

PLANT PHYLOGENETICS: A BIBLIOMETRIC ANALYSIS BASED ON VOSVIEWER AND CITESPACE

YANG, X. X. – ZHANG, S. J. – LUO, J.*

*Research Institute of Tibet Plateau Ecology, Tibet Agriculture & Animal Husbandry University,
Nyingchi, Tibet 860000, China
(e-mail: y15710463523@163.com)*

*Key Laboratory of Forest Ecology in Tibet Plateau, Ministry of Education, Nyingchi, Tibet
860000, China
(e-mail: 2234824532@qq.com)*

*National Key Station of Field Scientific Observation & Experiment, Nyingchi, Tibet 860000,
China*

Key Laboratory of Alpine Vegetation Ecological Security in Tibet, Nyingchi, Tibet 860000, China

**Corresponding author*

e-mail: luojian@xza.edu.cn; phone: +86-189-8904-5189

(Received 6th Apr 2023; accepted 1st Jun 2023)

Abstract. The study of phylogenetic zones of plants provides a good insight into the biogeographic and ecological processes of zone formation and a clear understanding of the nature and origin of biodiversity hotspots. The literature in the Web of Science core dataset was analyzed using bibliometric methods combined with CiteSpace 5.0, VOSviewer 1.6.18 visualization software, and Excel software to reveal the characteristics, hotspots, and evolutionary trends of this field over the past 35 years (1988–2022). The research on plant phylogenetic systematics has been increasing at China and abroad, and the main research force is mainly in the United States. The research conducted in this field primarily centers on biology, which exhibits clear interdisciplinary features, and the relationship between biology and other fields is particularly strong. In the field of plant phylogeny, these topics have a strong relationship in terms of knowledge transmission at each stage. The integration of diverse disciplines to advance mechanistic investigations, the amalgamation of various research techniques with phylogenetic tree building, and the utilization of model predictions across different plant species will continue to be a prominent research avenue in the realm of plant phylogenetic lineage research for the foreseeable future.

Keywords: *plant phylogenetics, literature measurement, VOSviewer and CiteSpace, research hotspots, development trends*

Introduction

Initially, plant phylogenetic studies focused on the classification and cluster analysis of plant composition based on the geographical distribution of families, genera, and species (the level of plant composition). This involved comparing the flora of a particular region with those of neighboring regions to explore the origin, nature, and status of the flora, and to reflect the evolutionary history of plant life in that region (Baskin and Baskin, 2016; Elton, 1946; Lu et al., 2018a; Yu et al., 2018). However, these analyses fail to consider the entirety of regional species, overlook the phylogenetic relationships among species or taxa, and complicate the identification of the degree of similarity in evolutionary history among different lineages (Borsch and Quandt, 2009).

With the continuous study of plant phylogeny, the concept of Plant Phylogenetics has emerged (Swenson and Umaña, 2014). This concept has been developed and

improved, and additional scientific methods have surfaced to solve the problem of studying the unity of lineage and interspecific relationships. Constructing phylogenetic trees using species from a particular region allows for the analysis of the evolutionary history of lineages. The resulting phylogenetic tree provides information on the interspecies affinities and the combination of evolutionary factors involved in the formation and development of the flora (Borsch and Quandt, 2009), thus revealing the patterns of lineage origin and evolution and predicting the future evolution of plants by building models (Yesson and Culham, 2006). The theory considers the evolutionary relationships of species as a whole in the study area, explains the biogeographic as well as ecological processes of lineage formation effectively, and provides quantifiable indicators and superior ways to influence modern flora and compare the degree of phylogenetic similarity among different lineages (Forest et al., 2007a; Kooyman et al., 2011; Qian et al., 2013). Li et al. (2015) conducted a plant phylogenetic study of the flora of Yunnan by utilizing the geographic distribution of 1983 genera of wild seed plants and their phylogenetic relationships. They analyzed the flora by calculating the composition among species and indicators of phylogenetic diversity, which allowed them to reclassify the flora based on an evolutionary perspective. They also analyzed the phylogenetic structure of different regions to understand the nature and origin of biodiversity hotspots in Yunnan effectively (Li et al., 2015).

A review of the existing literature reveals that only a few studies provide a complete picture of the developmental process of phylogenetic lineage studies. Most of the studies conducted in this field have primarily involved literature reviews, which have revealed a dearth of research on the long-term evolutionary processes of plant phylogeny throughout its developmental history. To address this gap, there is a need for the application of multiple research methods and tools to gain a more comprehensive understanding of plant evolution (Jaidka et al., 2013).

This study employed bibliometric analysis using CiteSpace 5.0 and VOSviewer 1.6.18 visualization software to investigate the trends in publications, research hotspot countries/regions, institutions (Feng et al., 2022; Li et al., 2019), major publishing journals, research hotspot themes, and the evolution of research on plant phylogenetic systematics using the Web of Science core dataset. The study summarized and analyzed the major research topics and their development, with the aim of providing insights into future research trends in this field. The research process is shown in *Figure 1*.

Data and methods

Data source

The Web of Science core database was used in this paper as the basis, and the search formula was constructed as “(ALL = plant OR ALL = plants) AND ((TS = (“phylogenetic diversity”) OR TS = (“phylogenetic structure”) OR TS = (“phylogenetic relatedness”)).” For this study, the type of literature was restricted to “Article,” “Review Article,” “Early Access,” or “Data Paper,” and the search results were exported in plain text format, the export date is October 25, 2022. The option “All records with cited references” was selected to ensure that all relevant articles were included in the analysis. A total of 2848 documents were finally obtained after filtering, removing duplicates, and eliminating irrelevant documents. The search formula is also constructed, and the data are exported as shown in *Figure 2*.

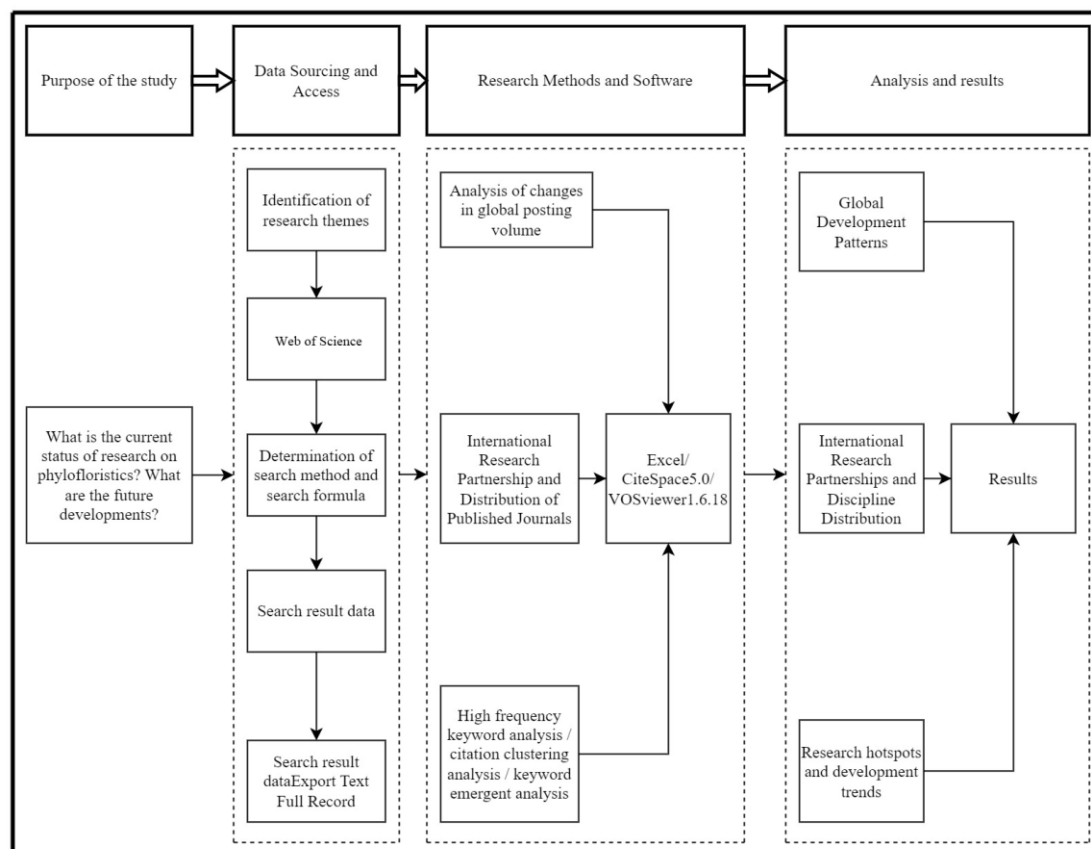


Figure 1. Research process roadmap



Figure 2. Data collection process

Research methodology

The frequency and centrality of the country, institution, and major journals, as well as the intensity and duration of country and keyword emergence, were calculated with the help of CiteSpace 5.0 software. In addition, VOSviewer 1.6.18 visualization software was utilized to map the distribution of countries, institutions, and journals, analyze the publication volume, publication countries, institutions, and disciplines in the field of plant phylogenetic systematics, and investigate the research hotspots and their development process by combining the keywords and citations in the literature. The number of publications, countries, institutions, and disciplines in the field of phylogeny,

as well as the hotspots of research and their development process, was also analyzed by combining literature keywords and citations to reveal the current status and future development of research in this field for 35 years (1988–2022).

Results

Analysis of the volume of published research literature

The change in the number of research literature publications conducted on Plant Phylogenetics during the period 1988–2022 (*Fig. 3*) shows an upward trend, and Plant Phylogenetics research can be divided into three phases based on the trend (*Table 1*). The growth rate of the data was used to divide it into three stages. The first stage was the exploration and development stage (1988–1999) and the cumulative number of articles published in this stage was 30, which has an annual average of 2.50 articles, accounting for 1.05% of the total number of articles published. This finding indicates a slow growth trend, which may be related to the immature scientific research tools and experiences at that time, the low importance attached to research in this area, as well as the limited online publication volume. The second phase is the accelerated growth phase (2000–2011) and the cumulative number of publications in this phase is 417, with an annual average of 34.75 publications, accounting for 14.64% of the total number of publications and demonstrating a rapid growth. This finding may be related to the deepening research on flora, plant composition, and phylogeny of plants and the increasing attention to this aspect of research; since then, Plant Phylogenetics research by scholars has continued to increase in interest (De Vries and Archibald, 2018; Hua, 2013; Lu et al., 2018b; Steinthorsdottir et al., 2021). The third phase is the explosive growth phase (2011–2022), in which the cumulative number of publications reached 2401, with an annual average of 218.27, accounting for 84.31% of the total number of publications and demonstrating a rapid growth. With further research, the maturation of research methods and techniques in the field of Plant Phylogenetics research considered the holistic nature between regional species and phylogenetic relationships among species or taxa, revealing the relevance and similarity of evolutionary history among different lineages (Cadotte et al., 2010; Erickson et al., 2014; Srivastava et al., 2012). The research of Plant Phylogenetics has provided additional research methods and popular directions for the study of flora (Donoghue, 2008), which has led to a new growth in the study of Plant Phylogenetics, which is still increasing.

Table 1. *Distribution of the number of papers output in the three stages*

Stage	Time horizon	Number of papers	Percentage of thesis output by stage	Average
Explore the development stage	1988–1999	30	1.05%	2.5
Accelerated growth phase	2000–2011	417	14.64%	34.75
Explosive growth phase	2012–2022	2401	84.31%	218.27

Global plant phylogenetics research international research partnerships and discipline distribution

International research partnerships

An important direction to promote development and innovation is reflected in research and cooperation between countries/regions (Liu et al., 2015). An analysis of

the literature originating from 89 countries/regions yielded the top 10 countries considering frequency of publication (Table 2; Fig. 4), while an analysis of the literature originating from 327 institutions yielded a mapping of institutional cooperation networks (Table 2; Fig. 5).

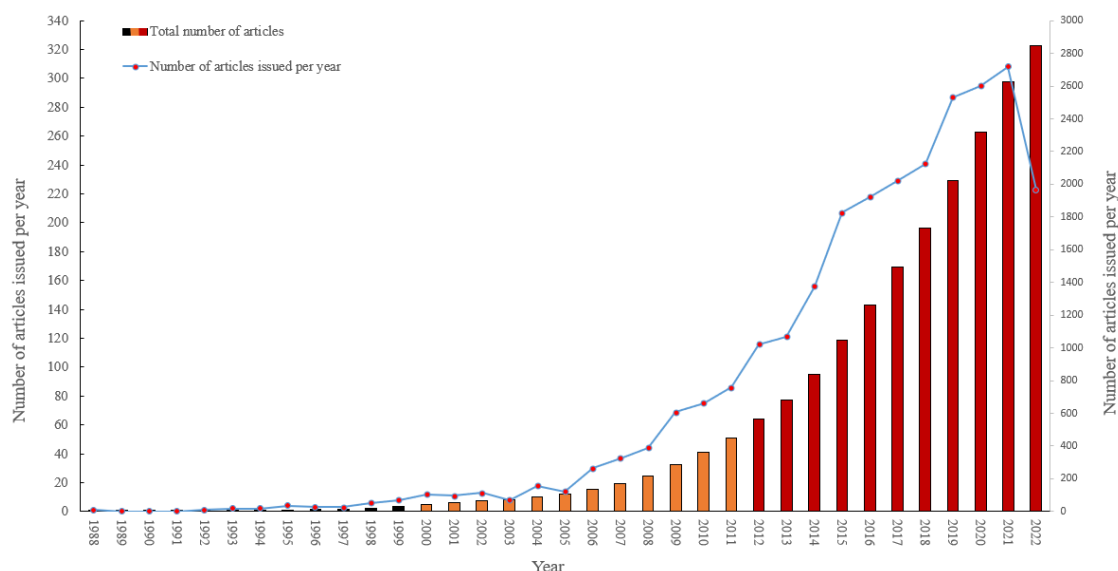


Figure 3. Number of publications and annual growth trend in the field of plant phylogenetic flora from 1990 to 2022

Table 2. Top 10 countries/regions and institutions considering number of articles issued

Country	Freq	Centrality	Time of first article	Country	Institution	Freq	Centrality	Time of first article
USA	1021	0.04	1988	China	Chinese Acad Sci	296	0.08	2004
China	618	0.00	2004	China	Univ Chinese Acad Sci	95	0.00	2014
Germany	307	0.34	2000	Spain	CSIC	82	0.07	2004
England	262	0.08	1997	USA	Univ Minnesota	74	0.10	2006
Canada	258	0.00	1995	USA	Univ Calif Berkeley	54	0.05	1998
French	253	0.46	1999	Switzerland	Univ Zurich	52	0.11	2011
Spain	240	0.00	2004	USA	Univ Florida	52	0.14	2008
Brazil	228	0.00	1994	USA	Univ Calif Davis	51	0.12	1998
Australia	203	0.12	1998	Canada	Univ Toronto	50	0.07	1999
Switzerland	175	0.49	1999	Germany	German Ctr Integrat Biodivers Res iDiv	50	0.19	2014

Considering frequency of publication, the United States tops the list, followed by China, Germany, England, Canada, and France, all of which are above 250; considering centrality, Switzerland (0.49) is the highest, followed by French (0.46); considering the time of entry into research, Switzerland (0.49) was the highest, followed by French (0.46). The study of plant phylogenetic systematics has formed a large network of cooperation between countries/regions, and the cooperation between different

countries/regions is relatively close. Switzerland has the closest cooperation with all countries/regions in the world and has a clear grouping. China ranks second in the number of relevant research publications but its centrality is low. This phenomenon indicates that China's cooperation with other countries in this field is slightly close, and international cooperation and influence must be further improved.

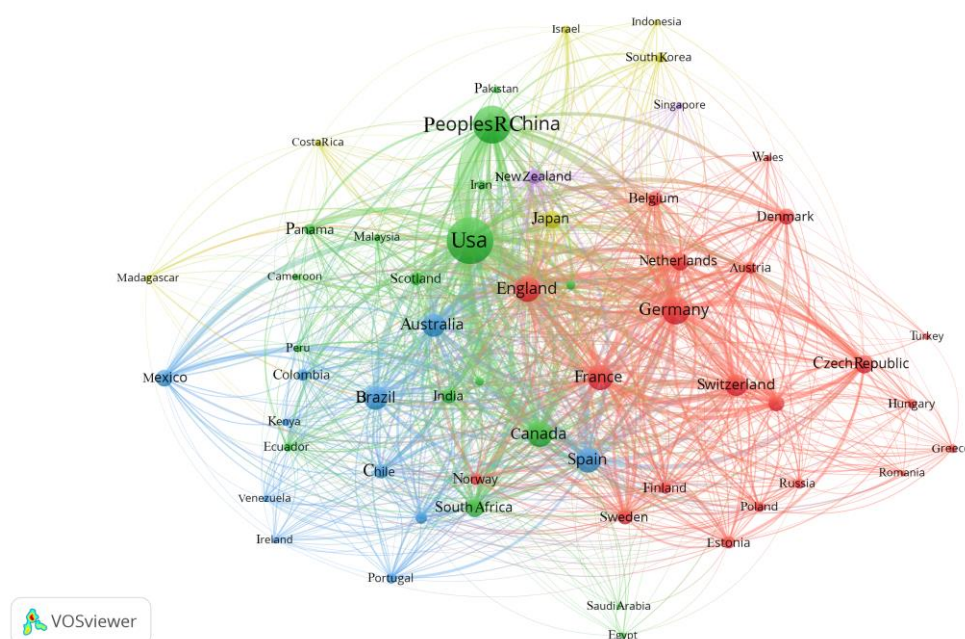


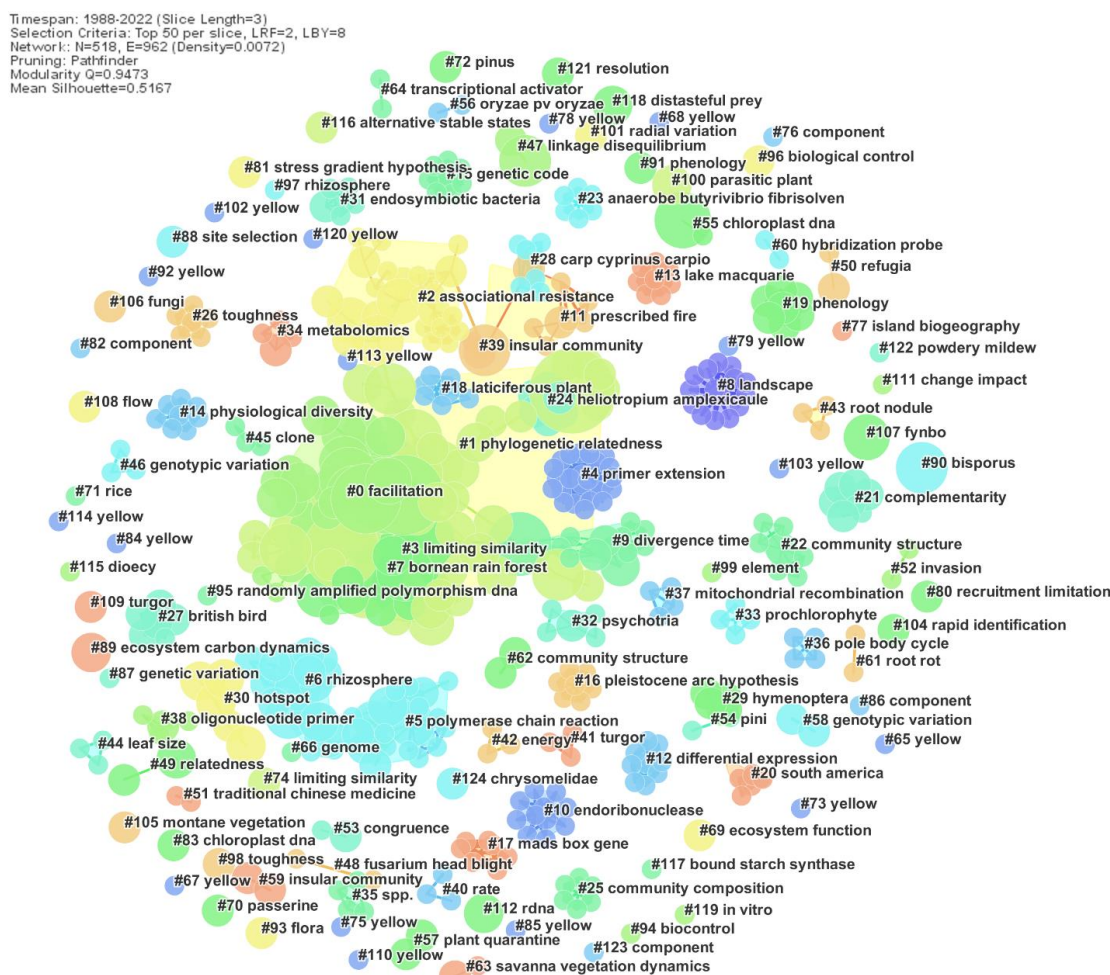
Figure 4. Mapping of national/regional cooperation networks in international literature

The analysis of research institutions provides a clear picture of the research units with a strong influence (Fang et al., 2018). The top 10 Chinese institutions conducting research in this field were identified by combining *Table 2* and *Figure 5*. The Chinese Academy of Sciences and the University of Chinese Academy of Sciences had the highest total publication frequency among these institutions. The frequency of publications of the Chinese Academy of Sciences far exceeded the other institutions up to 296, indicating that the institution has additional research in this field. The two Chinese institutions have a total publication frequency of 391 articles, accounting for 45.68% of the total publication frequency of the top 10 institutions. However, the centrality of their institutions is relatively low, further verifying that China has less close cooperation with other countries in this field; followed by the United States, with four of the top 10 institutions in this field, namely Univ Minnesota, Univ Calif Berkeley, Univ Minnesota, Univ Florida, and Univ Calif Davis, accounting for the largest number of the top 10 institutions. The four institutions published 231 articles, accounting for 26.99% of the total frequency of the top 10 institutions, and each institution has a high centrality, indicating close cooperation with other institutions. Among the top 10 institutions, Spain ranks third in the frequency of institutional publications in this field, with one CSIC among the top 10 institutions. Among the top 10 institutions, one CSIC had 82 articles, accounting for 9.58% of the total number of articles published by the top 10 institutions. In addition, the centrality of the German Centre for Integrative Biodiversity Research (iDiv) in Germany is 0.19, which is larger

The nodes and lines of different colors in the figure represent various time slices, transitioning from dark blue to dark red: dark blue (1988) and red (2022) represent the starting and end points of the time slice, respectively. Different circular nodes correspond to the equivalent keywords; a large node circle represents the high frequency of the keyword. Moreover, the position of the node indicates its earliest appearance: the keyword appears numerous times in the time slice represented by the color change when the keyword node has a thick layer of annual wheel. The line between the nodes indicates that the keyword appeared simultaneously in the same literature with another keyword. The color of the line corresponds to the year when the two keywords first appeared in the same article simultaneously, and the thickness of the line represents the number of co-occurrence and the closeness of the relationship: the relationship is close when the line is thick and vice versa (Li et al., 2017).

The general developmental characteristics of phylogenetic zoology studies of plants can be summarized in accordance with the timeline. *Figure 6* shows the following: (1) The main keywords in the 1990s were phylogenetic structure, identification, phylogeny, phylogenetic diversity, diversity, pattern, community, evolution, competition, and conservation. Research during this stage was mainly focused on exploring the species composition of various regions, the distribution of plant resources, the evolutionary history of plants in different regions, identification of species, interspecific relationships, and conservation research in biodiversity hotspots. The research direction was clear at this time. The term phylogenetic structure first appeared in 1992, indicating that the research on phylogenetic has gradually developed in the direction of interspecific relationships and ecological conservation, with increasing emphasis on the holistic nature of phylogeographic systems. This term has also begun to be applied to the phylogeny of different phylogeographic systems. (2) In the 21st century, terms such as biodiversity, biogeography, species richness, community structure, ecology, plant community, niche conservatism, trait, and species, as well as terms including diversity, community assembly, beta diversity, plant diversity, climate change, and forest, indicate that the study of a certain region has placed remarkable emphasis on the totality of the system and ecological niche with further research and optimization and innovation of research methods. Meanwhile, the study of phylogenetic systematics considers the influence of different factors on the formation and evolution of plants and then predicts the development and future evolution of plants in different regions (Wiens and Graham, 2005). The study of flora at this stage has become a new hotspot, and the methods for estimating a particular flora and the quantitative assessment of the plants of the region are rational, which, in turn, provides a basis for prioritizing different regions for conservation. (3) The keywords functional diversity, functional trait, productivity, mechanism, limiting similarity, gradient, facilitation, vegetation, impact, and phylogenetic diversity have been used to describe the phylogeny of plants. The emergence of assemblage, global pattern, and *r* package marked the enrichment of the hypothesis of plant phylogenetic systematics while considering the functional and diversity traits of different plant lineages. This enrichment aims to avoid overly intense interspecific competition leading to interspecific competitive exclusion (Götzenberger et al., 2012). The introduction of the term “*R* package” has generated significant interest in the totality of plant phylogenetic zones and the extent of phylogeny in the field of plant phylogenetic studies. In addition, the close connection of nodes between time zones indicates that the field of plant phylogenetic zoology still possesses strong knowledge transfer relationships and the tendency to further develop on the original basis in different time periods.

Citation clustering analysis



The small cluster serial number indicates additional literature. The cluster labels are extracted from the titles of the most influential articles; thus, the labels cannot summarize all the contents of the articles in the clusters. Therefore, the selected literature in this paper contained more than 20 (the first six clusters) for specific analysis, and the other clusters contained only a few literature and were insufficiently representative to conduct specific analysis. Cluster labels from 0–5 are presented

sequentially: #0 facilitation, #1 phylogenetic relatedness, #2 associational resistance, #3 limiting similarity, #4 primer extension, and #5 polymerase chain reaction.

The articles in Cluster #0 focus on different research methods to understand the processes of species assembly, coexistence, and future evolution in species ecological communities from a phylogenetic perspective. Lesson predicted how climate change would affect the future distribution of plants based on the BIOCLIM and Maxent models and analyzed the risk of future extinction of these plants (Yesson and Culham, 2006). The Vandercook study tested the hypothesis that soil moisture conditions drive habitat filtering and act on seed germination and seedling establishment as important ecological mechanisms for structuring temperate plant communities (Vandelook et al., 2012). Slingsby used quantile regression analysis and mean observations between co-occurring species and comparisons between expected phylogenetic distances to provide evidence for phylogenetic overdispersion in networks of closely related species (Slingsby and Verboom, 2006). This part of the paper mostly explores dialectical thinking using existing methods to assess or verify their accuracy.

The articles included in cluster #1 are mainly explored considering plant phylogenetic correlations. For example, Li Rong conducted a study on the phylogenetic lineages of Yunnan plants and showed that the integration of phylogenetic information can provide valuable insights for flora assessment and help effectively understand the structure of global biodiversity hotspots (Qian et al., 2013). The analysis of Alexandrou of the co-occurrence of paired assemblages of 325 algal groups in 1100 lakes in North America confirmed that phylogenetic distance may not explain the co-occurrence of freshwater green algae (Alexandrou et al., 2014). Using growth data, Kunstler estimated 275 interaction coefficients between tree species in the French mountains. The results showed that interaction strength was driven mainly by characteristic hierarchical structure rather than by functional or phylogenetic similarity. In addition to the influence of environmental filtering, these results also verified that functional and phylogenetic convergence of local tree communities over time is due to competing taxonomic units with different competitive capabilities (Kunstler et al., 2012).

The article in Cluster #2 focuses on the zonal plant composition or richness to predict the stability of the system and its overall resistance and thus identify priority areas for conservation. Expert scholars analyze the associated resistance of different zonations with different perspectives and methods. Iason conducted a comprehensive study on how forest tree resistance to pests and diseases is influenced by the manipulation of tree community characteristics of associated plants and other organisms. Their results indicated that constructing future forests to increase their overall resistance and reduce the likelihood of pest and disease impacts is possible (for example, through tree species and genotype diversity, using them as part of a long-term prevention strategy) (Iason et al., 2018). Zhou investigated the distribution patterns of a total of 1335 seed plants in Mount Kenya and calculated species richness and phylogenetic diversity in seven vegetation zones, concluding that moist forests have fewer herbaceous plants due to closed canopies of woody plants compared to open dry forests. Woody plants may have climate-dominated ecotopes while herbaceous plants may have microhabitat and microhabitat-dominated ecotopes, suggesting that low and upper mountain forests with high species richness or overdispersed phylogenetic structure as priority areas for conservation in Mount Kenya and other high mountains in the Eastern African mountain biodiversity hotspot (Zhou et al., 2018). Wang conducted a study in the huqin sands of the semi-arid agro-pastoral mosaic zone of China. A large-scale field survey

of 141 plots at 141 sites in the semi-arid agro-pastoral interface in China analyzed the effects of grazing disturbance on biodiversity patterns in semi-arid ecosystems from different aspects (Wang et al., 2019).

Cluster #3 contains articles that focus on the narrative of the unfolding restricted similarity hypothesis among plants. Related papers compare and examine the patterns observed in plant communities with a null model that simulates stochastic patterns in species assembly (Götzenberger et al., 2012). Functional trait differences among species are increasingly used to infer the effects of biotic and abiotic processes on species coexistence. De Bello proposed a functional species library framework based on this research outline, which detects patterns of simulated trait diversity more consistently than previous approaches and can also be applied to functional and phylogenetic diversity, allowing for a reinterpretation of community assembly processes and a better understanding of community assemblages (De Bello et al., 2012). Vandercook tested the hypothesis that soil moisture conditions drive habitat filtering and act on seed germination and seedling establishment as important ecological mechanisms for the construction of temperate plant communities (Vandelook et al., 2012). Paine assessed the effects of functional similarity, phylogenetic affinities, and stem density on seedling mortality in neighboring seedlings and adults in species-rich tropical forests (Paine et al., 2012).

Cluster #4 is described mainly around a method for studying the structure of RNA molecules in intact plant tissues, which uses dimethyl sulfate (DMS) to analyze the RNA structure. DMS modifies the substituents of adenine and cytosine residues within the single-stranded region of the RNA molecule, identifies the reactive sites by primer extension analysis, and uses DMS modification data to reveal the phylogenetic structure of plants (Senecoff and Meagher, 1992).

The literature related to cluster #5 has developed a narrative around plant inter-root microbial communities, with partial sequencing and analysis of cloned genes by molecular phylogenetic methods (Marilley and Aragno, 1999) and how phylogenetic diversity varies in the plant root system (Eisenhauer et al., 2017).

Analysis of intensity and frequency of sudden appearance of keywords

The business represents a steep increase in the number of occurrences of a keyword in a certain period: a large number of occurrences as keywords indicates a large number of related studies to these keywords in that period. The research frontier and the trend of development and evolution of a certain field is based on the temporal distribution and dynamic changeability of business (Pan et al., 2018). This paper aimed to have a clear and comprehensive understanding of the current frontier of plant phylogenetic zoology research and reflect the degree of attention and persistence of academics on specific keywords (Tucker et al., 2017). Thus, the business function in CiteSpace software was used in this paper to detect the business of keywords during 1988–2022 and generated the top 10 business lists for the business detection of keywords. The results are shown in Table 3, wherein each bar represents two years: a thick red bar represents the burst time period, and a large burst intensity value indicates the activity of research around this keyword in that time period (Munim et al., 2020). The study process was divided into three phases based on keyword chronology and emergent intensity in conjunction with the keyword time zone view to reflect the comprehensiveness of the study results (Fig. 6).

With the continuous development and improvement of gene technology, research on plant DNA genes has been promoted, that on plant genetic diversity in a certain region

has become a hot spot, and plant-related flora has also become increasingly popular. Such an improvement also marks the rapid change and development of plant taxonomy from traditional classification methods to molecular classification methods.

Table 3. Top 10 keywords with the strongest citation bursts

Keywords	Strength	Begin	End	Time period:1988–2022
DNA	17.2484	1996	2013	
Community ecology	13.1809	2008	2017	
Rain forest	13.079	2010	2017	
History	12.8187	2006	2015	
Bacteria	12.5815	2000	2011	
Genetic diversity	11.7828	1996	2011	
Phylogeny	10.18	2007	2011	
Ecosystem	8.9918	2008	2015	
Model	7.0999	2005	2011	
Extinction	6.9438	2008	2015	

The second stage: is the emergence of the words model, history, and phylogeny. This stage of academic focus is based on the rapid development of plant molecular biology and continues to deepen the theory and application while focusing on the innovation of research methods of flora and introducing different research methods model to reveal the historical evolution of plant phylogeny. For example, Faith proposed the use of branch length between species in the phylogenetic evolutionary tree to express the characteristics of phylogenetic diversity (PD), which made it possible to integrate the evolutionary history of species for a comprehensive and in-depth assessment of biodiversity (Tucker et al., 2017), and gradually formed a broad consensus (Eiserhardt et al., 2013; Forest et al., 2007; Pearse et al., 2014). With the accumulation of DNA barcode sequencing and data over time, the reconstruction of more highly accurate macro-phylogenetic trees has led to a more refined and credible study of plant phylogenetic lineages (Joly et al., 2014).

The words community ecology, ecosystem, extinction, and rain forest emerged in the third stage, and new research directions were provided as research methods became rich and increasingly sophisticated to understand the specific patterns of the lineages effectively. Phylogenetic systematics combines phylogenetic trees with traditional flora to study the evolutionary and biogeographic history of local flora and thus reveal the process of species formation within the system, which effectively explains the biogeographic and ecological processes of system formation (Li et al., 2018). Integrating phylogenetic trees with ecological factors, such as climate, altitude, and topography of species' locations, can provide insight into the history of vegetation composition, predict the future evolution of flora, and analyze the similarity between phylogeny and taxonomic composition, leading to an improved understanding of ecosystems. Meanwhile, the application of phylogenetic diversity measures in community phylogeny, phylogenetic zonation, and biodiversity conservation provides a new perspective to understand the dynamics of community, ecosystem, and global scale biodiversity and a scientific basis for effective and efficient conservation of species and their evolutionary history (Lu et al., 2018a). Tropical rainforests have become a new research hotspot area due to their high plant richness and complex phylogenetic structure.

Conclusions

The literature on phylogenetic systematics based on the WOS core dataset from 1990 to 2022, which reveals the growth trend of the literature, the countries and institutions included in the research fields involved, and the research progress and frontiers, is analyzed in this paper.

(1) From the basic characteristics of the research, the relevant research can be divided into the following three stages: the exploration and development stage, the accelerated growth stage, and the explosive growth stage. A strong knowledge linkage exists between the stages, and new hot spots are formed by further development on the original basis.

(2) From the study of international scientific research cooperation relations and disciplinary distribution, the scientific research strength of the United States leads this aspect and the cooperation between the United States and other countries is close. China still needs to further improve between cooperation with other countries; this area integrates the relevant research mainly concentrated in the field of ecology. This is followed by biology, plant science, natural science, and other disciplines, with strong interdisciplinarity between disciplines, among which ecology is most closely linked to other disciplines.

(3) From the perspective of the evolution of topics, plant phylogenetic studies have shown a strong dependence on technology and analytical methods. With the continuous improvement and development of the field of plant phylogenetics, the research themes at different stages have shown strong interdisciplinarity. The research at each stage is closely related to the times and has close inheritance, especially in the area of plant genetics. This close relationship fully reflects the deep and rational scientific problems of plant phylogenetic systematics in the context of social stability, ecological civilization, technological progress, and harmony between human and nature. Combining the research theory with the practical ecological problems and providing additional attention to the practicality of the research is reasonable.

The current research in this discipline is generally the era of quantitative interpretation of the zonal phenomena and exploration of their formation mechanisms, with a broad scale of research, a deep and thorough perspective, and a stringent and accurate requirement for data precision. Future research on phylogenetic systematics will further focus on the depth and breadth of the study and use the accumulation of biological information to enhance the research of modern flora and phylogenetic similarity among different systematics. Such research works will provide important reference values for biodiversity formation and maintenance mechanisms and present effective information for additional scientific and accurate assessment of systemic biodiversity from evolutionary and other dimensions. The phylogenetic similarity between the phylogeographic systems of the region is of considerable value for the formation and maintenance of biodiversity.

Acknowledgements. This work was supported by Special Foundation for National Science and Technology Basic Research Program of China [2021FY100201], the Second Tibetan Plateau Scientific Expedition and Research Program[2019QZKK05020110] and Graduate Innovation Program Funding Project YJS2022-15 of Tibet Agricultural and Animal Husbandry College.

Conflict of interests. The authors declare that they have no conflict of interests.

REFERENCES

- [1] Alexandrou, M. A., Cardinale, B. J., Hall, J. D., Delwiche, C. F., Fritschie, K., Narwani, A., Venail, P. A., Bentlage, B., Sabrina Pankey, M., Oakley, T. H. (2014): Evolutionary relatedness does not predict competition and co-occurrence in natural or experimental communities of green algae. – *Proceedings of the Royal Society B: Biological Sciences* 282(1799): 20141745.
- [2] Baskin, J. M., Baskin, C. C. (2016): Origins and relationships of the mixed mesophytic Forest of Oregon–Idaho, China, and Kentucky: review and synthesis – *Annals of the Missouri Botanical Garden* 101(3): 525-552.
- [3] Borsch, T., Quandt, D. (2009): Mutational dynamics and phylogenetic utility of noncoding chloroplast DNA – *Plant Systematics and Evolution* 282: 169-199.
- [4] Cadotte, M. W., Jonathan Davies, T., Regetz, J., Kembel, S. W., Cleland, E., Oakley, T. H. (2010): Phylogenetic diversity metrics for ecological communities: integrating species richness, abundance and evolutionary history – *Ecol Lett* 13(1): 96-105.
- [5] Chen, C., Hu, Z., Liu, S., Tseng, H. (2012): Emerging trends in regenerative medicine: a scientometric analysis in CiteSpace – *Expert opinion on biological therapy* 12(5): 593-608.
- [6] De Bello, F., Price, J. N., Münkemüller, T., Liira, J., Zobel, M., Thuiller, W., Pärtel, M. (2012): Functional species pool framework to test for biotic effects on community assembly – *Ecology* 93(10): 2263-2273.
- [7] De Vries, J., Archibald, J. M. (2018): Plant evolution: landmarks on the path to terrestrial life – *New Phytologist* 217(4): 1428-1434.
- [8] Donoghue, M. J. (2008): A phylogenetic perspective on the distribution of plant diversity – *Proceedings of the National Academy of Sciences* 105(supplement_1): 11549-11555.
- [9] Eisenhauer, N., Lanoue, A., Strecker, T., Scheu, S., Steinauer, K., Thakur, M. P., Mommer, L. (2017): Root biomass and exudates link plant diversity with soil bacterial and fungal biomass – *Sci Rep* 7(1): 44641.
- [10] Eiserhardt, W. L., Svenning, J. C., Baker, W. J., Couvreur, T. L. P., Balslev, H. (2013): Dispersal and niche evolution jointly shape the geographic turnover of phylogenetic clades across continents – *Sci Rep* 3(1): 1-8.

- [11] Elton, C. (1946): Competition and the structure of ecological communities. – *The Journal of Animal Ecology* 54-68.
- [12] Erickson, D. L., Jones, F. A., Swenson, N. G., Pei, N., Bourg, N. A., Chen, W., Kress, W. J. (2014): Comparative evolutionary diversity and phylogenetic structure across multiple forest dynamics plots: a mega-phylogeny approach. – *Frontiers in Genetics* 5: 358.
- [13] Fang, Y., Yin, J., Wu, B. (2018): Climate change and tourism: a scientometric analysis using CiteSpace. – *Journal of Sustainable Tourism* 26(1): 108-126.
- [14] Feng, L., Tang, H., Pu, T., Chen, G., Liang, B., Yang, W., Wang, X. (2022): Maize–soybean intercropping: a bibliometric analysis of 30 years of research publications. – *Agron J* 114: 3377-3388.
- [15] Forest, F., Grenyer, R., Rouget, M., Davies, T. J., Cowling, R. M., Faith, D. P., Balmford, A., Manning, J. C., Procheş, Ş., Van Der Bank, M., Reeves, G., Hedderson, T. A. J., Savolainen, V. (2007): Preserving the evolutionary potential of floras in biodiversity hotspots. – *Nature* 445(7129): 757-760.
- [16] Götzenberger, L., de Bello, F., Bråthen, K. A., Davison, J., Dubuis, A., Guisan, A., Zobel, M. (2012): Ecological assembly rules in plant communities—approaches, patterns and prospects. – *Biological Reviews* 87(1): 111-127.
- [17] Hou, J., Yang, X., Chen, C. (2018): Emerging trends and new developments in information science: a document co-citation analysis (2009–2016). – *Scientometrics* 115: 869-892.
- [18] Hua, Z. (2013): The floras of southern and tropical southeastern Yunnan have been shaped by divergent geological histories. – *PLoS One* 8(5): e64213.
- [19] Iason, G. R., Taylor, J., Helfer, S. (2018): Community-based biotic effects as determinants of tree resistance to pests and pathogens. – *For Ecol Manage* 417: 301-312.
- [20] Jaidka, K., Khoo, C. S. G., Na, J. C. (2013): Literature review writing: how information is selected and transformed. – *Aslib Proceedings: New Information Perspectives* 65: 303-325.
- [21] Joly, S., Davies, T. J., Archambault, A., Bruneau, A., Derry, A., Kembel, S. W., Wheeler, T. A. (2014): Ecology in the age of DNA barcoding: the resource, the promise and the challenges ahead. – *Molecular Ecology Resources* 14(2): 221-232.
- [22] Kooyman, R., Rossetto, M., Cornwell, W., Westoby, M. (2011): Phylogenetic tests of community assembly across regional to continental scales in tropical and subtropical rain forests. – *Global Ecology and Biogeography* 20(5): 707-716.
- [23] Kunstler, G., Lavergne, S., Courbaud, B., Thuiller, W., Vieilledent, G., Zimmermann, N. E., Kattge, J., Coomes, D. A. (2012): Competitive interactions between forest trees are driven by species' trait hierarchy, not phylogenetic or functional similarity: implications for forest community assembly. – *Ecol Lett* 15(8): 831-840.
- [24] Li, C., Ji, X., Luo, X. (2019): Phytoremediation of heavy metal pollution: a bibliometric and scientometric analysis from 1989 to 2018. – *International Journal of Environmental Research and Public Health* 16(23): 4755.
- [25] Li, R., Kraft, N. J. B., Yang, J., Wang, Y. (2015): A phylogenetically informed delineation of floristic regions within a biodiversity hotspot in Yunnan, China. – *Sci Rep* 5(1): 1-7.
- [26] Li, R., Qian, L., Sun, H. (2018): Current progress and future prospects in phylofloristics. – *Plant Diversity* 40(4): 141-146.
- [27] Li, X., Ma, E., Qu, H. (2017): Knowledge mapping of hospitality research - a visual analysis using CiteSpace. – *Int J Hosp Manag* 60: 77-93.
- [28] Liu, Z., Yin, Y., Liu, W., Dunford, M. (2015): Visualizing the intellectual structure and evolution of innovation systems research: a bibliometric analysis. – *Scientometrics* 103: 135-158.
- [29] Lu, L. M., Mao, L. F., Yang, T., Ye, J. F., Liu, B., Li, H. L., Sun, M., Miller, J. T., Mathews, S., Hu, H. H., Niu, Y. T., Peng, D. X., Chen, Y. H., Smith, S. A., Chen, M., Xiang, K. L., Le, C. T., Dang, V. C., Lu, A. M., Soltis, P. S., Soltis, D. E., Li, J. H., Chen,

- Z. D. (2018): Evolutionary history of the angiosperm flora of China. – *Nature* 554(7691): 234-238.
- [30] Marilley, L., Aragno, M. (1999): Phylogenetic diversity of bacterial communities differing in degree of proximity of *Lolium perenne* and *Trifolium repens* roots. – *Applied Soil Ecology* 13(2): 127-136.
- [31] Munim, Z. H., Dushenko, M., Jimenez, V. J., Shakil, M. H., Imset, M. (2020): Big data and artificial intelligence in the maritime industry: a bibliometric review and future research directions. – *Maritime Policy and Management* 47(5): 577-597.
- [32] Paine, C. E. T., Norden, N., Chave, J., Forget, P. M., Fortunel, C., Dexter, K. G., Baraloto, C. (2012): Phylogenetic density dependence and environmental filtering predict seedling mortality in a tropical forest. – *Ecol Lett* 15(1): 34-41.
- [33] Pan, X., Yan, E., Cui, M., Hua, W. (2018): Examining the usage, citation, and diffusion patterns of bibliometric mapping software: a comparative study of three tools. – *J Informetr* 12(2): 481-493.
- [34] Pearse, W. D., Purvis, A., Cavender-Bares, J., Helmus, M. R. (2014): Metrics and Models of Community Phylogenetics. – In: Garamszegi, L. Z. (ed.) *Modern Phylogenetic Comparative Methods and Their Application in Evolutionary Biology: Concepts and Practice*. Springer-Verlag, Berlin, pp. 451-464.
- [35] Qian, H., Swenson, N. G., Zhang, J. (2013): Phylogenetic beta diversity of angiosperms in North America. – *Global Ecology and Biogeography* 22(10): 1152-1161.
- [36] Senecoff, J. F., Meagher, R. B. (1992): In vivo analysis of plant RNA structure: soybean 18S ribosomal and ribulose-1, 5-bisphosphate carboxylase small subunit RNAs. – *Plant Molecular Biology* 18: 219-234.
- [37] Shen, Z., Wu, H., Chen, Z., Hu, J., Pan, J., Kong, J., Lin, T. (2022): The global research of artificial intelligence on prostate cancer: a 22-year bibliometric analysis. – *Frontiers in Oncology* 12.
- [38] Slingsby, J. A., Verboom, G. A. (2006): Phylogenetic relatedness limits co-occurrence at fine spatial scales: evidence from the schoenoid sedges (Cyperaceae: Schoeneae) of the Cape Floristic Region, South Africa. – *The American Naturalist* 168(1): 14-27.
- [39] Song, J., Zhang, H., Dong, W. (2016): A review of emerging trends in global PPP research: analysis and visualization. – *Scientometrics* 107: 1111-1147.
- [40] Srivastava, D. S., Cadotte, M. W., Macdonald, A. A. M., Marushia, R. G., Mirotchnick, N. (2012): Phylogenetic diversity and the functioning of ecosystems. – *Ecol Lett* 15(7): 637-648.
- [41] Steinthorsdottir, M., Coxall, H. K., De Boer, A. M., Huber, M., Barbolini, N., Bradshaw, C. D., Strömberg, C. A. E. (2021): The Miocene: the future of the past. – *Paleoceanography and Paleoclimatology* 36(4): e2020PA004037.
- [42] Swenson, N. G., Umaña, M. N. (2014): Plant Phylogenetics: an example from the Lesser Antilles. – *Journal of Plant Ecology* 7(2): 166-175.
- [43] Tucker, C. M., Cadotte, M. W., Carvalho, S. B., Jonathan Davies, T., Ferrier, S., Fritz, S. A., Grenyer, R., Helmus, M. R., Jin, L. S., Mooers, A. O., Pavoine, S., Purschke, O., Redding, D. W., Rosauer, D. F., Winter, M., Mazel, F. (2017): A guide to phylogenetic metrics for conservation, community ecology and macroecology. – *Biological Reviews* 92(2): 698-715.
- [44] Vandeloof, F., Verdú, M., Honnay, O. (2012): The role of seed traits in determining the phylogenetic structure of temperate plant communities. – *Ann Bot* 110(3): 629-636.
- [45] Wang, Y., Wang, J., Chen, C., Li, J., Chu, J. (2019): Grazing plays an important role in structuring alpha and beta components of taxonomic, functional, and phylogenetic diversity in semiarid sandy land of northern China. – *Glob Ecol Conserv* 20: e00790.
- [46] Wiens, J. J., Graham, C. H. (2005): Niche conservatism: integrating evolution, ecology, and conservation biology. – *Annu. Rev. Ecol. Evol. Syst.* 36: 519-539.
- [47] Wu, J., Jia, D., Wei, Z., Xin, D. (2020): Development trends and frontiers of ocean big data research based on CiteSpace. – *Water* 12(6): 1560.

- [48] Yesson, C., Culham, A. (2006): A phyloclimatic study of Cyclamen. – BMC Evolutionary Biology 6: 1-23.
- [49] Yu, X., Xiang, C., Peng, H. (2018): Taxonomy in the Kunming Institute of Botany (KIB): progress during the past decade (2008–2018) and perspectives on future development. – Plant Diversity 40(4): 147-157.
- [50] Zhou, Y., Chen, S., Hu, G., Mwachala, G., Yan, X., Wang, Q. (2018): Species richness and phylogenetic diversity of seed plants across vegetation zones of Mount Kenya, East Africa. – Ecol Evol 8(17): 8930-8939.