

Genomics in Endangered Species Conservation: A Bibliometric Analysis

Loso Judijanto
IPOSS Jakarta, Indonesia

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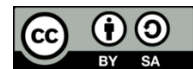
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ABSTRACT

This study presents a bibliometric analysis of research on genomics in endangered species conservation to map its intellectual structure, thematic evolution, and global collaboration patterns. Data were analyzed using bibliometric visualization techniques to identify keyword co-occurrence, thematic clusters, density distributions, co-authorship networks, institutional affiliations, and country-level collaborations. The results show that genomics and endangered species constitute the central knowledge base of the field, strongly connected with genetics, population genetics, and conservation genomics. Thematic evolution indicates a shift from traditional molecular genetics and phylogenetic studies toward high-throughput genomic approaches, particularly population genomics and single nucleotide polymorphism (SNP)-based analyses. Collaboration network analysis reveals a globally distributed but centralized structure, dominated by major research hubs such as the United States and China, with strong supporting contributions from Europe and emerging participation from developing regions.

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Corresponding Author:

Name: Loso Judijanto
Institution: IPOSS Jakarta
Email: losojudijantobumn@gmail.com

1. INTRODUCTION

The problem of biodiversity loss has emerged as one of the most serious environmental problems facing the world today in the 21st century [1], [2]. Habitat degradation, climate change, pollution, over-exploitation of natural resources, invasive species, and new emerging pathogens have increased the risk of extinction for many species around the world. The current international conservation assessments show that many species are considered to be vulnerable, endangered, or critically endangered, and there is an urgent need for proper conservation plans [3]. Classical

conservation efforts have largely depended on ecology, habitat conservation, and population management. While these have been useful techniques, they do not offer much insight about the underlying genetic mechanisms involved in species survival and adaptation. As a result of this realization, there has been an increased effort to incorporate molecular genomics in conservation programs [4]–[6].

The development of genomics has revolutionized the field of biology through the ability to perform complete genome analyses instead of analyzing individual genes. Genomics refers to the analysis of

genome structure, function, evolution, and variation through the use of next-generation sequencing and bioinformatics approaches. Improvements in NGS have made DNA sequencing much cheaper and more efficient, allowing large amounts of genetic information to be generated for further analysis [7]. Thus, with the help of genomics techniques, it became possible to conduct studies on non-model organisms, including those that are rare and endangered. With the aid of genomics, it is possible to analyze genetic diversity, population structure, evolutionary history, adaptations, inbreeding rates, and changes in populations' demographics with high accuracy. Therefore, genomics data have allowed opening new possibilities to address complex conservation issues that could not be resolved with the help of traditional genetic methods [8]–[10].

In this regard, conservation genomics is a relatively new discipline that combines genomics and conservation. This field involves the use of genomics technologies in conservation and species management. Unlike conventional conservation genetics, conservation genomics uses information from the entire genome in order to determine biological and evolutionary fitness of populations. Genome-wide analyses reveal information on genetic diversity, heterozygosity, levels of gene flow, adaptive differences, and loci with positive effects on fitness. This information is important since lower levels of genetic diversity and higher levels of inbreeding are often associated with poor adaptive potential and high chances of extinction in small populations. In addition, conservation genomics plays an important role in evidence-based management in breeding programs, translocations, hybridization programs, and identification of evolutionarily significant units. These examples illustrate the growing importance of genomics in contemporary conservation efforts [11]–[14].

The application of genomics to endangered species conservation has expanded considerably over the last two decades. Numerous studies have employed whole-genome sequencing, population

genomics, transcriptomics, environmental DNA (eDNA), and ancient DNA analyses to investigate species facing severe conservation threats. Genome sequencing projects involving threatened wildlife have generated valuable insights into demographic history, adaptive evolution, disease susceptibility, and responses to environmental change. In addition, paleogenomic approaches have enabled researchers to reconstruct historical population dynamics and extinction processes, thereby providing important perspectives for contemporary conservation management. The increasing adoption of genomic tools has also stimulated interdisciplinary collaboration among conservation biologists, geneticists, bioinformaticians, and policy makers. As genomic resources continue to expand globally, the scientific literature addressing endangered species conservation through genomic approaches has grown substantially, creating a complex and rapidly evolving body of knowledge that warrants systematic examination.

However, while there has been a significant increase in the number of publications related to conservation genomics, the current level of synthesis of the intellectual structure, development, collaboration patterns, and emerging research trends of the discipline remains inadequate. Review papers tend to emphasize certain aspects of the development of conservation genomics, such as particular groups of species studied, methodologies applied, and applications in practice. The growing number of publications makes it harder for researchers to track the most influential individuals, institutions, themes, and emerging areas in the field. Bibliometric analysis provides an objective tool that allows for the mapping of scientific knowledge based on publication trends, citation patterns, co-authorship networks, co-occurrence of keywords, and thematic developments. With the help of bibliometric tools, researchers will be able to detect research foci, intellectual bases, and future directions and provide an overview of the history of development of the field. Consequently, it is essential to conduct

bibliometric analysis of the development of genomics in endangered species conservation.

Despite the growing importance of genomics in the conservation of endangered species, there is no bibliometric mapping of the existing scientific literature on the topic. There are gaps in the available information on the topics of publication trends, key authors, top institutions, collaboration networks, highly cited papers, topic clusters, and trends in research. Such an approach does not allow for an adequate understanding of the intellectual architecture and evolution of the field by researchers, conservationists, and policymakers. Therefore, there is a need for a comprehensive bibliometric analysis of the scientific field of genomics in the conservation of endangered species. The objective of the study is to conduct a systematic bibliometric analysis of the global scientific landscape of genomics in endangered species conservation.

2. METHODS

In this research, a bibliometric analysis methodology has been applied to investigate the scientific progress of genomics in relation to the conservation of endangered species. Bibliometric analysis is a type of quantitative analysis that aims at analyzing publication trends, productivity in science, structure of science, and research trends in a certain field of study. In this research, the data have been extracted from the Scopus database, which is regarded as one of the biggest and most comprehensive multidisciplinary citation databases. Scopus database has been chosen because of its large

coverage of high-quality peer-reviewed journals, conference proceedings, and scholarly literature on different scientific fields. The relevant literature has been found through the search queries based on the set of keywords: genomics, conservation genomics, endangered species, threatened species, biodiversity conservation, wildlife conservation. The search was restricted by time range of publication and indexing in Scopus.

Bibliometric data analysis was performed with the use of VOSviewer, one of the most popular software for building and analyzing bibliometric networks. The following bibliometric methods were applied: co-authorship analysis, co-occurrence analysis of keywords, citations analysis, bibliographic coupling, and co-citations analysis. These methods helped to identify the key authors, organizations, countries, and journals, as well as to map the themes and intellectual structures in the area under research. Visualization of the network helped to visualize relationships between research actors and concepts, while visualization of overlay helped to analyze the time development of the research themes. Visualization of density was used to find out the themes which are studied most intensely. Thus, the paper gives a detailed view on the development, structure of knowledge and research directions in genomics of endangered species conservation.

3. RESULTS AND DISCUSSION

3.1 Keyword Co-Occurrence Network Visualization

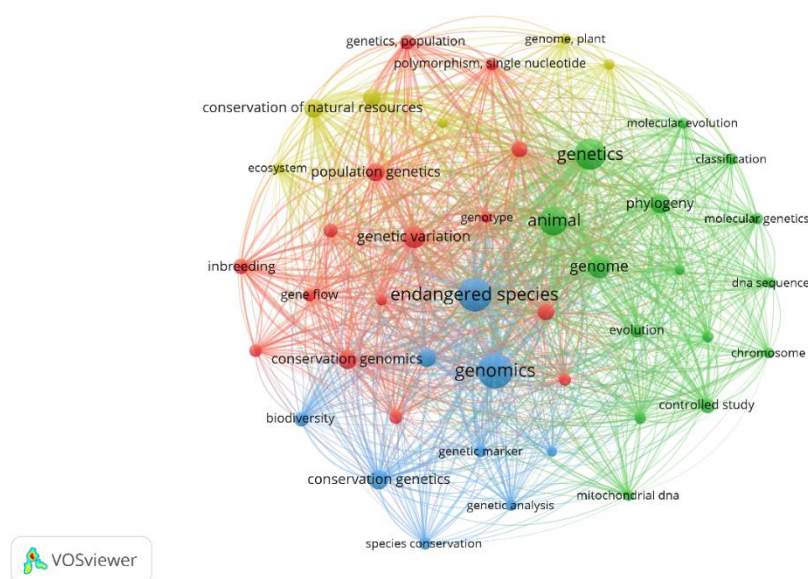


Figure 1. Network Visualization
Source: Data Analysis, 2026

Figure 1 represents a VOSviewer keyword co-occurrence network related to genomics in endangered species conservation. At the center of the map, the dominant nodes are “endangered species,” “genomics,” “genetics,” and “genetic variation”, indicating that the field is structurally anchored around the integration of molecular genetics and conservation biology. The central positioning of these terms reflects high frequency and strong co-occurrence links, suggesting that most publications in this domain are focused on applying genomic tools to understand and manage endangered populations.

The network is organized into several distinct clusters, each representing thematic subdomains. The green cluster is heavily associated with molecular and evolutionary biology concepts such as phylogeny, genome, DNA sequence, molecular genetics, and chromosome. This indicates a strong emphasis on evolutionary reconstruction and molecular characterization of species. These terms are tightly interconnected, suggesting that genomic sequencing and phylogenetic analysis are foundational methods in conservation genomics research.

The red cluster centers on population-level processes, including genetic variation, population genetics, inbreeding, gene flow,

and conservation genomics. This cluster reflects applied conservation concerns, particularly the management of genetic diversity in small or fragmented populations. The presence of “inbreeding” and “gene flow” highlights a focus on genetic risks faced by endangered species, such as loss of diversity and reduced adaptive potential.

The blue cluster is more conservation-policy and application-oriented, containing terms like conservation genetics, species conservation, biodiversity, and genetic markers. This cluster bridges scientific findings with practical conservation strategies, indicating how genomic data is translated into monitoring and management tools. The linkage between “genetic markers” and “species conservation” suggests the operational use of molecular tools in field conservation programs.

The network demonstrates a multidisciplinary convergence where genomics, evolutionary biology, and conservation science intersect. The central role of “genomics” connecting all clusters indicates its function as an integrative framework unifying molecular data with ecological and conservation applications. The structure also suggests a research trend moving from traditional conservation genetics toward more advanced genomic

approaches, reinforcing the growing importance of high-throughput sequencing

and molecular data in endangered species management.

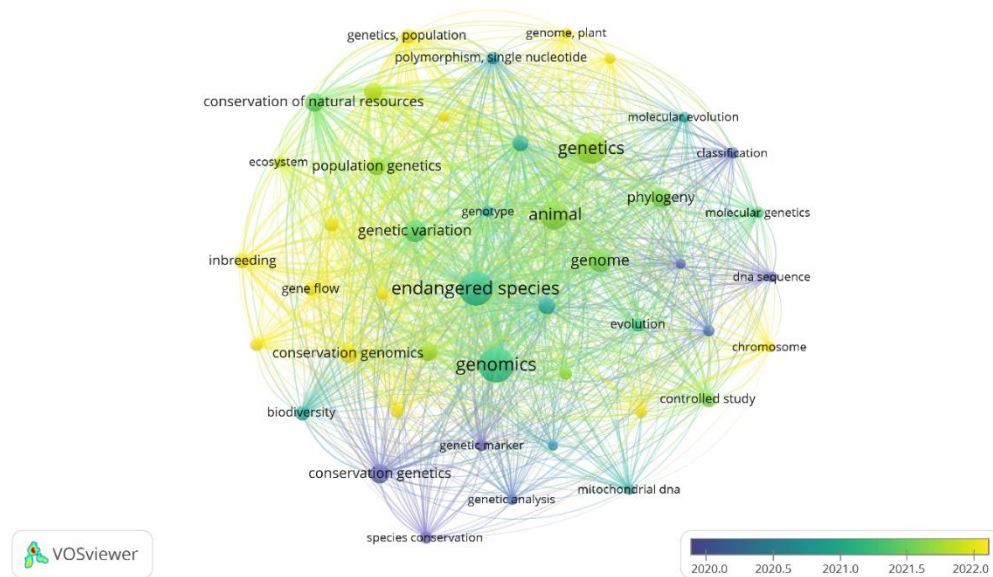


Figure 2. Overlay Visualization

Source: Data Analysis, 2026

Figure 2 indicates a temporal evolution of research themes in genomics for endangered species conservation, with colors representing publication recency (blue $\approx$ earlier, yellow $\approx$ most recent, around 2020–2022). The central position of “endangered species” and “genomics” remains stable, confirming them as persistent core concepts across the time window. These nodes function as a bridge connecting classical conservation genetics with newer genomic and evolutionary approaches. Earlier dominant themes (bluish–green tones) are concentrated around phylogeny, molecular genetics, mitochondrial DNA, genetic analysis, and species conservation. This suggests that foundational work in the field was initially driven by phylogenetic reconstruction,

marker-based genetics, and mitochondrial studies. These topics reflect a pre-genomic or early genomic phase where studies relied heavily on limited genetic markers and evolutionary inference to understand endangered populations. More recent topics (yellow nodes) are clearly shifting toward population genetics, conservation of natural resources, gene flow, inbreeding, conservation genomics, and SNP-related polymorphism (single nucleotide polymorphism). This indicates a transition toward high-resolution genomic data and population-level management applications. The increasing prominence of SNPs and population genetic structure reflects the adoption of next-generation sequencing and more data-intensive conservation strategies.

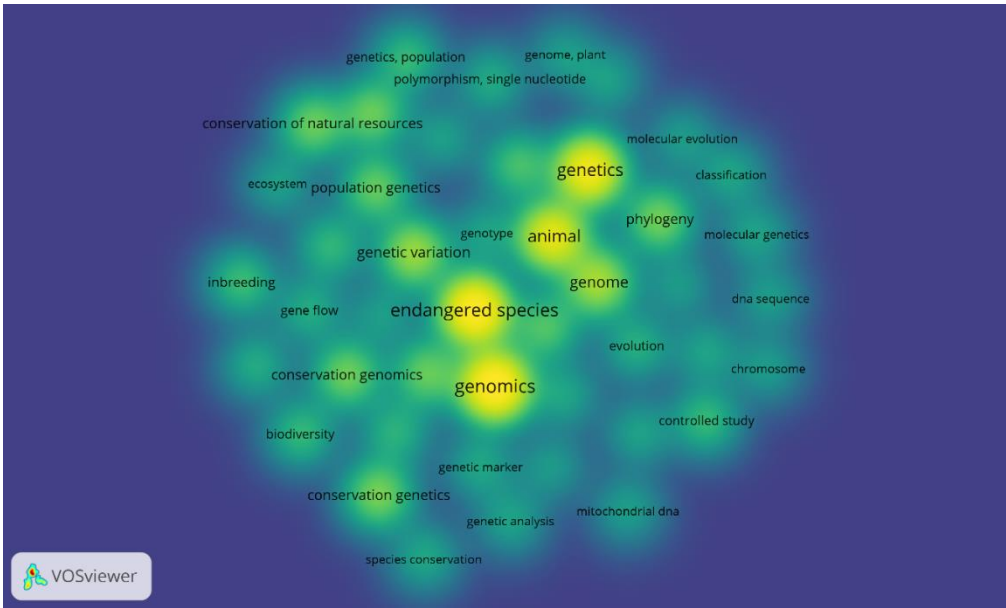


Figure 3. Density Visualization
Source: Data Analysis, 2026

Figure 3 represents the intellectual concentration of research on genomics in endangered species conservation. Areas with higher intensity (yellow) indicate stronger co-occurrence and higher keyword frequency. The most prominent hotspot is “genomics”, followed closely by “endangered species”, “genetics,” and “animal”, showing that the core of this research domain is strongly centered on applying genomic tools to understand and manage threatened biological populations. These nodes form a dense central core, indicating that most studies are clustered around integrated conservation-genomic applications rather than isolated thematic strands.

Moderate-density regions (green tones) expand outward to include genetic variation, genome, phylogeny, population genetics, gene flow, inbreeding, and conservation genomics. This suggests an intermediate conceptual layer where evolutionary biology and population-level genetic processes connect core genomic research with applied conservation outcomes. Peripheral and lower-density zones (blue areas) such as mitochondrial DNA, chromosome, DNA sequence, species conservation, and genetic analysis reflect more specialized or foundational methodologies that are still relevant but less dominant in current literature intensity.

3.2 Citation Analysis

Table 1. Top Cited Documents

Citations	Authors and Year	Title
1040	[15]	A molecular phylogeny of living primates
879	[16]	Harnessing genomics for delineating conservation units
724	[17]	Earth BioGenome Project: Sequencing life for the future of life
719	[18]	Genetic rescue to the rescue
529	[19]	EST-SSRs as a resource for population genetic analyses
480	[20]	Challenges and opportunities of genetic approaches to biological conservation
344	[21]	Mountain gorilla genomes reveal the impact of long-term population decline and inbreeding
270	[22]	Plant DNA barcodes: Applications today and in the future

229	[23]	The rough edges of the conservation genetics paradigm for plants
225	[24]	Using neutral, selected, and hitchhiker loci to assess connectivity of marine populations in the genomic era

Source: Scopus, 2026

3.3 Co-Authorship Analysis

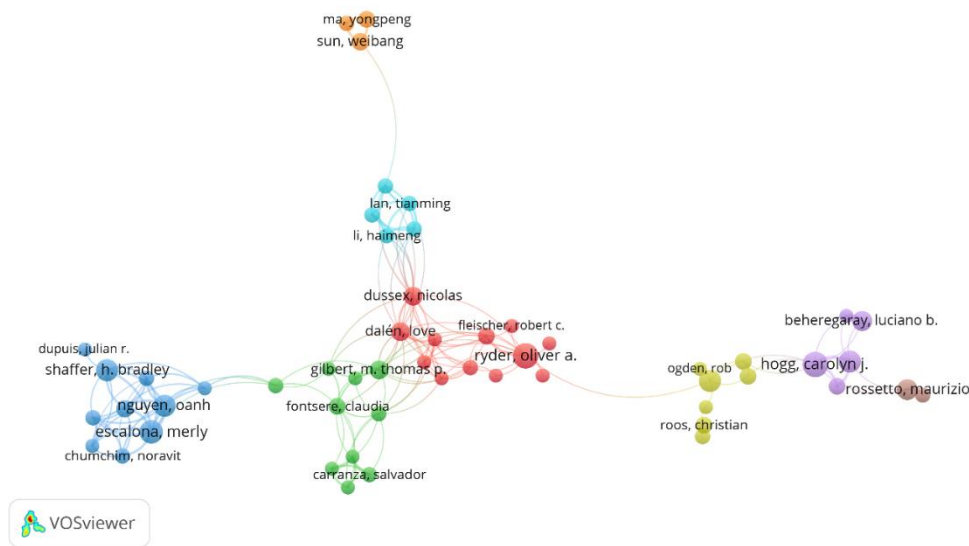


Figure 4. Author Visualization
Source: Data Analysis, 2026

Figure 4 represents a co-authorship structure within the field, showing several clearly separated research clusters connected by a limited number of bridging authors. On the left, a blue cluster (e.g., Shaffer, Nguyen, Escalona) forms a tightly interconnected group, indicating strong internal collaboration and a relatively established research team. In the central region, green and red clusters (including Gilbert, Fontserè, Dussix, Dalén, Ryder) act as the main structural hub, with multiple inter-cluster

links suggesting these authors play a coordinating or highly collaborative role across subgroups. On the right, yellow and purple clusters (e.g., Hogg, Roos, Rossetto, Beheregaray) appear more specialized and somewhat peripheral, but still connected through key intermediaries, indicating thematic or geographic specialization with selective collaboration. The upper isolated nodes (e.g., Ma Yongpeng, Sun Weibang) suggest emerging or less integrated contributors.

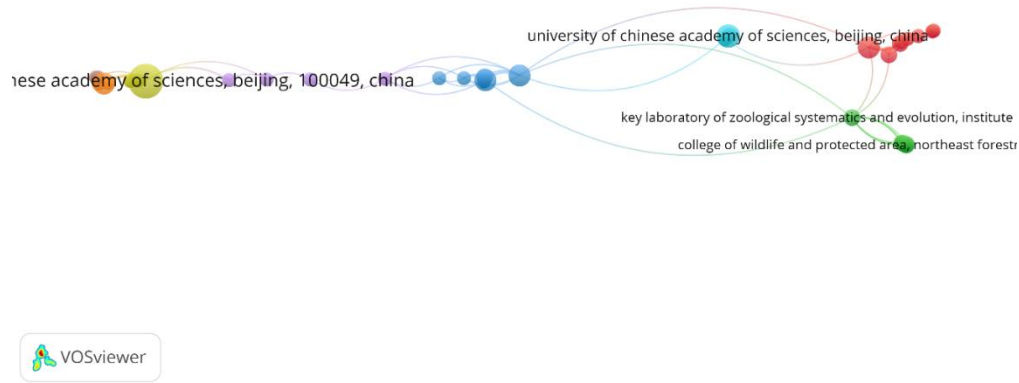


Figure 5. Institution Visualization
Source: Data Analysis, 2026

Figure 5 depicts an institutional collaboration network centered on Chinese research organizations involved in zoological systematics, evolution, and wildlife conservation. The structure is relatively linear, with the Chinese Academy of Sciences, Beijing and the University of Chinese Academy of Sciences acting as primary hubs, indicated by their central positioning and multiple connecting links. These institutions function as the main coordination centers, bridging collaborations across affiliated

laboratories and research units. On the right side, the Key Laboratory of Zoological Systematics and Evolution and the College of Wildlife and Protected Area (Northeast Forestry University) form a secondary cluster, showing strong internal linkage but partial dependence on the central CAS network for broader collaboration. The left-side node cluster associated with CAS (Beijing 100049) suggests administrative or institutional subdivision connections feeding into the main research system.

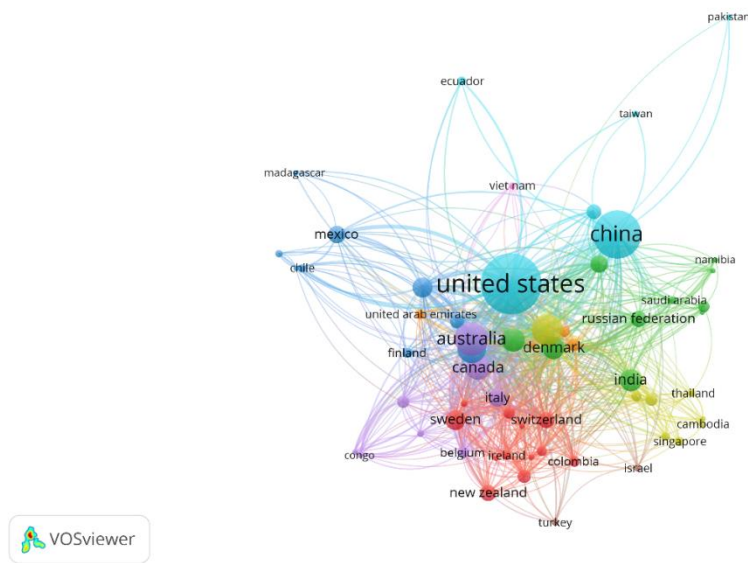


Figure 6. Country Visualization
Source: Data Analysis, 2026

Figure 6 represents a country-level collaboration network in the field, showing how research output is distributed and interconnected globally. The United States and China appear as the two dominant central hubs, with the largest nodes and the highest number of co-authorship links, indicating their leadership role in international research production and collaboration intensity. Surrounding them, countries such as Australia, Canada, and Denmark function as important secondary connectors, bridging interactions between major hubs and regional clusters. Denmark in particular appears highly central relative to its size, suggesting a strong mediating role across European and Asian collaborations.

A dense European cluster is visible, including Italy, Sweden, Switzerland, Belgium, Ireland, Finland, and the United Kingdom-related networks, characterized by strong intra-regional collaboration and frequent cross-links. This reflects a well-integrated research ecosystem within Europe, where partnerships are both internal and transcontinental. Meanwhile, Asian and Middle Eastern countries such as India, Thailand, Singapore, Saudi Arabia, and Russia form another collaborative belt, often linked through China as a primary hub. peripheral nodes such as Madagascar, Chile,

Congo, and Pakistan indicate emerging or less-integrated contributors with more limited collaboration intensity.

4. CONCLUSION

This bibliometric study on genomics in endangered species conservation demonstrates a rapidly evolving and increasingly interdisciplinary research landscape, where genomics has become the central analytical framework connecting molecular genetics, population biology, and conservation science. The keyword and thematic analyses reveal a clear transition from traditional approaches based on phylogenetics and mitochondrial DNA toward high-throughput genomic methods, particularly population genomics and SNP-based analyses, which are now driving research on genetic diversity, inbreeding, and gene flow in endangered populations. The co-authorship and institutional networks further highlight a moderately centralized but globally distributed collaboration structure, with leading contributions from major research hubs such as the United States and China, supported by strong European integration and emerging participation from developing regions.

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