryptic Diversity (#2), emphasize the role played by hybridization in the evolution of species, lineage diversification, and genetics of conservation. With 239 and 165 papers each, the clusters consist of seminal work on the genetic composition of hybrid species, evolutionary dynamics, and cryptic biodiversity. World-leading scientists such as Pritchard JK, Rieseberg LH, and Mallet J are the pacesetters in population genetics and hybrid speciation research that has inspired the subsequent research on gene movement and adaptive hybridization. The presence of the two clusters indicates that hybridization is no longer viewed as a genetic bane but also an evolutionary innovation process and a tool to guarantee species persistence.

Further specialization within the network is evident in Cluster #3 (Homoploid Hybrid Speciation) and Cluster #4 (Captive Breeding as a Conservation Tool), both consisting of

104 and 70 individuals. The clusters reflect the application of hybridization research within the field of evolutionary biology and the application of hybridization within conservation programs. Research within homoploid hybrid speciation examines how hybridization yields species formation but does not include the manipulation of chromosomes, whereas research within the conservation arena examines the repercussions of hybridization within wildlife management and captive breeding programs. The fact that there are such specific clusters means that hybridization is being employed more within the context of biodiversity conservation programs rather than considered a disruptive force.

The emergence of compact but thematically coherent clusters such as Cluster #6 (Ecological Diversity) and Cluster #7 (Human Intestinal Microbiota) indicates the expanding scope of hybridization research beyond genetics. The clusters that are large in silhouette values (0.964–0.976) are the ones that indicate research on the connection between hybridization and ecological adaptation. The fact that themes such as hybridization of the gut microbiota, hybridization of the coral reef, and plant hybridization are covered indicates the expanding multidisciplinary of hybridization research. The fact that the seminal papers within these themes are highly cited further indicates that hybridization research is being done not merely at the species but also microbial and ecosystem scales.

Network visualization of co-citation links provides a comprehensive view of the historical evolution of hybridization research within the research on biodiversity. The large clusters represent core genetic and microbial research, while the small clusters represent expanding applications to conservation, ecology, and evolutionary biology. The multidisciplinary character of hybridization research arises through the intersection of molecular techniques, ecological models, and conservation strategies to create an improved understanding of species interactions. This bibliometric analysis highlights the shift away from the historical view of hybridization as a genetic threat toward an understanding of the complexity of hybridization within the enrichment of biodiversity, adaptation, and evolution.

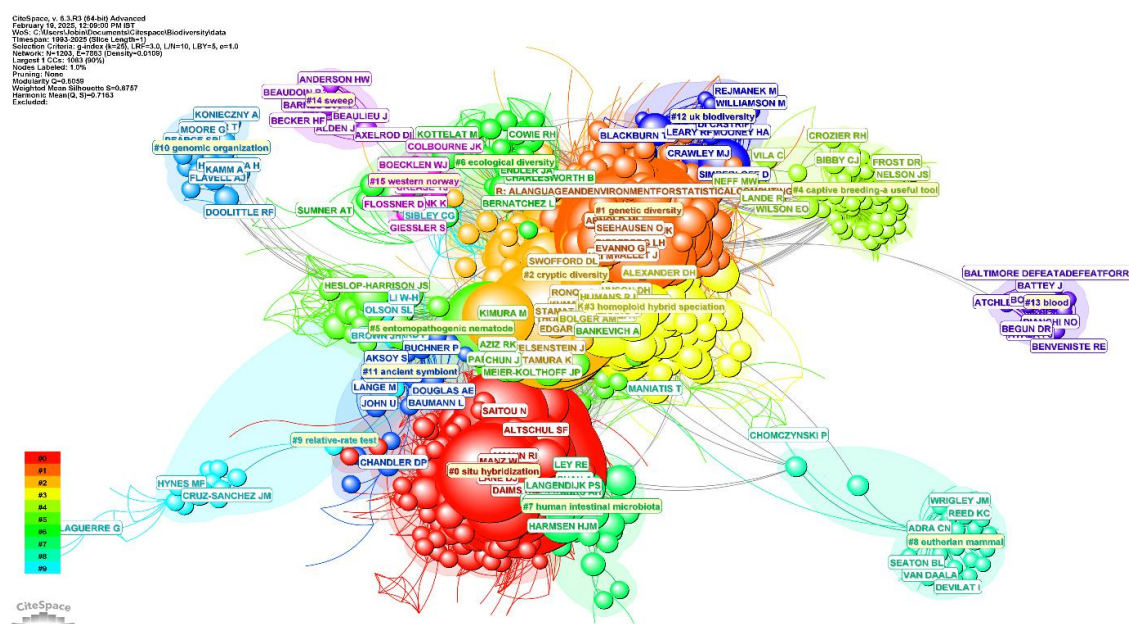


Figure 4. Network visualization of co-citation of cited authors

Most relevant sources

The data presented in *Table 1* demonstrates that research on hybridization and biodiversity is heavily concentrated in journals specializing in microbiology, genetics, and evolutionary biology. Applied and Environmental Microbiology, with 133 articles, leads as the most prominent source, indicating a strong focus on microbial hybridization and its environmental implications. PLOS ONE (85 articles) and Scientific Reports (26 articles) reflect the interdisciplinary nature of the topic, accommodating diverse research spanning molecular, ecological, and evolutionary perspectives. Notably, Molecular Ecology and Molecular Phylogenetics and Evolution collectively contribute 100 articles, underscoring the centrality of genetic analysis in understanding hybridization events and their evolutionary outcomes. Journals such as FEMS Microbiology Ecology and ISME Journal highlight the growing interest in microbial interactions and hybrid strains in natural ecosystems. Meanwhile, Theoretical and Applied Genetics emphasizes the role of plant genetics in biodiversity studies. Overall, the publication landscape reveals a comprehensive integration of ecological, genetic, and evolutionary frameworks in the study of hybridization and its impact on biodiversity.

Table 1. Most relevant sources

Sources	Articles
Applied and environmental microbiology	133
Plos one	85
Molecular ecology	57
Molecular phylogenetics and evolution	43
Environmental microbiology	42
Fems microbiology ecology	38
Theoretical and applied genetics	36
Isme journal	33
Ecology and evolution	28
Scientific reports	26

Timezone network visualization of co-citation of cited journals

Figure 5 displays a co-cited journals' network that provides information regarding influential sources that contributed to hybridization and research on biodiversity. The nine clusters that the network contains are nine research themes. The DNA Barcoding (#0) cluster contains 220 members and has a measure of 0.898. This signifies the dominance of research conducted using molecular genetics in hybridization. The highly cited journals contained within this cluster, such as PLOS ONE, Evolution, Genetics, Heredity, and Molecular Ecology, are reflective of the widespread use of DNA sequencing and DNA barcoding methodologies to ascertain species identification and evolutionary research. The presence of the journals indicates that genomics and molecular ecology are the underlying methodological techniques employed within hybridization research.

The second-largest group, Microbial Community Structure (#1), consists of 160 journals with a silhouette value of 0.892 showing strong theme coherence. The highest cited journals are Nucleic Acids Research, Applied and Environmental Microbiology, and FEMS Microbiology Ecology that address microbial hybridization, metagenomics,

and microbiome diversity. This group shows that hybridization is also studied within the context of microbial ecology, namely within the study of the gut microbiota, the creation of biofilms, and microbial interactions within extreme environments. The third-largest group, Genetic Structure (#2), consists of 155 journals that include Science, Bioinformatics, Molecular Biology and Evolution, and Proceedings of the National Academy of Sciences (PNAS). The highest cited journals represent research interest in the genomic architecture, evolutionary history, and computational biology methodologies employed within hybridization research.

Figure 5. Timezone Network visualization of co-citation of cited journals

Some clusters reflect the specific applications of hybridization research to various biological disciplines. Cluster #3 (Wild Sunflower) and Cluster #5 (Domestic Cat) reflect research on hybridization research, species evolution, and phylogenetics within plant and animal species. Journals under these clusters like Molecular Phylogenetics and Evolution, Genome Biology and Evolution, and Frontiers in Plant Science reflect the role hybridization has within the knowledge of evolutionary mechanisms and genetics to be used for the conservation. The Situ Hybridization cluster (#4), made up of 109 members, has top journals like Nature and Applied and Environmental Microbiology that reflect the use of hybridization within microbial diversity and molecular diagnosis.

The co-citation pattern of the journals depicts the extensive reach of hybridization research to the various subfields of science, ranging from genomics and microbiology to ecology and conservation biology. The large clusters represent a firm core in molecular genetics, evolutionary research, and microbial ecology, while the small clusters represent specialized applications to plant and animal hybridization, anthropological systematics, and biotechnology. That the highly cited journals like Nature, Science, and PLOS ONE are highly represented means that hybridization research continues to evolve along the trajectories of technological innovation in sequencing, computational modeling, and bioinformatics to deliver new knowledge about biodiversity and evolution of species.

Countries scientific productions

Table 2 presents the top ten contributing nations/territories based on the number of papers that have been published. The United States has the highest contribution with 638 papers, an affirmation of the strong lead role that the country has played to promote research in this sector. The sheer number of publications signifies a strong research system, funding availability, and institutional interest to conduct research on biodiversity and hybridization. Germany comes next with 270 papers, the United Kingdom follows with 261 papers, then comes France with 211 papers. This signifies the strong research and academic interest that Europe has towards evolutionary genetics and conservation biology. The countries have strong research institutes and funding mechanisms that encourage research on biodiversity and ecological sustainability.

Table 2. *Countries scientific productions*

Country/territory	Documents
United States	638
Germany	270
United Kingdom	261
France	211
China	200
Italy	167
Spain	159
Japan	142
Canada	137
Australia	136

China (200 documents) stands out as the leading Asian contributor, emphasizing the country's growing influence in biodiversity research. With its diverse ecosystems and increasing focus on conservation, China's research contributions are expected to rise further in the coming years. Similarly, Italy (167), Spain (159), and Japan (142) reflect significant contributions from Southern and Eastern Europe as well as East Asia, regions known for their rich biodiversity and conservation efforts. Canada (137) and Australia (136), both countries with vast and unique ecosystems, also rank among the top contributors. Their strong research presence aligns with national priorities in ecological conservation, particularly regarding hybridization's impact on species adaptation and ecosystem stability. Overall, the geographical distribution of publications indicates a strong presence of biodiversity and hybridization research in North America, Europe, and

Asia, with developed countries leading the discourse. The variation in contributions may be influenced by factors such as research funding, biodiversity concerns, and policy focus in each region. Future bibliometric studies could explore international collaborations to assess how these leading countries are working together on hybridization research.

Timeline network visualization of countries collaborations

Figure 6, the timeline network visualization of country collaborations, highlights the global nature of scientific partnerships, with North America, Europe, and East Asia leading in genomic and evolutionary studies, while Africa and Latin America contribute significantly to species-specific and ecological research. The largest cluster, Evolutionary Radiation (#0), is dominated by the United States, United Kingdom, China, Japan, and Australia, reflecting strong investments in phylogenetics, species diversification, and genomic sequencing. Similarly, Gene Flow (#1) includes European leaders like Switzerland, the Netherlands, Russia, Czech Republic, and Sweden, indicating a regional focus on hybridization in freshwater ecosystems, plant gene flow, and amphibian species. The Cichlid Fishes cluster (#2) highlights African biodiversity research, with key contributors from France, Spain, South Africa, Israel, and Kenya, emphasizing genetic adaptation in aquatic species, particularly in the African Great Lakes region.

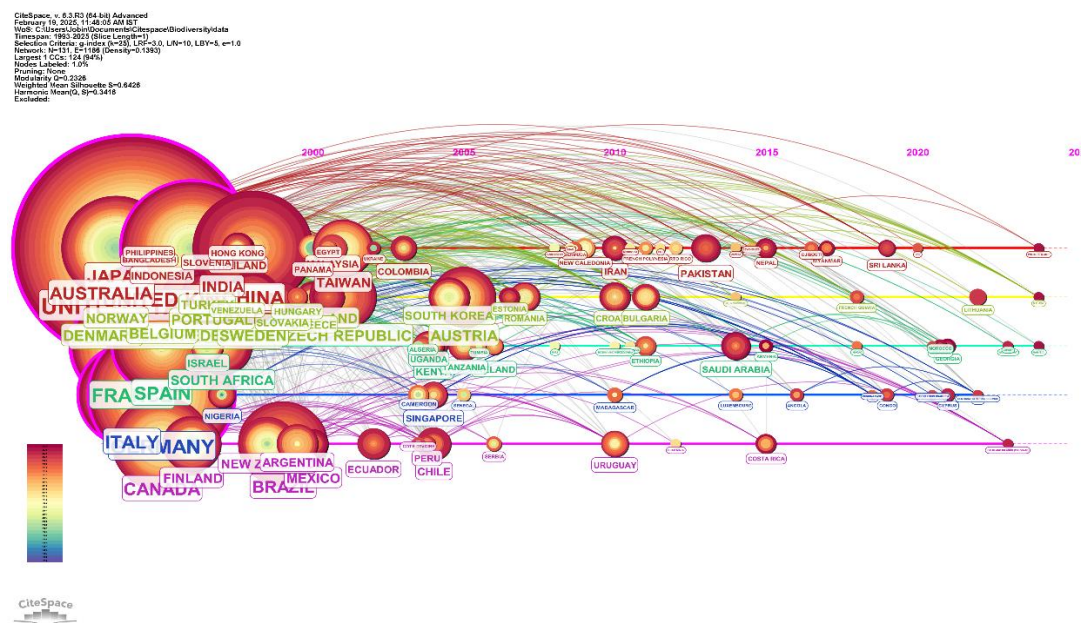


Figure 6. Timeline Network visualization of countries collaborations

Regional and cross-continental collaborations are evident in Identity Abundance (#3) and New Biogeographic Suture (#4), where countries such as Germany, Italy, Singapore, Nigeria, and Cameroon focus on species conservation, genetic differentiation, and hybridization in tropical ecosystems. Meanwhile, Canada, Brazil, Mexico, Finland, and New Zealand are leading marine hybridization and conservation genetics studies, particularly in apex predator species and rainforest biodiversity. These international partnerships demonstrate that hybridization research is increasingly interdisciplinary, requiring global cooperation to address challenges like climate change, habitat fragmentation, and species adaptation. As hybridization continues to influence biodiversity

and conservation policies, strengthening global research networks will be essential to uncovering new insights into genetic diversity, species resilience, and ecosystem stability.

Network visualization of citation of documents

Figure 7 visualizes the citation network of key scientific publications in hybridization and biodiversity using VOSviewer. The network is based on a minimum citation threshold of 30, meaning only publications cited at least 30 times were included. Out of 2284 sources, 938 met this threshold, and the network consists of 92 items grouped into 17 clusters. Each node represents a publication, with node size indicating the number of citations received, while edges (links) show citation relationships between publications. The most highly cited publication is Sokol (2008), as indicated by its large node size, signifying its major influence in the field. Other highly cited works include Schmid (2003), Juretschko (2002), Rosenberg (2009), and Ravenschlag (1999), each forming central hubs in different clusters. The presence of multiple interconnected clusters suggests that research on hybridization is multidisciplinary, spanning across evolutionary biology, conservation, microbial genetics, and molecular ecology. The structure of the network reveals research subfields, with closely linked nodes representing thematic connections in research. The presence of distinct clusters indicates specialized research areas, where certain publications influence specific subdomains within hybridization studies. The citation relationships between clusters suggest that these subfields interact, with foundational works influencing multiple research directions. The network analysis underscores the importance of key publications in shaping the knowledge base on hybridization and biodiversity conservation. Future research could explore emerging clusters and citation bursts to identify rising trends in the field.

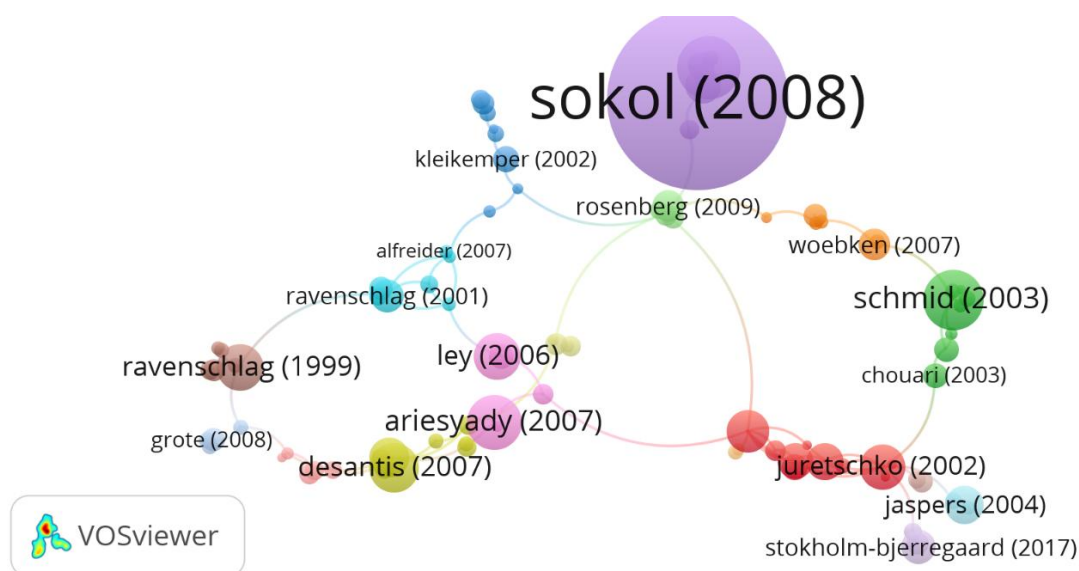


Figure 7. Network visualization of citation of documents

Co-occurrence of all keywords

Figure 8 illustrates the co-occurrence network and visualizes the interrelation of author keywords in hybridization and biodiversity research. The network is built using a minimum occurrence threshold of 5, meaning only keywords that appeared at least five

times were included. Out of 5598 keywords, 196 met this threshold, and these were categorized into 10 clusters of varying sizes and colors. The size of each node represents the frequency of a keyword, while edges (links) represent co-occurrence relationships, indicating how frequently these keywords appear together in research articles.

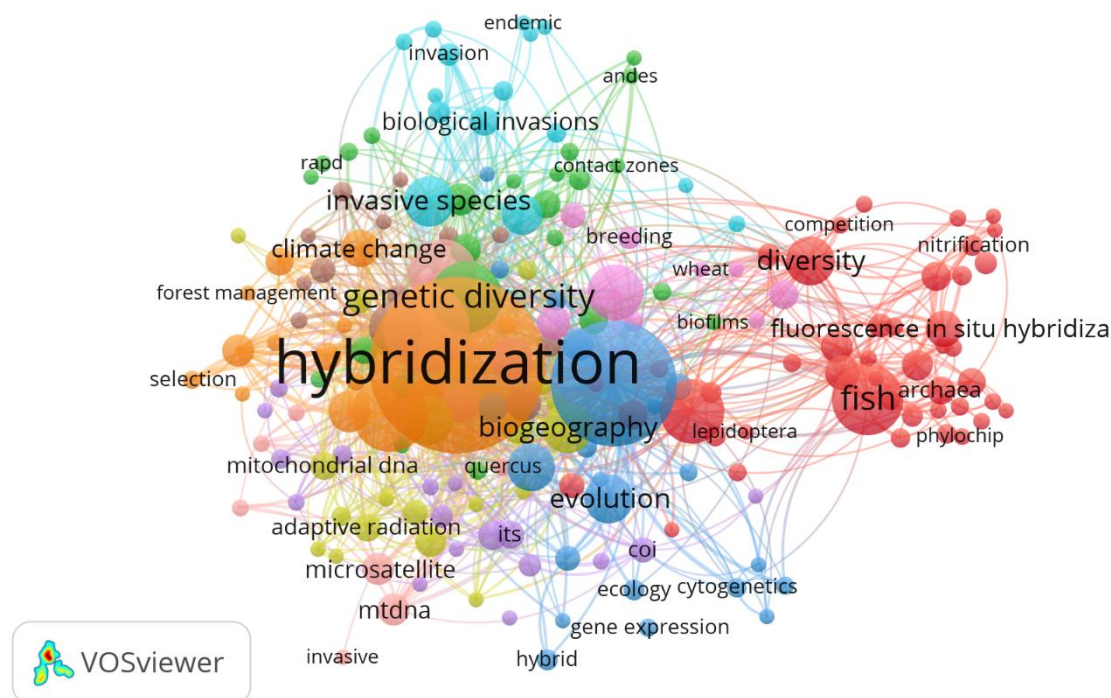


Figure 8. Co-occurrence of author keywords

The largest cluster (Cluster 1) contains 45 keywords, showing a strong thematic focus on core topics like “hybridization,” “genetic diversity,” “biogeography,” and “invasive species.” These terms form the central hub of the network, reflecting their high connectivity within hybridization research. Other major clusters include Cluster 2 (24 keywords) and Cluster 3 (22 keywords), which feature topics related to “evolution,” “climate change,” and “mitochondrial DNA.” Clusters 4 to 10 contain fewer keywords, but they represent specialized research areas such as molecular techniques (e.g., “fluorescence in situ hybridization”), microbial studies (e.g., “archaea”), and conservation strategies.

The interconnected structure of the network suggests that hybridization research is highly interdisciplinary, linking genetics, ecology, conservation biology, and evolutionary studies. The presence of distinct clusters indicates diverse research directions, while the strong central connections suggest that hybridization remains a unifying theme across multiple scientific domains. The wide-ranging co-occurrence of terms highlights the increasing complexity of hybridization studies, where researchers integrate genetic tools, ecological factors, and environmental challenges to explore the role of hybridization in biodiversity conservation and species evolution.

Trend topics

Figure 9 depicts a temporal pattern of salient research themes in hybridization and biodiversity research from 1997 to 2023, showing the appearance and frequency of the

words over the years. The frequency of the words was represented by the sizes of the bubbles where the larger bubbles indicate higher research interest. Early research from 1997 to 2005 was focused on molecular techniques such as PCR, RAPD, in situ hybridization, and plant breeding, an indication of the early genetic and evolution research in hybridization. Over time, research diversified to other themes such as biodegradation, evolution of the genome, hybridization across species, and microbial diversity, an indication of an expansion from plant genetics to other ecological themes. Keywords such as molecular ecology, phylogeny, and reproductive isolation gained popularity during the mid-2000s, an indication of the shift towards the understanding of genetic mechanisms underlying hybridization.

Beginning 2010 onwards, the research agenda was quite different, with the agenda themes of biodiversity conservation, adaptation, systematics, and invasive species gaining prominence. The recent period (2015–2023) saw an explosion of climate change, hotspots of biodiversity, phylogenomics, and biological invasions that reflect the increasing salience of hybridization under global environmental transitions. The ongoing usage of core terms such as genetic diversity, hybridization, and introgression reflect the centrality played by them within the domain of research on biodiversity. The recent ascendance to prominence of the words based on conservation reflect an integration of hybridization research within policy-guided biodiversity management. This shift underscores the multidisciplinary of hybridization research that draws upon genetics, ecology, conservation, and climate science to address pressing issues.

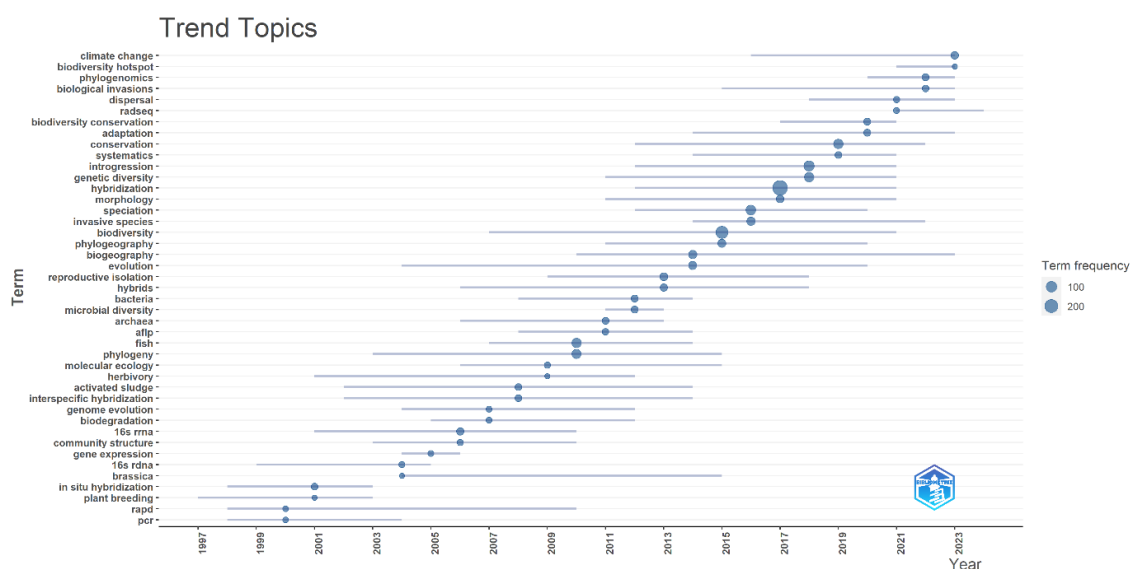


Figure 9. Visualization of trending topics in the realm of research

Thematic map

Figure 10 presents a thematic map categorizing key research topics in hybridization and biodiversity based on development degree (density) and relevance (centrality). The top-right quadrant (Motor Themes) includes well-developed and highly relevant topics such as “hybridization,” “introgression,” and “speciation.” These terms indicate that the core research focus revolves around how hybridization affects biodiversity, genetic variation, and species formation. Additionally, “genetic diversity,” “biodiversity

conservation,” and “microsatellite” appear as strong themes, emphasizing the use of genetic tools in biodiversity studies. These motor themes drive the field forward and represent active research areas with high impact.

The top-left region (Niche Themes) consists of very specific themes like “16S rRNA gene,” “DNA barcoding,” “microbial diversity,” and “archaea,” which are well-defined research themes that are not very connected to other themes. The themes indicate an emerging use of molecular techniques to investigate genetic interactions during hybridization. The bottom-right region (Basic Themes) consists of “biodiversity,” “phylogeny,” and “taxonomy,” which are basic but less rapidly evolving themes. These are a basic understanding of the impact of hybridization on species classification and evolutionary relationships but are not as highly developed as motor themes.

The lower left quadrant (Declining or Emerging Themes) contains the words “diversity,” “in situ hybridization,” and “biological invasions,” which reflect that these themes are losing research attention or picking up speed. With the increasing global interest in invasive species and the contribution made by hybridization to ecosystem dynamics, these themes will once again be research agendas. Also present are words that are specific to bacteria and to flow cytometry, which reflect that microbiological thought regarding hybridization has not yet reached widespread use but is an important one to track in the future. This analysis of themes tells us that future research will need to integrate molecular methodologies and conservation strategies to determine the long-term ecological and evolutionary consequences of hybridization.

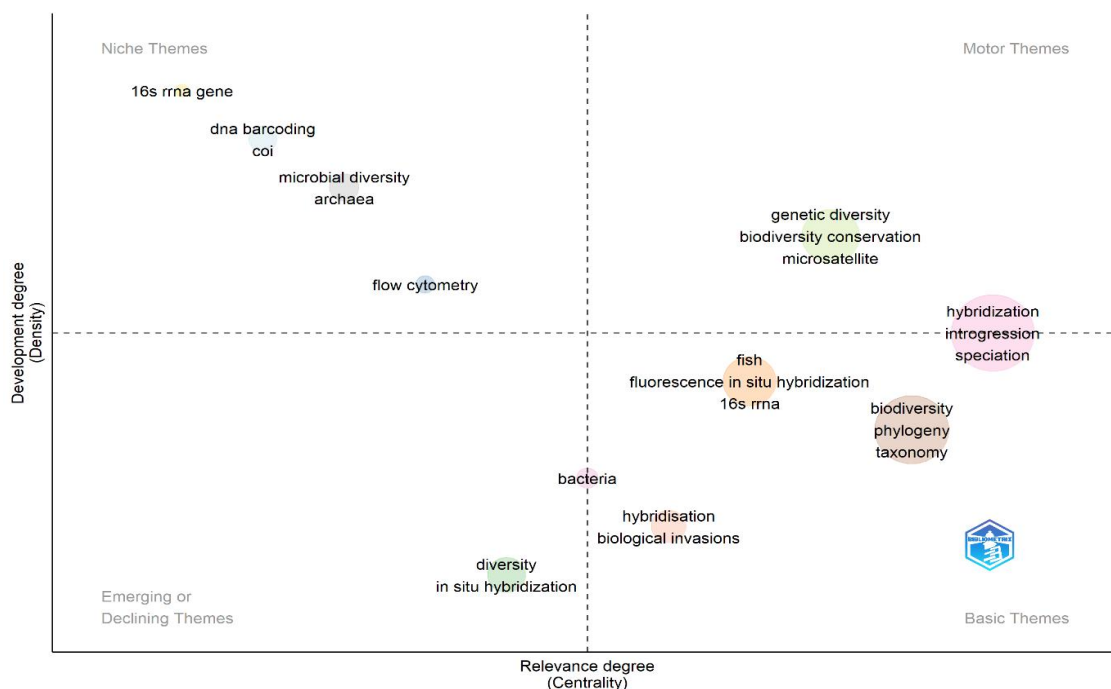


Figure 10. Thematic visualization of keywords

Network visualization co-authorship of organizations

Figure 11 illustrates the network visualization of co-authorship across organizations reveals 11 distinct clusters, each representing a major research focus related to hybridization and biodiversity. Cluster #0, labeled “Social Insect,” is the largest with 46

show cross-continental collaborations, such as between the University of Queensland and Wageningen University in Cluster #7 (“Oxidizing Bacteria”). The silhouette values across all clusters are high (ranging from 0.916 to 1.0), indicating clear thematic boundaries, while the citation strengths suggest that a few institutions are pivotal nodes driving research impact within their respective clusters.

Network visualization co-authorship of authors

Figure 12 illustrates the co-authorship network among the most prolific authors in the field of hybridization and biodiversity, based on VOSviewer analysis. The network comprises 175 authors grouped into 17 distinct clusters, each representing a research community with shared scholarly interests. At the center of the network is Rudolf Amann from the Max Planck Institute for Marine Microbiology, whose large node size and extensive linkages highlight his pivotal role as a central collaborator. Amann’s strong co-authorship ties with researchers like Andrew J. Weightman and Marie-Anne Cambon-Bonavita suggest a cohesive and highly productive research group. Cluster 1, comprising 19 authors including Gary L. Andersen, Gabriele Berg, and Joanne Bertaux, reflects another influential collaboration hub, though variations in author name entries (e.g., Andersen, Gary and Andersen, Gary L.) may indicate data duplication. Simona Rossetti, associated with the Istituto di Ricerca sulle Acque, forms a significant cluster with Yunhong Kong and David G. Bourne, demonstrating transnational research collaborations. Similarly, Per H. Nielsen and Tim Tolker-Nielsen, both affiliated with Aalborg University in Denmark, form a strong cluster indicative of regional scientific synergy. Peripheral clusters containing authors such as Stephen J. Giovannoni, Zackary I. Johnson, and Didier Debroas represent more specialized or emerging research groups. The thickness of connecting lines illustrates the strength of collaborative ties, with prominent linkages observed between authors like Michael Schlöter and Gary L. Andersen. Overall, the visualization underscores the interdisciplinary and collaborative nature of the field, highlighting both dominant research leaders and a diverse network of contributors advancing knowledge in hybridization and biodiversity.

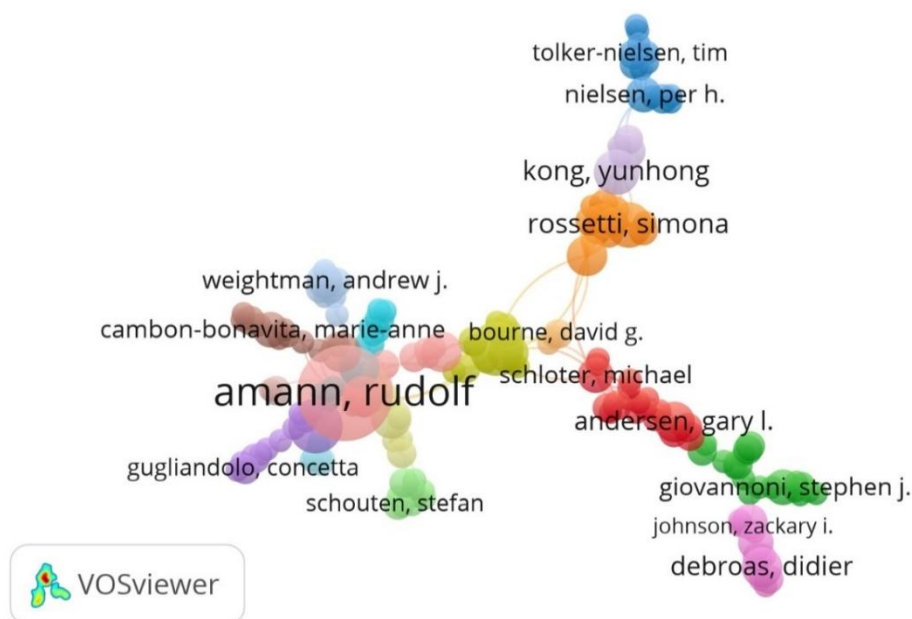


Figure 12. Network visualization co-authorship of authors

Discussion

The bibliometric analysis of hybridization and biodiversity research reveals a steady increase in scientific interest over the past three decades, with a notable rise in publications from 2000 onwards. The United States, United Kingdom, China, Germany, and France emerge as dominant contributors, reflecting their strong research infrastructure and funding support. The interdisciplinary nature of hybridization research is evident, with contributions spanning genomics, evolutionary biology, conservation science, microbial ecology, and environmental studies. The network visualization of co-cited authors and journals highlights the central role of molecular techniques, particularly DNA barcoding, genetic diversity analysis, and evolutionary modeling, in advancing the field. While early research focused on fundamental genetics and phylogenetics, recent studies integrate hybridization within climate change, invasive species management, and biodiversity conservation, signifying a shift towards applied ecological research.

The co-occurrence analysis of keywords and thematic mapping reveal key research themes, with hybridization, introgression, speciation, and genetic diversity being the most frequently explored topics. Emerging themes include adaptive hybridization, ecological resilience, and conservation genomics, indicating a growing recognition of hybridization's role in species adaptation to environmental changes. Network analysis of country collaborations underscores global scientific partnerships, particularly between North America, Europe, and East Asia, with developing regions such as Africa and Latin America contributing significantly to studies on regional biodiversity, hybrid speciation, and ecosystem stability.

The co-citation analysis of cited journals indicates that molecular genetics, conservation biology, and microbial ecology are the leading disciplines driving hybridization research. The integration of computational biology, environmental monitoring, and biotechnological applications suggests a broader scope for hybridization studies beyond traditional evolutionary biology. The citation network analysis further confirms that a few highly influential studies shape the field, with landmark papers on hybrid speciation, genetic introgression, and biodiversity conservation receiving the highest citations. This highlights the need for future research to expand beyond these foundational studies and explore emerging areas such as the role of hybridization in ecosystem services, microbiome interactions, and global biodiversity shifts.

The findings indicate that hybridization is no longer viewed solely as a threat to biodiversity but also as a mechanism for adaptation and resilience. However, research gaps remain in understanding long-term ecological consequences, the role of hybridization in rapid environmental change, and policy-driven conservation strategies. The future of hybridization research lies in integrating genomics with ecological and conservation frameworks, fostering collaborative research initiatives, and ensuring that scientific advancements translate into effective biodiversity management policies. Addressing these gaps will provide a comprehensive understanding of hybridization's role in shaping global biodiversity in an era of accelerating environmental change.

Research gaps and practical implications

Despite the significant advancements in hybridization and biodiversity research, several research gaps remain that require further investigation. The trend topics analysis (*Fig. 10*) reveals a shift from foundational genetic studies to broader ecological and conservation-oriented research, yet long-term ecological consequences of hybridization

remain understudied. While genetic diversity, introgression, and reproductive isolation are well-established topics, their interaction with climate change, habitat fragmentation, and ecosystem resilience needs further exploration. Additionally, the role of hybridization in microbial diversity and host-microbe interactions remains a niche area (as highlighted in the thematic map's niche quadrant), suggesting a gap in linking microbial genomics with macro-ecological processes. The thematic analysis also identifies biological invasions and in situ hybridization as emerging or declining themes, indicating a potential research gap in understanding how invasive hybrid species alter ecosystem dynamics and contribute to biodiversity loss or adaptation. Furthermore, while policy-driven biodiversity conservation has gained attention in recent years, the integration of hybridization research into global conservation frameworks and legal policies remains limited, calling for interdisciplinary approaches that combine genomics, ecological modeling, and biodiversity management strategies.

From a practical standpoint, these research trends have direct implications for conservation strategies, ecosystem management, and environmental policy. The increasing relevance of climate change and hybridization studies suggests that conservation practitioners need to adapt management strategies to account for hybrid species' resilience or vulnerability in changing environments. The prominence of biodiversity conservation and genetic diversity as motor themes (*Fig. 10*) indicates that integrating molecular tools such as DNA barcoding and phylogenomics into conservation planning can improve species monitoring and identification of hybrid populations. Additionally, the emerging focus on microbial diversity and archaea suggests that microbiome studies should be incorporated into conservation genomics to assess the role of microbial hybridization in species adaptation. As hybridization plays a dual role in both preserving genetic diversity and posing risks to species integrity, conservation policies must move beyond simplistic approaches that treat hybridization as purely detrimental. Instead, a case-by-case evaluation of hybrid populations, their adaptive potential, and their ecological functions should inform sustainable biodiversity policies. Finally, enhancing global collaboration, particularly between developed and biodiversity-rich developing nations, will be crucial for advancing hybridization research and implementing effective conservation interventions at a global scale.

Conclusion

The bibliometric analysis of hybridization and biodiversity research highlights the growing scientific interest in understanding its ecological, evolutionary, and conservation implications. Over the past three decades, research output has steadily increased, with contributions from leading countries such as the United States, China, Germany, and the United Kingdom. The findings emphasize the interdisciplinary nature of hybridization studies, integrating genetics, conservation biology, microbial ecology, and environmental sciences. While hybridization is often perceived as a threat to biodiversity, emerging research underscores its role in species adaptation, genetic diversity, and ecosystem resilience. However, significant research gaps remain in assessing long-term ecological consequences, microbial hybridization, and policy-driven conservation strategies. Future studies should prioritize integrating genomic tools, ecological models, and conservation frameworks to address these gaps effectively. Strengthening global collaborations and funding support will be essential for advancing hybridization research and ensuring its application in sustainable biodiversity management.

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