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Review

Development in Soil Chronosequence Research from 1994 to 2024: A Bibliometric Analysis Using CiteSpace

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Abstract: Soil chronosequences are crucial for understanding pedogenesis and ecosystem dynamics, yet a systematic bibliometric analysis of this field remains absent. To investigate hotspots and trends, this study used CiteSpace to analyze 4075 publications from the Web of Science Core Collection (1994–2024). The results revealed a steady increase in publications over time, led by the USA (1287 articles) and China (1093 articles). Wardle David A. emerged as the most influential researcher (67,519 citations) for his contributions regarding microbial-driven pedogenic feedbacks. The Chinese Academy of Sciences was the top institution, contributing 13.3% of articles and achieving the highest centrality of 0.21. Geoderma (IF = 5.6) was the most cited journal (2258 citations), with key contributors including Vitousek (530 citations) and Walker (415 citations) from the USA and Wardle (411 citations) from Sweden. Research hotspots in this field were nutrient cycling, vegetation succession/ecological restoration, and soil microbial community dynamics. Three thematic shifts were identified: early focus on conceptual frameworks, expansion to ecological restoration and carbon dynamics, and recent diversification into microbial communities, coastal ecosystems (e.g., mangroves, Spartina alterniflora), and anthropogenic impacts (e.g., heavy metals). The research has evolved significantly from 1994 to 2024, with a growing emphasis on interdisciplinary approaches and practical applications. This analysis provides a comprehensive synthesis of soil chronosequence research, advancing our understanding of pedogenesis and informing sustainable land-management strategies.

Keywords: bibliometric analysis; soil chronosequence; hotspot; pedogenesis; CiteSpace

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1. Introduction

Soil, as a fundamental natural resource, supports agriculture, controls ecosystem functions, and helps to maintain climate factors [1]. Soil age is a key indicator of soil development, illuminating soil evolution and guiding resource management and ecological assessments [2,3]. Recent decades have witnessed a paradigm shift in soil age research. Beyond traditional soil science, it now addresses multidisciplinary challenges such as nutrient cycling, heavy metal mobility, paleoclimate reconstruction, and the restoration of degraded land [4–7]. Therefore, measuring soil properties dynamics across chronosequences is significant for strengthening pedogenic theory and promoting sustainable soil management.

A soil chronosequence refers to a genetically related soil sequence spanning distinct time periods under similar parent material, climate, topography, and biotic factors [8,9].

This concept serves as a powerful tool for understanding how soil develops and changes over time. Throughout the past few decades, researchers have created chronosequences for various landscapes, including river terraces, volcanic lava flows, geological landslides, marine erosion platforms, coastal dunes, and reclaimed tidal flats, in order to explore soil development processes and rates [10–15]. These studies demonstrate that soil property variations directly link to soil age and pedogenic processes such as weathering, organic matter accumulation, element migration, and microbial dynamics [16–18]. These findings provide new insights into the evolution and sustainability of soil under both natural and anthropogenic influences.

Previous studies have created soil chronosequences by employing alternative approaches, including historical document analysis and field surveys, sampling soils with differing ages of development, dating based on the construction of irrigation canals, changing periods of rice paddy cultivation in reclaimed tidal flats (space-for-time substitution), defining the ages of soil terrace formation, remote-sensing image interpretation (space-for-time substitution), and advanced dating techniques such as optically stimulated luminescence (OSL) dating, radiocarbon (^{14}C) dating, cesium-137 (^{137}Cs) dating, and lead-210 (^{210}Pb) dating [19–23]. These methodologies not only provided technical support for the precise determination of soil age but also promoted the diversification of soil chronosequence research. For instance, the application of high-precision OSL dating and accelerator mass spectrometry-based ^{14}C dating has significantly enhanced the accuracy and reliability of soil age determination [21,22].

In recent years, significant advancements in the study of soil chronosequence have been witnessed. On the one hand, improvements in high-precision dating methods, such as single-grain luminescence dating, have enhanced the resolution of soil age determination across diverse temporal scales [20]. For instance, in reclaimed tidal flats in East China, a chronosequence of rice paddy soils (50, 100, 300, and 700 years) revealed that soil carbon and nitrogen exhibited exponential growth with cultivation time and stabilized rapidly at approximately 100 years due to paddy management practices such as fertilization and flooding [24]. Furthermore, an analysis of a 22,000-year landslide-derived soil chronosequence revealed that topsoil carbon and nitrogen increased with soil age, while carbon accumulation rates decreased significantly between 5500 and 22,000 years ago [5]. These findings align with the ISO/IWA (International Organization for Standardization/International Workshop Agreement) 48:2024 requirements for material circularity in ESG (Environmental, Social, and Governance) frameworks.

On the other hand, research has increasingly expanded from focused attention on individual soil properties to extensive investigations of numerous constituents [25–27]. Research shows that soil phosphorus fractions vary during soil formation: bioavailable phosphorus rises and residual phosphorus declines as soil formation lengthens [28–32]. These changes are primarily caused by iron–aluminum oxides, vegetation, and soil pH variations. For example, in glacial retreat chronosequences, progressive vegetation succession was found to induce pH-mediated shifts in iron–aluminum oxide speciation, thereby exerting direct control over phosphorus bioavailability dynamics. [15,33]. A study by Zhang et al. (2016) used high-throughput sequencing of the 16S rRNA gene to investigate the changes in soil properties and soil microbial communities for abandoned cropland, revealing that land use played an important role in soil nutrients and bacterial diversity [34]. The above findings support SDG 15.3's land degradation neutrality targets through the identification of thresholds for sustainable land use. Similarly, millennial-scale coastal dune sequences (e.g., Australian Last Glacial Maximum sites) demonstrate soil carbon accumulation rates synchronized with sea-level-driven vegetation shifts, offering proxies for Paris Agreement carbon market baselines [35]. Moreover, the soil chronosequence

approach has also been employed to study the evolution of soil quality. For instance, in the lower Yangtze River alluvial plain, the development of chronosequences based on different reclamation periods has indicated anthropogenic impacts on soil quality [36,37]. These works have extended the uses of soil chronosequences and established a scientific basis for the rational development and conservation of soil resources. However, limited attention has been given to a comprehensive analysis of research on soil chronosequences.

This study was conducted using CiteSpace to analyze the literature in this field systematically. The objectives of this study were as follows: (1) to trace the historical progress and current trends in soil chronosequence research; (2) to evaluate the influences of scholars, institutions, and countries on soil chronosequence research; and (3) to detect research hotspots and future directions. The hypotheses tested were as follows: (1) the number of publications in soil chronosequence research has experienced a growth; (2) the research influence of different countries and institutions varies significantly in soil chronosequence studies; and (3) the research focus in this field has evolved from individual soil properties to integrated studies of multiple elements. The findings of this study allow for proper identification of the current research hotspots and trends in soil chronosequence studies, therefore providing scientific references and knowledge for future research.

2. Materials and Methods

2.1. Date Collection

The data used in this study were obtained from the Web of Science Core Collection (WoSCC) database on 7 January 2025. We selected the Science Citation Index Expanded (SCIE) and the Social Sciences Citation Index (SSCI) of the WoSCC. The search term was set as "soil chronosequence", with the search period spanning from 1 January 1994 to 31 December 2024. The language was specified as English, and the document types were designated as "Article" and "Review Article". After eliminating the literature not related to the topic and filtering the duplicates, 4075 relevant articles were finally selected as the samples for analysis. The articles were then exported in "plain text" format, and the record content was set as "full record and cited references" to preserve complete records, including information on abstracts, keywords, and cited references. These articles were used to statistically analyze and draw knowledge maps of publication years, authors, journals, and keywords, among other aspects, in order to clearly reflect the research status and development trends in the soil chronosequence field. The search and analysis process is depicted in Figure 1.

2.2. Data Analysis

Bibliometric analysis, which leverages quantitative methods to examine literature characteristics such as citation patterns and keyword frequencies, was employed in this study. CiteSpace is a tool developed by Professor Chaomei Chen using the Java platform, which has been widely recognized for its capabilities in terms of visualizing and analyzing bibliometric data [38]. It can identify key articles, journals, authors, institutions, and more to explore hotspots and development trends. This study utilized CiteSpace 6.3.1 to create a comprehensive set of knowledge maps. When using CiteSpace 6.3.1, the following parameter settings were made. We screened the imported literature in CiteSpace, with the time slice set to one year to track temporal trends year by year. The threshold (top N per slice) was set to 50, and the Pathfinder clipping was used to simplify the atlas. Regarding node types, countries, institutions, authors, keywords, and journals were extracted from titles, abstracts, and keywords provided by authors. First, we analyzed the number of publications and the associated growth rate based on the data. Then, to better understand the current status in this field, we performed a co-occurrence analysis focusing on key nodes

such as country, institution, author, journal, and significant articles. We also conducted a keyword clustering analysis and burst analysis to identify the hotspots and trends in this field. Based on these analyses, we intuitively revealed the evolving trends and dynamics in soil chronosequence studies published between 1994 and 2024, offering insights for potential future research directions. The quantitative tables that involved the rating of publications, institutions, authors, countries, and keywords were created employing Excel. Graphs of annual publications and high-impact journals were obtained using Origin 2018. CiteSpace was employed to explore the co-occurrence maps of countries, authors, institutions, and keywords, as well as keyword clusters and keyword bursts. The flowchart and trend map in this study were developed using Visio 2019.

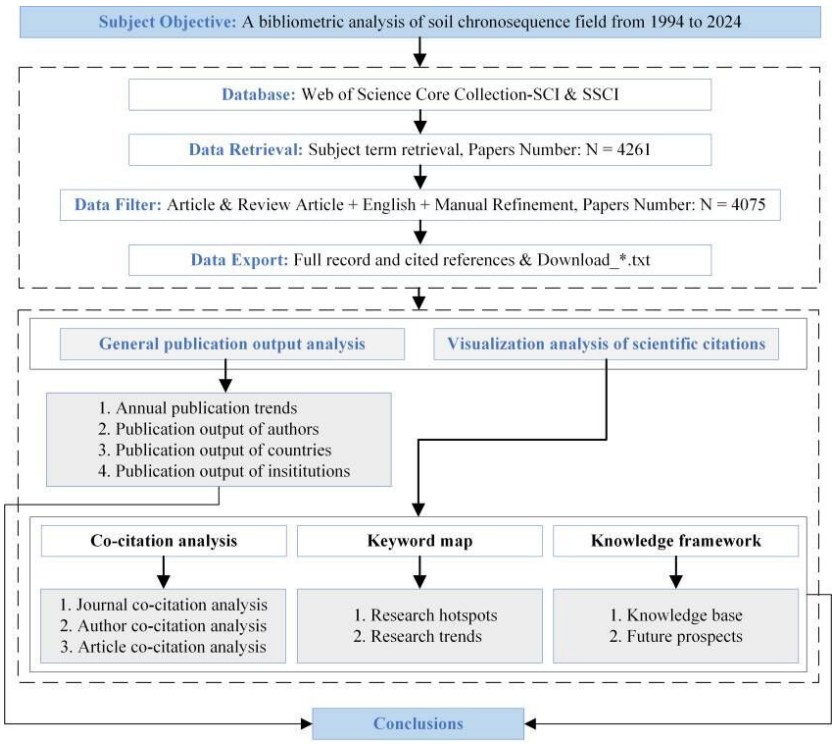


Figure 1. Research workflow chart of this study.

As exhibited in the knowledge maps, the nodes and links form a scientific analysis network, where nodes represent discrete academic entities (including countries, institutions, keywords, authors, and references), while links between nodes describe the degree of co-occurrence or co-citation relationships between these entities. Node size is proportional to the citation or occurrence frequency of the represented entity, with a larger size indicating a higher scholarly impact. The width of a link corresponds to the connection strength (weighted by co-citation counts), the length inversely reflects association proximity, and the color gradient (from cool to warm hues) indicates the chronological emergence of linkages relative to the analyzed time slices [38]. Network analysis was modulated by the G-index scaling factor k, where higher k values increase the node density by retaining more low-frequency entities [39]. To quantify the importance of the nodes in the network, their centrality was estimated, with the obtained values ranging from 0 to 1. The higher the centrality, the stronger the correlation and the greater the importance of the index [40]. When the centrality values of nodes exceed 0.1, they are classified as pivotal pivots, often bridging disparate research clusters. Burst detection within CiteSpace allows for the identification of keywords that show a significant increase in usage over a specific period, pinpointing emerging research hotspots; in particular, this function pinpoints terms

with sudden prominence, offering insights into evolving trends and potential frontiers in the field.

3. Results

3.1. Analysis of Annual Publications

This study was based on data collected from the WoSCC database, which is known for its comprehensive research capabilities. A total of 4075 soil chronosequence publications were analyzed from 1994 to 2024, averaging approximately 131 articles annually. Overall, the number of publications exhibited a constant increase. Soil chronosequence research can be generally categorized into three stages: the initial stage, the development stage, and the booming stage (Figure 2). The initial stage (1994–2005) accounted for roughly 13.8% of the total publications on soil chronosequences. These early studies focused on the pedogenic process and application of dating methods such as Rb-Sr isotope dating [41,42]. These studies laid the theoretical foundations for future studies on soil development and enhanced the understanding of pedogenesis.

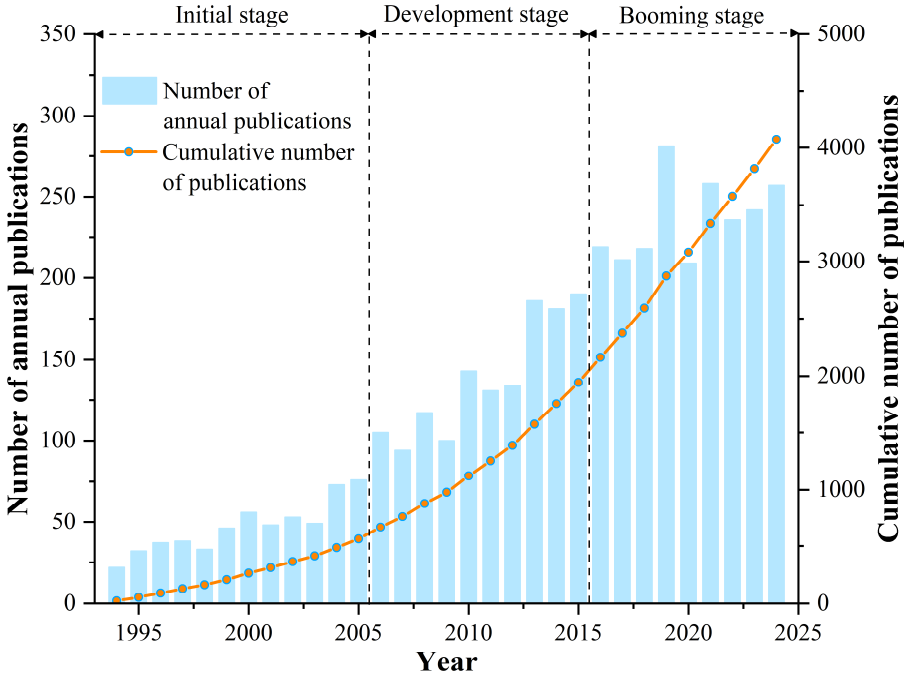


Figure 2. Annual distribution of publications on soil chronosequences from 1994 to 2024.

Figure 2 shows that publications increased continuously during the development stage (2006–2015), accounting for 33.9% of the total publications. This increase could be explained by the growing concerns relating to soil science and environmental science. The rapid economic growth during this period exacerbated issues such as soil degradation, food security, and climate change. Soil chronosequence studies gained prominence as a tool to address these challenges, elucidating soil carbon dynamics and the impacts of land-use on soil quality [43]. Since 2016, the field has entered the "booming stage", with the number of articles increasing steadily. The number of articles exceeded 200 per year for the first time in 2016, reaching its peak in 2019 with 281. Between 2016 and 2024, 52.3% of all articles in this field were published. The booming stage (2016–2024) reflects a surge in research activity, fueled by technological advancements and the alignment of soil science with global sustainability agendas, such as the UN SDGs and the Paris Agreement [44].

3.2. Analysis of Authors, Countries, and Institutions

A total of 14,324 authors participated in research involving soil chronosequences. This study picked out the top 10 authors in terms of their impact, combined total citations, H-index, and domain, as depicted in Table 1. Wardle David A. emerged as the most influential researcher, with his work on microbial-mediated pedogenic feedbacks in chronosequences accumulating 67,519 citations, predominantly having been published in high-impact journals. Notably, although Lal Rattan (USA) had the highest total citations and H-index, he ranked second, as his research mainly focuses on soil carbon sequestration and its role in mitigating climate change. Most of the top 10 authors were from developed countries, except for Han Xinhui and Wu Yanhong, who were from China. This disparity indicates that developed countries have made substantial investments in research related to soil chronosequences. Furthermore, China also places a significant emphasis on this field compared to other developing countries, reflecting its commitment to advancing scientific research in this area. High-impact authors tend to focus on globally relevant themes (e.g., soil carbon sequestration and its role in mitigating global climate change by Rattan Lal, H-index = 131), while the contributions of those in developing countries centered on localized systems (e.g., China's loess hilly region and alpine glacial area).

Table 1. Top 10 authors in soil chronosequence research ranked by impact, combined total citations, H-index, and domain.

Rank	Author	Country	Total Citations *	H-Index *	Key Contribution Domain
1	Wardle, David A	Sweden	67,519	103	Microbial-mediated pedogenic feedbacks in glacial retreat chronosequences
2	Lal, Rattan	USA	74,843	131	Soil carbon sequestration and its role in mitigating climate change
3	Kuzyakov, Yakov	Germany	58,826	112	Carbon flux partitioning across alluvial soil chronosequences
4	Lambers, Hans	Australia	39,727	100	Phosphorus bioavailability dynamics in nutrient-depleted dune chronosequences
5	Turner, Benjamin L	Korea	28,341	87	Phosphorus fractionation mechanisms in tropical rainforest chronosequences
6	Chadwick, Oliver A	USA	21,936	77	Silicate weathering kinetics and mineral transformation in millennial-scale chronosequences
7	Richter, Daniel D	USA	11,769	58	Anthropogenic acceleration of soil erosion and carbon loss in agricultural chronosequences
8	Frouz, Jan	Czechia	8969	46	Ecological succession and soil organic matter recovery in post-mining chronosequences
9	Han, Xinhui	China	5864	44	Responsiveness of soil carbon, nitrogen, and bacterial communities to afforestation in the loess hilly region
10	Wu, Yanhong	China	3649	32	Permafrost thaw-driven soil development in alpine glacial forefield chronosequences

* Total citations and H-index were collected from the Web of Science Core Collection.

To explore global scholarly collaboration, we analyzed the author network in this field (Figure 3). It was observed that Lambers Hans had a strong cooperation relationship with Wu Yanhong from China and Turner Benjamin L. from Gyeongsang National University, Republic of Korea, while Wardle David A. was also found to collaborate with Turner Benjamin L. from the Republic of Korea and Fang Jingyun from China. This im-

plies that these scholars have built strong collaborative relationships in the field of soil chronosequence studies. Their cooperative work has mainly focused on the biogeochemical process of nutrient mobilization during pedogenesis and primary succession along chronosequences, successional trajectories of soil microbiomes, and plant acquisition of nutrients along chronosequences [45–48].

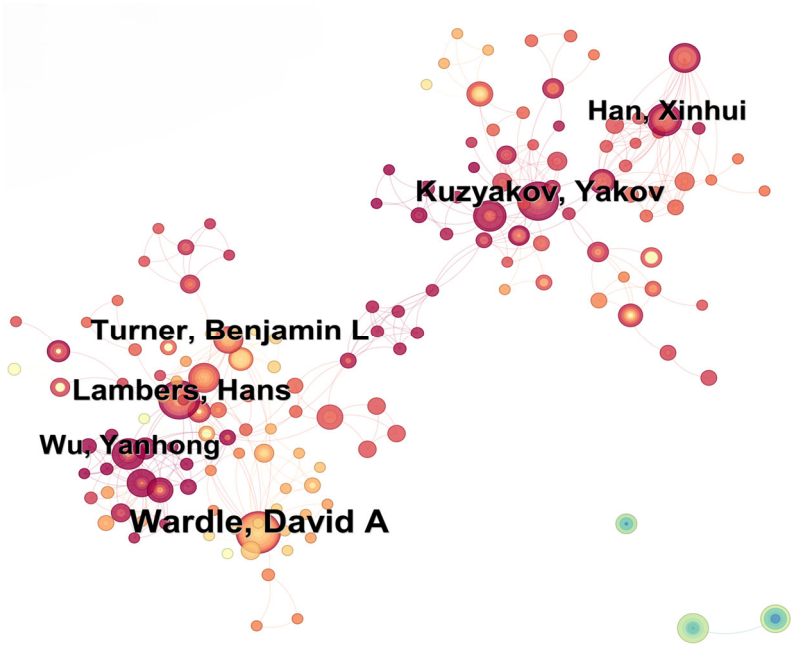


Figure 3. Mapping of author network in soil chronosequence research from 1994 to 2024.

To explore global contributions and collaboration, we analyzed literature from 796 countries active in soil chronosequence research. The top 10 most productive countries are listed in Table 2. The USA led research in this field, with the most publications at 1287. Chinese publications ranked second, with 1093 publications, followed by Germany (376), Canada (312), Australia (232), and France (213). The other countries have published fewer than 200 articles; however, some of them exhibited high centrality, such as Brazil (0.09) and Switzerland (0.08).

Table 2. Top 10 countries in soil chronosequence research (1994–2024) ranked by publication count.

Rank	Country	Publication	Centrality	Year *
1	USA	1287	0.34	1994
2	CHINA	1093	0.19	1996
3	GERMANY	376	0.19	1996
4	CANADA	312	0.07	1994
5	AUSTRALIA	232	0.14	1998
6	FRANCE	213	0.33	1995
7	UK	186	0.07	1994
8	BRAZIL	184	0.09	1994
9	SPAIN	160	0.03	1994
10	SWEDEN	1287	0.34	1994

* "Year" represents the earliest publication year in which the term was used in the country.

A network map of countries based on the collected literature was constructed, as shown in Figure 4, which consisted of 117 nodes and 906 links. The USA peaked with the highest centrality (0.34), followed by France (0.33), Germany and China (0.19), Australia (0.14), Brazil (0.09), and Switzerland (0.08). The USA has cooperated with almost all the

other countries, including Germany, Canada, the UK, China, and Spain. China has also established close cooperation with many countries such as Switzerland, Spain, the USA, and France. These results indicated that the USA has contributed the most to the publications and that it also exhibits significant influence in the collaborative network.

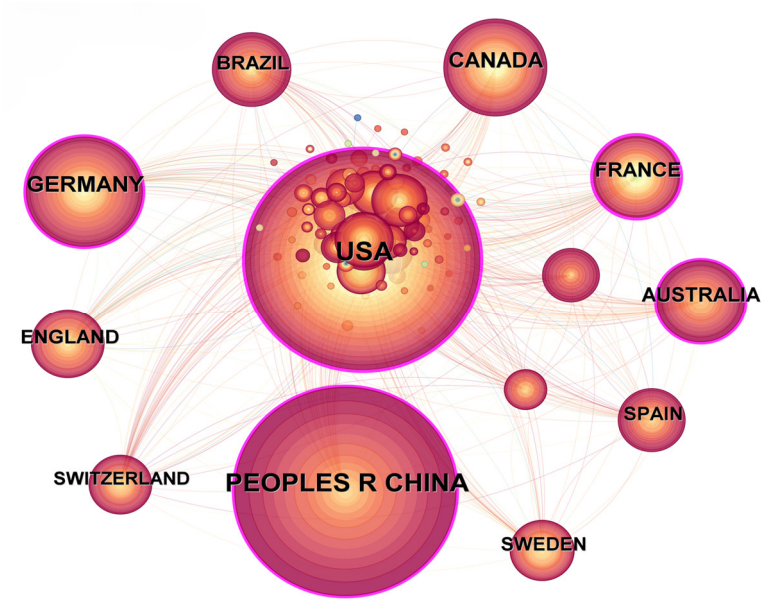


Figure 4. Collaboration network of countries in terms of soil chronosequence articles published from 1994 to 2024.

The analysis of the collected literature indicated that 9717 institutions contributed to soil chronosequence publications. The top 10 most productive institutions are listed in Table 3. From 1994 to 2024, the Chinese Academy of Sciences was noted as having published a notable portion of articles, representing approximately 13.3% of all articles published in this context. Among the ten leading institutions, four were from China, collectively accounting for 24.5% of the total articles. Three USA institutions contributed about 10.2% of the total publications. Meanwhile, the institutions coming from France and Sweden together contributed only 7.7% of these articles. The investments into soil chronosequence research made by China are likely influenced by various motivations, including the essential requirement for ensuring food security as well as maintaining the quality of soil. It is well known that the nation produces a significant portion, roughly 25%, of the global food while having just about 10% of the land that is arable, which presents many challenges related to sustainable agricultural practices [49].

Table 3. Top 10 institutions in soil chronosequence research (1994–2024) ranked by publication count.

Rank	Institution	Publication	Percentage	Centrality	Year *	Country
1	Chinese Academy of Sciences	541	13.3%	0.21	1996	China
2	University of California	192	4.71%	0.19	1995	USA
3	Northwest A&F University	184	4.52%	0.03	2011	China
4	University of Chinese Academy of Sciences	178	4.37%	0.03	2010	China
5	United States Department of Agriculture (USDA)	127	3.12%	0.07	1995	USA
6	Swedish University of Agricultural Sciences	107	2.63%	0.13	1996	Sweden
7	National Research Institute for Agriculture, Food and Environment (INRAE)	102	2.50%	0.06	1995	French
8	Centre National de la Recherche Scientifique (CNRS)	101	2.48%	0.12	1995	French
9	United States Department of the Interior	97	2.38%	0.03	1997	USA
10	Institute of Soil & Water Conservation (ISWC)	94	2.31%	0	2011	China

* "Year" represents the earliest publication year in which the term was used by the institution.

A map illustrating the networks among institutions involved in this research field is shown in Figure 5. It is composed of 574 nodes with 3331 connections in total. Figure 5 shows that the Chinese Academy of Sciences was the largest node, appearing the most frequently, which highlights its active collaborations across institutions. The Chinese Academy of Sciences engages in cooperative efforts with numerous institutions such as the CNRS, USDA, University of California, and ISWC. In terms of centrality, the Chinese Academy of Sciences stands out with the highest rating of 0.21. Other institutions, such as the University of California along with the Swedish University of Agricultural Science and the CNRS, also displayed high centrality values, in the range of approximately 0.12 to 0.19. The centrality of other institutions remained below 0.1, suggesting that their significance is moderate compared with the leading institutions.

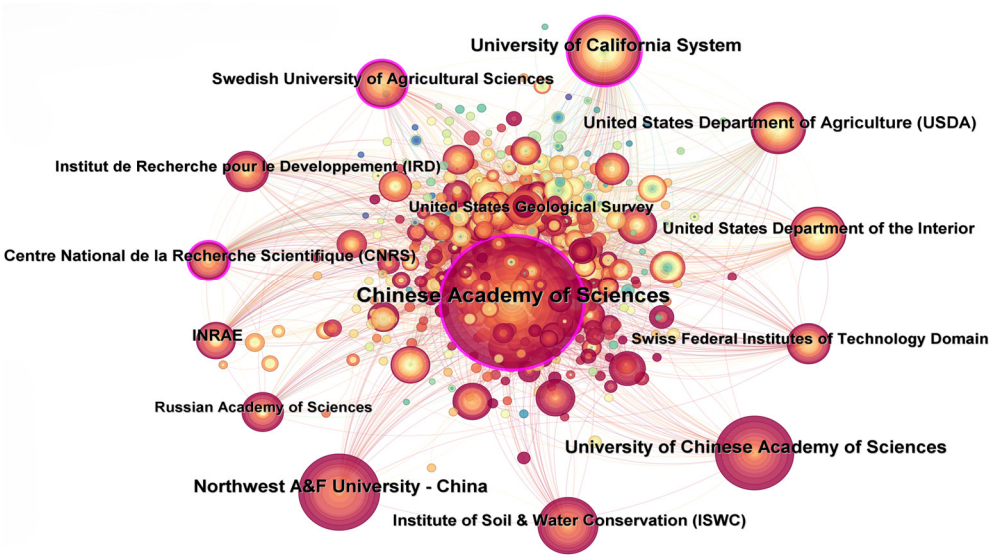


Figure 5. Collaboration network of institutions in terms of soil chronosequence articles published from 1994 to 2024.

3.3. Co-Citation Analysis of Hot Journals, Authors, and Articles

From 1994 to 2024, a total of 500 journals published studies on soil chronosequences, and the top 10 most cited journals are listed in Figure 6. Geoderma (IF = 5.6) led the field with 2258 citations. The journal emphasizes the importance of comprehensive soil science research, covering areas such as soil water, environmental chemistry, hydrology, mineralogy, and interdisciplinary studies examining dynamic soil processes and their spatiotemporal dynamics.

This was followed by Soil Biology and Biochemistry (2242 counts, IF = 9.8), Plant and Soil (2109 counts, IF = 3.9), Ecology (2012 counts, IF = 4.4), Soil Science Society of America Journal (1942 counts, IF = 2.4), Nature (1922, IF = 50.5), Science (1745, IF = 44.8), and Global Change Biology (1668, IF = 10.8). Notably, Nature, Science, and Global Change Biology, with their high-impact factors, underscore the considerable influence of soil chronosequences. The high citation counts and impact factors of these journals highlight the significance of soil chronosequence research, which attracts interdisciplinary attention spanning fields such as soil science, environmental science, and ecology.

Table 4 lists the top eight highest-centrality journals, from which it can be observed that both Catena and Vegetatio had the highest centrality with 0.04, followed by another six journals with a centrality of 0.03. This suggests that these journals have built strong interconnections within the academic network in this field, despite their relatively fewer citations (Table 4). Accordingly, both citation frequency and centrality play crucial roles in assessing a journal's academic importance.

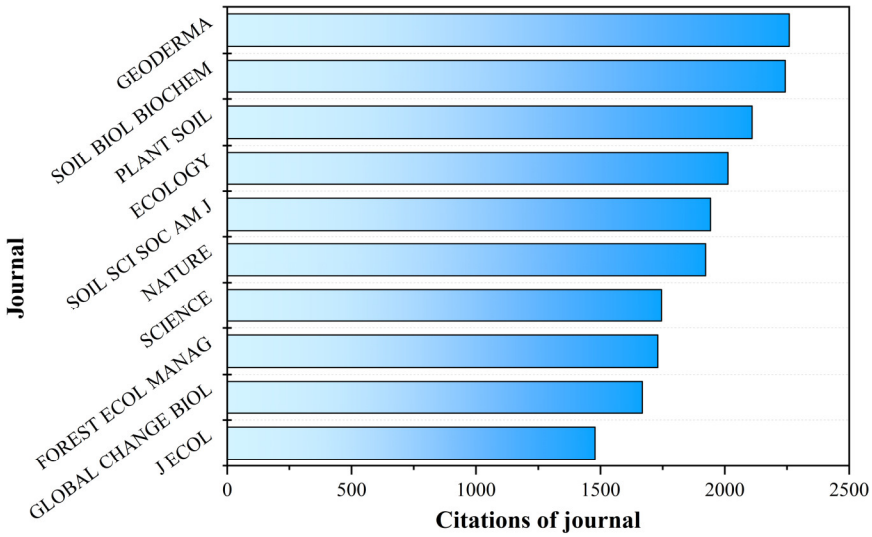


Figure 6. Top 10 most cited journals publishing soil chronosequence articles from 1994 to 2024.

Table 4. Top 8 journals in soil chronosequence research (1994–2024) ranked by centrality.

Rank	Journal	Citation	Centrality	Year *
1	CATENA	1313	0.04	1994
2	VEGETATIO	295	0.04	1994
3	APPL ENVIRON MICROB	696	0.03	1994
4	GEOCHIM COSMOCHIM AC	606	0.03	1995
5	J SOIL SCI	482	0.03	1994
6	GEOMORPHOLOGY	449	0.03	1995
7	AM NAT	353	0.03	1994
8	ANNU REV ECOL SYST	320	0.03	1994

* "Year" represents the earliest publication year in which the term was used in the journal.

The top 10 most cited authors in soil chronosequence research from 1994 to 2024 are listed in Table 5. The authors with a large number of citations include Vitousek (530) and Walker (415) from the USA, as well as Wardle from Sweden (411). Their research has mainly focused on ecosystem dynamics, biogeochemical cycles, plant–soil interactions, and the impacts of human activities on these systems [50–52]. Lal Rattan is also among the top 10 authors, concentrating on sustainable agriculture, soil carbon sequestration, and agricultural management practices to address climate change and enhance global food security [53]. This implies that a good understanding of soil carbon dynamics will further enhance soil chronosequence research.

Table 5. Top 10 authors in the field of soil chronosequence research (1994–2024) ranked by citations.

Rank	Author	Country	Citation *	Centrality	Year *
1	Vitousek, Peter M.	USA	530	0.08	1994
2	Walker, Lawrence R.	USA	415	0.03	1995
3	Wardle, David A.	Sweden	411	0.05	2001
4	Lal, Rattan	USA	390	0.03	2003
5	Six, Johan	Switzerland	354	0.04	2006
6	Fierer, Noah	USA	293	0.04	2008
7	F. Stuart Chapin III	USA	276	0.07	1995
8	Schlesinger, William H.	USA	262	0.04	1997
9	Davidson, Eric A.	USA	253	0.05	1994
10	Bardgett, Richard D.	UK	252	0.05	2002

* "Year" represents the earliest publication year in which the term was used by the author; Citation refers to the citation frequency of each author from 1994 to 2024.

The analysis of the top 10 publications ranked by citations (Table 6) revealed distinct thematic clusters that have shaped soil chronosequence research. For instance, Walker's 2010 study "The use of chronosequences in studies of ecological succession and soil development" (81 citations) [45], published in the Journal of Ecology, established a foundational framework for linking soil development to ecological succession. This work explored how soil chronosequences serve as proxies for studying ecosystem succession and soil development. The key findings are that soil development lags plant succession by 50–200 years in post-glacial systems and that phosphorus availability emerges as a critical limiting factor during mid-succession (100–500 years). By framing chronosequences as tools for studying long-term ecosystem trajectories, Walker's study laid the groundwork for subsequent investigations into climate change impacts on soil–plant systems. Similarly, Peltzer's 2010 article "Understanding ecosystem retrogression" (46 citations) [51] in Ecological Monographs advanced the concept of ecosystem retrogression—a process where ecosystems gradually degrade due to environmental stressors. The study used chronosequences to demonstrate how soil nutrient depletion and microbial community shifts drive ecosystem decline, highlighting the utility of chronosequences in predicting ecosystem resilience.

Table 6. Top 10 publications in soil chronosequence research (1994–2024) ranked by citations.

Rank	Title	Reference	Citation	Centrality	Year *	Journal
1	The use of chronosequences in studies of ecological succession and soil development	[45]	81	0.01	2010	J ECOL
2	Soil bacterial community dynamics reflect Changes in plant community and soil properties during the secondary succession of abandoned farmland in the Loess Plateau	[34]	48	0.06	2016	SOIL BIOL BIOCHEM
3	Understanding ecosystem retrogression	[51]	46	0.04	2010	ECOL MONOGR
4	Total carbon and nitrogen in the soils of the world	[54]	46	0.35	2014	EUR J SOIL SCI
5	Divergent assemblage patterns and driving forces for bacterial and fungal communities along a glacier forefield chronosequence	[55]	35	0.02	2018	SOIL BIOL BIOCHEM
6	Chemical and biological gradients along the Damma Glacier soil chronosequence, Switzerland	[56]	35	0.04	2011	VADOSE ZONE J
7	Conceptualizing soil organic matter into particulate and mineral-associated forms to address global change in the 21st century	[57]	31	0.01	2020	GLOBAL CHANGE BIOL
8	Bacterial, archaeal and fungal succession in the forefield of a receding glacier	[58]	31	0.05	2012	MICROB ECOL
9	Foliar nutrient concentrations and resorption efficiency in plants of contrasting nutrient-acquisition strategies along a 2-million-year dune chronosequence	[46]	29	0.02	2014	J ECOL
10	Persistence of soil organic matter as an ecosystem property	[59]	28	0.01	2011	NATURE

* "Year" represents the publication year of the literature.

Turning to microbial ecology, the 2016 study by Zhang et al. "Soil bacterial community dynamics reflect changes in plant community and soil properties during the secondary succession of abandoned farmland in the Loess Plateau" (48 citations) [34] in Soil Biology & Biochemistry illustrated the role of chronosequences in tracking microbial responses to land-use changes. By analyzing bacterial communities across a chronosequence of aban-

doned farmland, the authors showed how soil microbial diversity and functionality evolve alongside vegetation succession, underscoring the importance of microbial processes in soil development. Soil organic matter (SOM) emerges as another critical theme. In the 2020 article "Conceptualizing soil organic matter into particulate and mineral-associated forms to address global change in the 21st century" [57] in Global Change Biology (IF = 10.8), a novel framework for categorizing SOM fractions was proposed, arguing that this distinction is vital for predicting SOM stability under climate change. Meanwhile, the 2011 paper "Persistence of soil organic matter as an ecosystem property" published in Nature (IF = 50.5) [59] highlighted the role of soil mineralogy and microbial activity in determining SOM persistence, positioning chronosequences as essential tools for understanding long-term carbon sequestration.

These studies, published in influential journals such as the Journal of Ecology and Soil Biology & Biochemistry, reflect the journals' focus on integrative ecological and soil science research. For example, Journal of Ecology publishes foundational studies linking soil chronosequences to ecosystem theory (e.g., Walker's framework). Soil Biology & Biochemistry has consistently published cutting-edge work on microbial mechanisms in soil development (e.g., Loess Plateau and glacier forefield studies) [34,55]. Similarly, Nature and Global Change Biology have prioritized research with global implications, such as SOM stability under climate change, amplifying the visibility of studies linking soil chronosequences to global challenges [57,59]. Collectively, the core thematic areas—ecological succession, microbial dynamics, and SOM stability—demonstrate that soil chronosequences provide a multifaceted framework to investigate intricate, time-dependent interactions among pedogenic processes, biotic communities, and environmental perturbations. Future research could capitalize on these foundations by exploring how chronosequences can guide soil management strategies aligned with global sustainability goals.

3.4. Analysis of Keyword Co-Occurrence, Clustering, and Evolution

To explore the research hotspots, this study constructed the co-occurrence map of the keywords used in soil chronosequence research, as shown in Figure 7. There are 872 keywords occurring in the articles involving soil chronosequences, among which 22 keywords had a frequency of more than 200 (Figure 7).

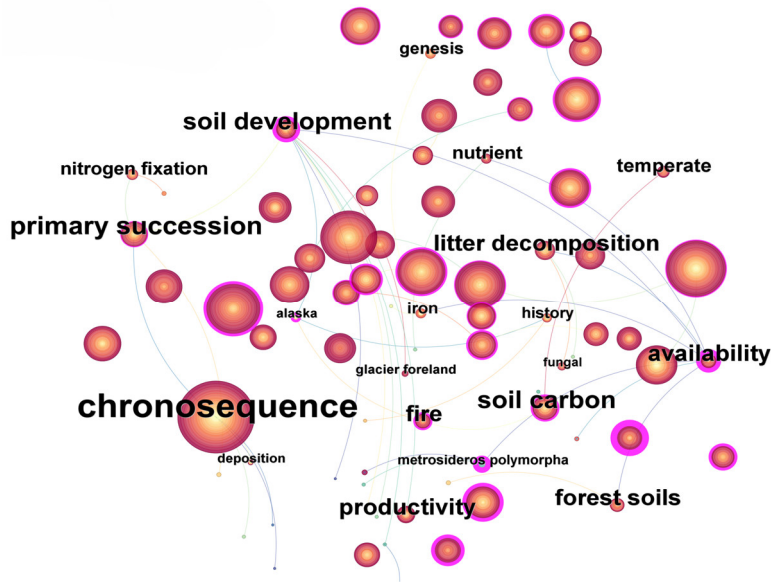


Figure 7. Mapping of keyword co-occurrence in soil chronosequence research from 1994 to 2024.

The burst analysis results for keywords used from 1994 to 2024, along with their strength and occurrence timespan, are shown in Figure 8. These keywords represent emerging research topics in the soil chronosequence field and can be used to track the evolution in this field. In the inception stage, research was primarily focused on foundational aspects of soil chronosequences, such as soil development, nitrogen mineralization, and nitrification [60,61]. The keywords "California" and "New Zealand" highlight regional studies central to understanding soil development in specific ecosystems. Strong citation bursts for "soil chronosequence" and "ecosystems" indicate the significance of these terms early in the research period. Then, the research shifted its focus to specific processes and components of soil chronosequences. Keywords such as "organic matter dynamics" and "turnover" imply growing interest in nutrient cycling, while "forest succession" and "ecosystem services" reflect growing interest in ecosystem-level changes [50,62]. The citation bursts for "organic matter dynamics" and "respiration" indicate the importance of carbon cycling as an issue in soil chronosequence research. Since 2010, research has increasingly focused on microbial communities in soil chronosequences, highlighted by high citation bursts for the keywords "bacterial community", "fungal community", and "soil microbial community". These publications have emphasized the role of microbial communities in soil chronosequences and their impact on ecosystem services and nutrient cycling [63].

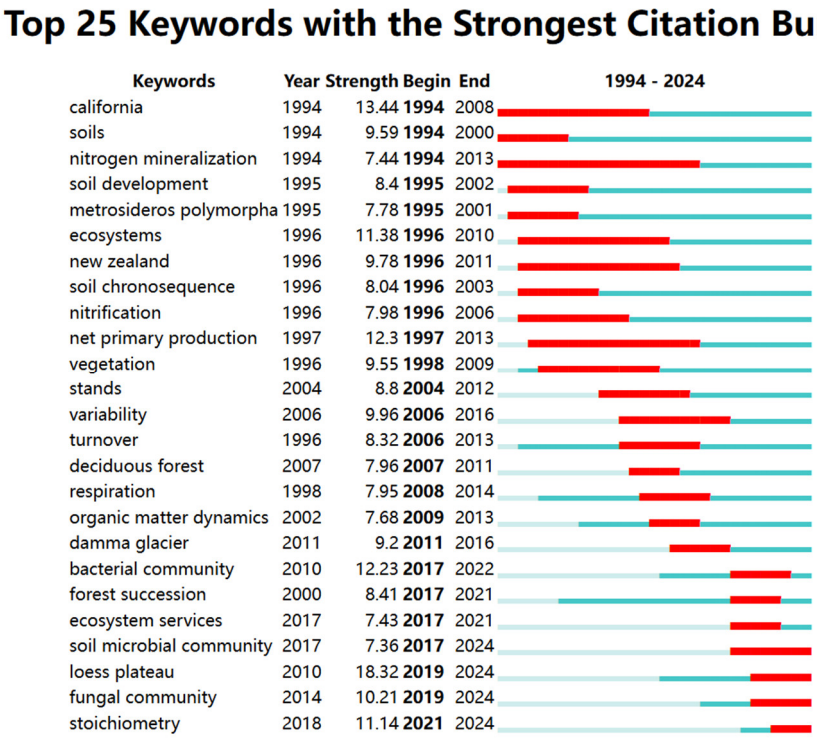


Figure 8. Top 25 keywords with the strongest citation bursts in soil chronosequence research from 1994 to 2024.

The keyword clustering map visualizes significant research topics in the soil chronosequence field, as presented in Figure 9. The largest cluster, soil chronosequence (#0), underscores the importance of understanding the formation and development of soil over time, which is fundamental for predicting soil behavior under different environmental scenarios and managing soil resources sustainably. Other notable clusters include soil organic carbon (#1), which is crucial for carbon sequestration and mitigating climate change, and bacterial community (#4), which emphasizes the role of soil bacteria in nutrient cycling and ecosystem health.

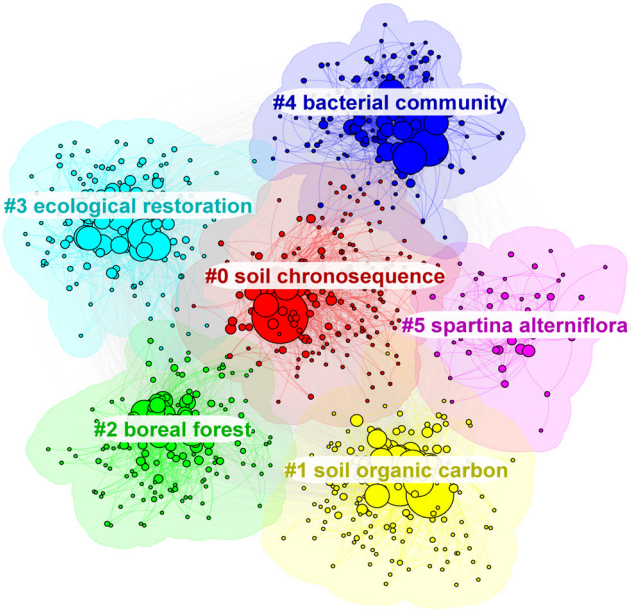


Figure 9. Cluster map of keywords used in soil chronosequence research from 1994 to 2024.

Based on the cluster map analysis, we extracted the top six clusters to further explore the hotspots in this field (Table 7). The most important keywords in the cluster of "soil chronosequence" were weathering, pedogenesis, evolution, and soil development. Within this cluster, researchers primarily researched soil chronosequences, examining soil development, weathering, and soil property evolution [64,65]. For instance, Cheng et al. (2009) studied the chronosequential changes of selected pedogenic properties in paddy versus non-paddy soils in Cixi, Zhejiang, China [19]. They found that paddy soils had higher soil organic carbon, clay, and total Fe in the topsoil but lower Mn than non-paddy soils, showing that paddy management significantly affects soil formation [19]. The most common keywords under the "soil organic carbon" cluster were SOM, carbon sequestration, and soil quality. Over time, research has evolved from general studies on the properties of soil organic carbon to deeper explorations of its role in climate change mitigation and soil fertility enhancement. Recent studies have increasingly focused on the processes of soil organic carbon decomposition and accumulation, as well as the contributions of soil aggregates and microbial biomass to these processes [17,21]. A study by Aydın and Rages (2024) revealed the dynamics of soil respiration and organic carbon changes in Pinus nigra forests in Kastamonu, Turkey [65]. They measured soil respiration, temperature, and moisture across three age classes using an automated dynamic survey chamber (Li-8100A) over a year. The study found that soil respiration rose with stand age, then stabilized, while soil organic carbon showed no significant age-related changes in mineral soil layers but increased in forest litter.

The prevalent keywords in the "boreal forest" and "ecological restoration" groups were soil respiration, fire, soil temperature, climate change, secondary succession, and functional diversity. The research focus has shifted from characterizing individual factors such as soil respiration and temperature to investigating their interactive effects on ecosystem function and soil formation. Recently, researchers have increasingly emphasized how these parameters interact with climate change and disturbance regimes, such as fires, to shape ecosystem resilience and recovery [14,66]. The main keywords in the cluster "bacterial community" were microbial community, soil microbiome, and primary succession. Research in this cluster has evolved from characterizing the composition of microbial communities to understanding its functional roles in nutrient cycling and the succession of vegetation. Recent studies have increasingly integrated multi-omics approaches to explore

the mechanisms through which microbial communities drive soil processes and ecosystem dynamics [67–69].

Table 7. Top 6 clusters of keywords and the keywords included in these clusters obtained from soil chronosequence research from 1994 to 2024.

ID	Cluster Name	Size	Main Keywords (Top 5)
0	soil chronosequence	182	soil chronosequence; weathering; pedogenesis; evolution; soil development
1	soil organic carbon	173	soil organic carbon; soil organic matter; carbon sequestration; sequestration; soil quality
2	boreal forest	158	boreal forest; soil respiration; fire; soil temperature; climate change
3	ecological restoration	154	ecological restoration; secondary succession; species richness; functional diversity; succession
4	bacterial community	149	bacterial community; diversity; primary succession; microbial community; soil microbiome
5	spartina alterniflora	47	spartina alterniflora; blue carbon; mangrove forest; heavy metals; chronosequence

3.5. Knowledge Framework

By integrating the keyword co-occurrence, clustering, and timeline map results in soil chronosequence research, we categorized the hotspots over the past three decades into three key topics. The first one was nutrient cycling processes along soil chronosequences (including keywords such as soil age, soil organic carbon, nitrogen, phosphorus, and nutrient availability). Soil age plays a critical role in nutrient cycling, including nutrient transformation and availability, and it affects the activities of key enzymes [70–72]. It also influences the abundance of microbial functional genes, which, in turn, affects plantation productivity by modulating the supply of bio-available nitrogen [73,74]. Young soils have low available nitrogen and phosphorus, while intermediate-aged soils have greater nitrogen and phosphorus; meanwhile, the oldest soils have low phosphorus and cation availability but high nitrogen availability [52]. Some studies have reported that older soils have greater stable organic carbon due to increased microbial activity [16,69]. Soil respiration, which is pivotal in carbon cycling, varies with soil age. This variation is due to differences in the microbial community and the soil organic carbon decomposition rate [75]. Soil age also influences nitrogen cycling, with young soils generally undergoing more nitrogen fixation, while older soils present higher rates of ammonification and nitrification [75,76]. Phosphorus availability rises with soil age due to the increased decomposition of organic matter and microbial activity [26,28]. Nutrient availability serves as a key soil fertility indicator, as mature soils with higher nutrient availability generally enhance plant productivity. Nutrient loss from erosion and leaching increases with soil age, which highlights the need for sustainable soil management. Future research should prioritize long-term studies and sustainable practices to maintain nutrient balance and boost soil health.

The second topic focuses on vegetation succession and ecological restoration along soil chronosequences, where the keywords consisted of vegetation succession, ecological restoration, species richness, and functional diversity. Vegetation succession and ecological restoration are strongly related to soil age, as variations in soil properties and microbial communities play important roles in controlling plant dynamics and ecosystem recovery [23,30,77]. In younger soils, pioneer species that can tolerate harsh conditions and contribute to soil development are likely to dominate [47]. These species, such as nitrogen-fixing plants, enhance the fertility of the soil and make the environment more favorable for

the growth of later successional species [45]. With the increasing age of soils, increased organic matter and nutrient accumulation support the growth of more advanced and diverse vegetation communities, enabling the transition from early to late successional stages [31]. Ecological restoration can gain insights by examining vegetation succession dynamics across soil chronosequences. For example, studies have proven that the restoration of degraded ecosystems through afforestation or reforestation can accelerate the development of soil as well as soil quality [23]. Diversifying plant functional groups is essential for identifying soil characteristics and microbial communities, as these factors influence ecosystem resistance and functioning [77]. Restoration strategies such as reintroducing native species and planting cover crops can restore soil health and promote plant community recovery.

The third topic was soil microbial community dynamics along chronosequences (appearing with keywords such as primary succession, bacterial community, fungal community, and soil microbiome). Soil microbial communities play a key role in ecosystem functions, and their structure and activity are significantly regulated by soil age [18,66,78]. As soil develops over time, microbial communities undergo substantial shifts in composition, diversity, and function, mirroring the intricate relationships between biological processes and soil properties. Microbial diversity generally increases with soil age, as older soils are more stable and have more available nutrients to support microbial growth. For example, fungi and bacteria diversity is higher in mature and over-mature forests than in young forests, reflecting that soil maturation promotes more complex microbial communities [25]. Diversity shifts often drive soil property changes, such as higher organic matter content and nutrient availability, boosting microbial activity and ecosystem functions [68]. Bacterial communities exhibit high sensitivity to soil age, with dominant phyla shifts occurring across soil development stages. For example, proteolytic soil bacteria involved in nitrogen cycling display more diverse responses to soil conditions [79,80]. Similarly, fungal communities, especially mycorrhizal fungi, play a critical role in nutrient uptake and soil structure formation, and their abundance and diversity tend to increase with soil age [63,81]. These fungi form symbiotic relationships with plant roots, facilitating nutrient cycling and enhancing soil stability [21]. Microbial processes such as enzyme synthesis and decomposition also change with soil age [82]. Enzymes such as dehydrogenase, catalase, and phosphatase, which are responsible for nutrient cycling, are generally more active in older soils, reflecting greater microbial metabolism and nutrient turnover. This increased activity can lead to the more efficient decomposition of organic matter and greater nutrient availability for plant uptake, enhancing overall ecosystem productivity [68].

Building on our comprehensive analysis of soil chronosequence research, we observed various research dimensions and hotspots that are dynamically evolving. Therefore, a comprehensive trend map based on previous figures and keywords is presented (Figure 10). The knowledge base of this field has covered a wide range of topics, including soil chronosequences, ecological restoration, organic carbon, boreal forests, bacterial communities, Spartina alterniflora, blue carbon, mangrove forests, heavy metals, and chronosequences. These topics have evolved over time, reflecting the development and expansion of research interests in the field. In the period from 1994 to 2005, the research on soil chronosequences was mainly focused on the basic concepts and methodologies related to soil chronosequences (C = 182) [41,42]. This period laid the foundation for subsequent studies by establishing theoretical and methodological frameworks for understanding soil development over time. From 2006 to 2015, the field expanded to include topics such as ecological restoration (C = 154) and organic carbon (C = 173). These topics indicate a growing interest in the ecological implications of soil chronosequence research, particularly in terms of how soil development affects ecosystem services and carbon sequestration [83–86]. In the most recent period from 2016 to 2024, the research has further diversified into ar-

eas such as bacterial communities (C = 149), Spartina alterniflora (C = 47), blue carbon, mangrove forests, heavy metals, and chronosequences. These topics reflect the increasing recognition of the role of soil chronosequences in understanding microbial ecology, coastal ecosystem management, and the impacts of human activities on soil quality and environmental health [87–89]. In conclusion, the intellectual base of soil chronosequence research has evolved significantly from 1994 to 2024, with a growing emphasis on interdisciplinary approaches and practical applications. Future research in this field should continue investigating how soil development interacts with ecosystem dynamics while tackling urgent environmental challenges. Long-term monitoring and advanced technologies, such as remote sensing, GIS, and molecular biology methods, will be crucial to forecast soil dynamics and guide sustainable land management, thereby safeguarding soil quality and ecosystem resilience.

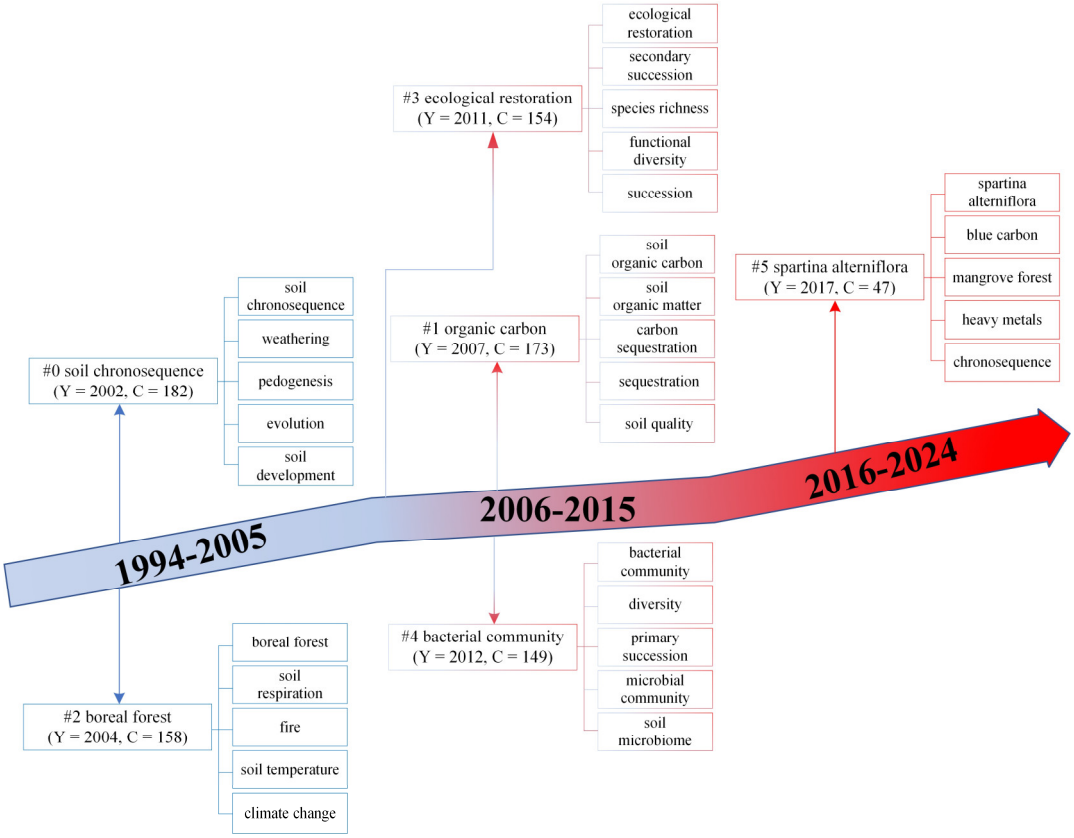


Figure 10. Trend map of the top 6 document co-citation analysis clusters. (#number denotes the cluster ID, where a larger number corresponds to a smaller cluster size. Y represents the publication year of the document, and C signifies the cluster size).

4. Conclusions and Challenges

This study offers a bibliometric analysis of soil chronosequence research published from 1994 to 2024, revealing key insights for future research. The field has received increasing attention, with an increasing number of publications. The USA leads in terms of article count and collaborative influence, while China shows the fastest growth in recent years. The Chinese Academy of Sciences stands out with 13.3% of publications and the highest institutional centrality of 0.21. The journal Geoderma leads the field with 2258 citations, while Soil Biology & Biochemistry and the Journal of Ecology also hold considerable influence and esteemed reputations within this domain. Research hotspots predominantly include nutrient cycling, vegetation succession, ecological restoration, and the dynamics of soil microbial communities. Soil chronosequence research has advanced significantly from

1994 to 2024, with a growing emphasis on interdisciplinary approaches and practical applications. Future studies should focus on how soil development interrelates with ecosystem dynamics while addressing pressing environmental issues.

However, this study has limitations. It relied solely on the WoSCC database, potentially excluding relevant studies from other sources such as Scopus and CNKI. Future analyses should include multiple databases for broader coverage. Additionally, this study focused on articles and reviews in English, overlooking conference reports, books, and non-English publications. Despite these limitations, the analysis results adequately represent current research on soil chronosequences. In summary, this work highlighted major hotspots and trends in soil chronosequence research. Future studies in this line ought to incorporate multiple data sources and methods to develop a more holistic and integrative view of research in soil chronosequences.

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Data Availability Statement: The data presented in this study are available on request from the corresponding author.

Conflicts of Interest: The authors declare no conflicts of interest.

Abbreviations

AM NAT	American Naturalist
ANNU REV ECOL SYST	Annual Review of Ecology Evolution and Systematics
APPL ENVIRON MICROB	Applied and Environmental Microbiology
CATENA	Catena
ECOL MONOGR	Ecological Monographs
EUR J SOIL SCI	European Journal of Soil Science
EUR J SOIL SCI	European Journal of Soil Science
FOREST ECOL MANAG	Forest Ecology and Management
GEOCHIM COSMOCHIM AC	Geochimica et Cosmochimica Acta
GEOMORPHOLOGY	Geomorphology
GLOBAL CHANGE BIOL	Global Change Biology
J ECOL	Journal of Ecology
MICROB ECOL	Microbial Ecology
PLANT SOIL	Plant and Soil
SOIL BIOL BIOCHEM	Soil Biology & Biochemistry
SOIL SCI SOC AM J	Soil Science Society of America Journal
VADOSE ZONE J	Vadose Zone Journal
VEGETATIO	Vegetatio

References

1. Sun, W.; Ye, J.; Lin, H.; Yu, Q.; Wang, Q.; Chen, Z.; Ma, J.; Ma, J. Dynamic characteristics of heavy metal accumulation in agricultural soils after continuous organic fertilizer application: Field-scale monitoring. *Chemosphere* **2023**, *335*, 139051. [CrossRef] [PubMed]
2. Zheng, Y.; Yang, S.; Deng, C. Provenance and climate changes inferred from magnetic properties of the sediments from the lower Yangtze River (China) during the last 130 years. *J. Asian Earth Sci.* **2019**, *175*, 128–137. [CrossRef]

3. Newman, G.S.; Hart, S.C. Shifting soil resource limitations and ecosystem retrogression across a three million year semi-arid substrate age gradient. *Biogeochemistry* **2015**, *124*, 177–186. [CrossRef]
4. Bing, H.; Wu, Y.; Zhou, J.; Sun, H.; Luo, J.; Wang, J.; Yu, D. Stoichiometric variation of carbon, nitrogen, and phosphorus in soils and its implication for nutrient limitation in alpine ecosystem of Eastern Tibetan Plateau. *J. Soil. Sediment.* **2016**, *16*, 405–416. [CrossRef]
5. He, J.B.; Wu, Y.H.; Bing, H.J.; Zhu, H.; Zhou, J. Soil chronosequence derived from landslides on the upper reach of Minjiang River, western China. *J. Mt. Sci.* **2023**, *20*, 1282–1292. [CrossRef]
6. Ninin, J.M.L.; Muehe, E.M.; Kölbl, A.; Mori, A.H.; Nicol, A.; Gilfedder, B.; Pausch, J.; Urbanski, L.; Lueders, T.; Planer-Friedrich, B. Changes in arsenic mobility and speciation across a 2000-year-old paddy soil chronosequence. *Sci. Total Environ.* **2024**, *908*, 168351. [CrossRef]
7. Qiu, L.; Yang, L.; Yu, Z.; Lyu, H.; Zhu, J.; Pan, Y.; Wu, S. Chronosequential changes in soil-related ecosystem services after coastal reclamation: Insights for coastal cropland protection. *Agric. Ecosyst. Environ.* **2024**, *363*, 108877. [CrossRef]
8. Stevens, P.R.; Walker, T.W. The chronosequence concept and soil formation. *Q. Rev. Biol.* **1970**, *45*, 333–350. [CrossRef]
9. Harden, J.W. A quantitative index of soil development from field descriptions: Examples from a chronosequence in central California. *Geoderma* **1982**, *28*, 1–28. [CrossRef]
10. Fu, Q.; Ding, N.; Liu, C.; Lin, Y.; Guo, B. Soil development under different cropping systems in a reclaimed coastal soil chronosequence. *Geoderma* **2014**, *230*, 50–57. [CrossRef]
11. Badía, D.; Martí, C.; Casanova, J.; Gillot, T.; Cuchí, J.A.; Palacio, J.; Andrés, R. A Quaternary soil chronosequence study on the terraces of the Alcanadre River (semiarid Ebro Basin, NE Spain). *Geoderma* **2015**, *241*, 158–167. [CrossRef]
12. Turner, B.L.; Laliberté, E. Soil development and nutrient availability along a 2 million-year coastal dune chronosequence under species-rich Mediterranean shrubland in southwestern Australia. *Ecosystems* **2015**, *18*, 287–309. [CrossRef]
13. Turner-Meservy, C.; Vilmundardóttir, O.K.; Lal, R.; Gísladóttir, G. Soil chemical properties in glacial moraines across a chronosequence influenced by avifauna and volcanic materials: Breiðamerkurjökull, Iceland. *Catena* **2022**, *209*, 105836. [CrossRef]
14. De Marco, A.; Berg, B.; Zarrelli, A.; De Santo, A.V. Shifts in soil chemical and microbial properties across forest chronosequence on recent volcanic deposits. *Appl. Soil Ecol.* **2021**, *161*, 103880. [CrossRef]
15. Rasigraf, O.; Wagner, D. Landslides: An emerging model for ecosystem and soil chronosequence research. *Earth-Sci. Rev.* **2022**, *231*, 104064. [CrossRef]
16. Zhang, H.; Wu, P.; Fan, M.; Zheng, S.; Wu, J.; Yang, X.; Zhang, M.; Yin, A.; Gao, C. Dynamics and driving factors of the organic carbon fractions in agricultural land reclaimed from coastal wetlands in eastern China. *Ecol. Indic.* **2018**, *89*, 639–647. [CrossRef]
17. Wissing, L.; Kölbl, A.; Vogelsang, V.; Fu, J.R.; Cao, Z.H.; Kögel-Knabner, I. Organic carbon accumulation in a 2000-year chronosequence of paddy soil evolution. *Catena* **2011**, *87*, 376–385. [CrossRef]
18. Su, B.; Gao, C.; Ji, J.; Zhang, H.; Zhang, Y.; Mouazen, A.M.; Shao, S.; Jiao, H.; Yi, S.; Li, S. Soil bacterial succession with different land uses along a millennial chronosequence derived from the Yangtze River flood plain. *Sci. Total Environ.* **2023**, *908*, 168531. [CrossRef]
19. Cheng, Y.Q.; Yang, L.Z.; Cao, Z.H.; Ci, E.; Yin, S. Chronosequential changes of selected pedogenic properties in paddy soils as compared with non-paddy soils. *Geoderma* **2009**, *151*, 31–41. [CrossRef]
20. Lair, G.J.; Zehetner, F.; Hrachowitz, M.; Franz, N.; Maringer, F.J.; Gerzabek, M.H. Dating of soil layers in a young floodplain using iron oxide crystallinity. *Quat. Geochronol.* **2009**, *4*, 260–266. [CrossRef]
21. Mardhiah, U.; Caruso, T.; Gurnell, A.; Rillig, M.C. Just a matter of time: Fungi and roots significantly and rapidly aggregate soil over four decades along the Tagliamento River, NE Italy. *Soil Bio. Biochem.* **2014**, *75*, 133–142. [CrossRef]
22. Bronić, I.K.; Barešić, J.; Sironić, A. Application of 14C method to chronology of the Croatian Dinaric karst—A case of the Plitvice Lakes. *Radiocarbon* **2022**, *64*, 805–817. [CrossRef]
23. Zheng, H.; Liu, D.; Yuan, J.; Li, Y.; Li, J.; Miao, Y.; Chen, Z.; He, T.; Ding, W. Wetland restoration after agricultural abandonment enhances soil organic carbon efficiently by stimulating plant-rather than microbial-derived carbon accumulation in Northeast China. *Catena* **2024**, *241*, 108077. [CrossRef]
24. Wang, J.; Zhuang, S.; Zhu, Z. Soil organic nitrogen composition and mineralization of paddy soils in a cultivation chronosequence in China. *J. Soils Sediments* **2017**, *17*, 1588–1598. [CrossRef]
25. Jiang, S.; Xing, Y.; Liu, G.; Hu, C.; Wang, X.; Yan, G.; Wang, Q. Changes in soil bacterial and fungal community composition and functional groups during the succession of boreal forests. *Soil Biol. Biochem.* **2021**, *161*, 108393. [CrossRef]
26. Luo, Y.J.; Huang, L.M.; Yuan, D.G. Characteristics and controls of inorganic and organic phosphorus transformation during long-term paddy soil evolution. *Soil Tillage Res.* **2022**, *224*, 105524. [CrossRef]
27. Chen, Y.; Chi, J.; Lu, X.; Cai, Y.; Jiang, H.; Zhang, Q.; Zhang, K. Fungal-bacterial composition and network complexity determine soil multifunctionality during ecological restoration. *Catena* **2023**, *230*, 107251. [CrossRef]
28. Huang, L.M.; Thompson, A.; Zhang, G.L. Long-term paddy cultivation significantly alters topsoil phosphorus transformation and degrades phosphorus sorption capacity. *Soil Tillage Res.* **2014**, *142*, 32–41. [CrossRef]

29. Joss, H.; Patzner, M.S.; Maisch, M.; Mueller, C.W.; Kappler, A.; Bryce, C. Cryoturbation impacts iron-organic carbon associations along a permafrost soil chronosequence in northern Alaska. *Geoderma* **2022**, *413*, 115738. [CrossRef]
30. Kim, Y.J.; Laffly, D.; Kim, S.E.; Nilsen, L.; Chi, J.; Nam, S.; Lee, Y.B.; Jeong, S.; Mishra, U.; Lee, Y.K.; et al. Chronological changes in soil biogeochemical properties of the glacier foreland of Midtre Lovénbreen, Svalbard, attributed to soil-forming factors. *Geoderma* **2022**, *415*, 115777. [CrossRef]
31. Cao, X.; Ji, Q.; Wei, C.; Xiao, L.; Zhang, P.; Mao, R.; He, X.; Wang, W. Plant succession and geo-topography determined forest soil P and nine fraction-Ps across a larch forest chronosequence in the northmost region of China. *Plant Soil* **2023**, *486*, 681–703. [CrossRef]
32. He, J.; Wu, Y.; Zhu, H.; Zhou, J.; Luo, C.; Bing, H. Soil phosphorus fractions dynamics along a 22-ka chronosequence of landslides, western Sichuan, China. *Catena* **2024**, *235*, 107674. [CrossRef]
33. Zhou, J.; Li, X.; Peng, F.; Li, C.; Lai, C.; You, Q.; Xue, X.; Wu, Y.; Sun, H.; Chen, Y.; et al. Mobilization of soil phosphate after 8 years of warming is linked to plant phosphorus-acquisition strategies in an alpine meadow on the Qinghai-Tibetan Plateau. *Glob. Change Biol.* **2021**, *27*, 6578–6591. [CrossRef]
34. Zhang, C.; Liu, G.; Xue, S.; Wang, G. Soil bacterial community dynamics reflect changes in plant community and soil properties during the secondary succession of abandoned farmland in the Loess Plateau. *Soil Biol. Biochem.* **2016**, *97*, 40–49. [CrossRef]
35. Jones, M.L.M.; Sowerby, A.; Williams, D.L.; Jones, R.E. Factors controlling soil development in sand dunes: Evidence from a coastal dune soil chronosequence. *Plant Soil* **2008**, *307*, 219–234. [CrossRef]
36. Wang, F.; Wang, T.; Gustave, W.; Wang, J.; Zhou, Y.; Chen, J. Spatial-temporal patterns of organic carbon sequestration capacity after long-term coastal wetland reclamation. *Agric. Ecosyst. Environ.* **2023**, *341*, 108209. [CrossRef]
37. Yan, D.; Sun, W.; Ye, L.; Liu, B. Changes of microbial residues over century-long soil development after tidal flat reclamation in eastern China. *Catena* **2024**, *238*, 107864. [CrossRef]
38. Chen, C. CiteSpace II: Detecting and visualizing emerging trends and transient patterns in scientific literature. *J. Am. Soc. Inf. Sci. Technol.* **2006**, *57*, 359–377. [CrossRef]
39. Huang, S.; Li, S.; Wu, M.; Wang, C.; Yang, D. A Scientometric Analysis of Research Trends and Knowledge Structure on the Climate Effects of Irrigation between 1993 and 2022. *Agronomy* **2023**, *13*, 2482. [CrossRef]
40. Hu, J.; Dong, J.; Xu, D.; Yang, Q.; Liang, J.; Li, N.; Wang, H. Trends in Global Agricultural Carbon Emission Research: A Bibliometric Analysis. *Agronomy* **2024**, *14*, 2617. [CrossRef]
41. White, A.F.; Blum, A.E.; Schulz, M.S.; Bullen, T.D.; Harden, J.W.; Peterson, M.L. Chemical weathering rates of a soil chronosequence on granitic alluvium: I. Quantification of mineralogical and surface area changes and calculation of primary silicate reaction rates. *Geochim. Cosmochim. Acta* **1996**, *60*, 2533–2550. [CrossRef]
42. Huggett, R.J. Soil chronosequences, soil development, and soil evolution: A critical review. *Catena* **1998**, *32*, 155–172. [CrossRef]
43. Lal, R. Soil carbon sequestration impacts on global climate change and food security. *Science* **2004**, *304*, 1623–1627. [CrossRef] [PubMed]
44. Luo, Z.; Luo, Y.; Wang, G.; Xia, J.; Peng, C. Warming-induced global soil carbon loss attenuated by downward carbon movement. *Glob. Change Biol.* **2020**, *26*, 7242–7254. [CrossRef]
45. Walker, L.R.; Wardle, D.A.; Bardgett, R.D.; Clarkson, B.D. The use of chronosequences in studies of ecological succession and soil development. *J. Ecol.* **2010**, *98*, 725–736. [CrossRef]
46. Hayes, P.; Turner, B.L.; Lambers, H.; Laliberté, E. Foliar nutrient concentrations and resorption efficiency in plants of contrasting nutrient-acquisition strategies along a 2-million-year dune chronosequence. *J. Ecol.* **2014**, *102*, 396–410. [CrossRef]
47. Zemunik, G.; Turner, B.L.; Lambers, H.; Laliberté, E. Diversity of plant nutrient-acquisition strategies increases during long-term ecosystem development. *Nat. Plants* **2015**, *1*, 15050. [CrossRef]
48. Zhou, J.; Wu, Y.; Turner, B.L.; Sun, H.; Wang, J.; Bing, H.; Luo, J.; He, X.; Zhu, H.; He, Q. Transformation of soil organic phosphorus along the Hailuogou post-glacial chronosequence, southeastern edge of the Tibetan Plateau. *Geoderma* **2019**, *352*, 414–421. [CrossRef]
49. Hu, Y.; Su, M.; Wang, Y.; Cui, S.; Meng, F.; Yue, W.; Liu, Y.; Xu, C.; Yang, Z. Food production in China requires intensified measures to be consistent with national and provincial environmental boundaries. *Nat. Food* **2020**, *1*, 572–582. [CrossRef]
50. Amatangelo, K.L.; Vitousek, P.M. Stoichiometry of ferns in Hawaii: Implications for nutrient cycling. *Oecologia* **2008**, *157*, 619–627. [CrossRef]
51. Peltzer, D.A.; Wardle, D.A.; Allison, V.J.; Baisden, W.T.; Bardgett, R.D.; Chadwick, O.A.; Condron, L.M.; Parfitt, R.L.; Porder, S.; Richardson, S.J.; et al. Understanding ecosystem retrogression. *Ecol. Monogr.* **2010**, *80*, 509–529. [CrossRef]
52. Chadwick, O.A.; Derry, L.A.; Vitousek, P.M.; Huebert, B.J.; Hedin, L.O. Changing sources of nutrients during four million years of ecosystem development. *Nature* **1999**, *397*, 491–497. [CrossRef]
53. Lal, R. Carbon farming by recarbonization of agroecosystems. *Pedosphere* **2023**, *33*, 676–679. [CrossRef]
54. Batjes, N.H. Total carbon and nitrogen in the soils of the world. *Eur. J. Soil Sci.* **2014**, *65*, 10–21. [CrossRef]

55. Jiang, Y.; Lei, Y.; Yang, Y.; Korpelainen, H.; Niinemets, Ü.; Li, C. Divergent assemblage patterns and driving forces for bacterial and fungal communities along a glacier forefield chronosequence. *Soil Biol. Biochem.* **2018**, *118*, 207–216. [CrossRef]
56. Bernasconi, S.M.; Bauder, A.; Bourdon, B.; Brunner, I.; Bünemann, E.; Chris, I.; Derungs, N.; Edwards, P.; Farinotti, D.; Frey, B.; et al. Chemical and biological gradients along the Damma glacier soil chronosequence, Switzerland. *Vadose Zone J.* **2011**, *10*, 867–883. [CrossRef]
57. Lavallee, J.M.; Soong, J.L.; Cotrufo, M.F. Conceptualizing soil organic matter into particulate and mineral-associated forms to address global change in the 21st century. *Glob. Change Biol.* **2020**, *26*, 261–273. [CrossRef]
58. Zumsteg, A.; Luster, J.; Göransson, H.; Smittenberg, R.H.; Brunner, I.; Bernasconi, S.M.; Zeyer, J.; Frey, B. Bacterial, archaeal and fungal succession in the forefield of a receding glacier. *Microb. Ecol.* **2012**, *63*, 552–564. [CrossRef]
59. Schmidt, M.W.; Torn, M.S.; Abiven, S.; Dittmar, T.; Guggenberger, G.; Janssens, I.A.; Kleber, M.; Kögel-Knabner, I.; Lehmann, J.; Manning, D.A.C.; et al. Persistence of soil organic matter as an ecosystem property. *Nature* **2011**, *478*, 49–56. [CrossRef]
60. Muhs, D.R. A soil chronosequence on Quaternary marine terraces, San Clemente Island, California. *Geoderma* **1982**, *28*, 257–283. [CrossRef]
61. Marsan, F.A.; Barberis, E.; Arduino, E. A soil chronosequence in northwestern Italy: Morphological, physical and chemical characteristics. *Geoderma* **1988**, *42*, 51–64. [CrossRef]
62. Lilienfein, J.; Qualls, R.G.; Uselman, S.M.; Bridgham, S.D. Soil formation and organic matter accretion in a young andesitic chronosequence at Mt. Shasta, California. *Geoderma* **2003**, *116*, 249–264. [CrossRef]
63. Brown, S.P.; Jumpponen, A. Contrasting primary successional trajectories of fungi and bacteria in retreating glacier soils. *Mol. Ecol.* **2014**, *23*, 481–497. [CrossRef]
64. White, A.F.; Schulz, M.S.; Vivit, D.V.; Blum, A.E.; Stonestrom, D.A.; Harden, J.W. Chemical weathering rates of a soil chronosequence on granitic alluvium: III. Hydrochemical evolution and contemporary solute fluxes and rates. *Geochim. Cosmochim. Acta* **2005**, *69*, 1975–1996. [CrossRef]
65. Aydın, M.; Rages, A.A. Soil respiration and organic carbon changes along a chronosequence of Pinus nigra forest stands. *BioResources* **2024**, *19*, 6095–6119. [CrossRef]
66. Benalcazar, P.; Seuradge, B.; Diochon, A.C.; Kolka, R.K.; Phillips, L.A. Conversion of boreal forests to agricultural systems: Soil microbial responses along a land-conversion chronosequence. *Environ. Microbiome* **2024**, *19*, 32. [CrossRef]
67. Ding, L.J.; Su, J.Q.; Li, H.; Zhu, Y.G.; Cao, Z.H. Bacterial succession along a long-term chronosequence of paddy soil in the Yangtze River Delta, China. *Soil Biol. Biochem.* **2017**, *104*, 59–67. [CrossRef]
68. Guo, R.; Chen, Y.; Xiang, M.; Yang, S.; Wang, F.; Cao, W.; Yue, H.; Peng, S. Soil nutrients drive changes in the structure and functions of soil bacterial communities in a restored forest soil chronosequence. *Appl. Soil Ecol.* **2024**, *195*, 105247. [CrossRef]
69. Jiao, H.; Xu, M.; Ji, J.; Wang, Y.; Zhang, Y.; Su, B.; Zhang, H.; Gao, C. Bacterial and fungal diversity, community composition, functional groups, and co-occurrence network succession in dryland and paddy soils along a 3000-year chronosequence. *Catena* **2025**, *248*, 108582. [CrossRef]
70. Turner, B.L.; Condron, L.M.; Wells, A.; Andersen, K.M. Soil nutrient dynamics during podzol development under lowland temperate rain forest in New Zealand. *Catena* **2012**, *97*, 50–62. [CrossRef]
71. Huang, L.; Hu, W.; Tao, J.; Liu, Y.; Kong, Z.; Wu, L. Soil bacterial community structure and extracellular enzyme activities under different land use types in a long-term reclaimed wetland. *J. Soil. Sediment.* **2019**, *19*, 2543–2557. [CrossRef]
72. Zhang, H.; Liu, Y.; Miao, Y.; Cao, D.; Wang, X.; Wang, S.; Wang, F.; Chen, J.; Ge, T.; Zhu, Z. Synergistic regulation of salinity and nutrients on organic carbon mineralization in a 700-year cultivated saline soil chronosequence. *Appl. Soil Ecol.* **2024**, *203*, 105667. [CrossRef]
73. Schulz, S.; Brankatschk, R.; Dümig, A.; Kögel-Knabner, I.; Schloter, M.; Zeyer, J. The role of microorganisms at different stages of ecosystem development for soil formation. *Biogeosciences* **2013**, *10*, 3983–3996. [CrossRef]
74. Liu, Y.; Wang, P.; Cai, G.; Ge, T.; Wang, J.; Guggenberger, G. Divergent accumulation of microbial and plant necromass along paddy soil development in a millennium scale. *Soil Tillage Res.* **2023**, *232*, 105769. [CrossRef]
75. Vindušková, O.; Pánek, T.; Frouz, J. Soil C, N and P dynamics along a 13 ka chronosequence of landslides under semi-natural temperate forest. *Quat. Sci. Rev.* **2019**, *213*, 18–29. [CrossRef]
76. Basdediós, N.; Hardegger, S.; Mestrot, A.; Wang, J.; Zhou, J.; Bing, H.; Wu, Y.; Wilcke, W. Shift of the ecosystem nitrogen cycle from open to closed within a century along a glacial retreat chronosequence at Mount Gongga, southwest China. *Plant Soil* **2025**, 1–19. [CrossRef]
77. Chen, C.; Yin, G.; Hou, L.; Jiang, Y.; Sun, D.; Liang, X.; Han, P.; Zheng, Y.; Liu, M. Reclamation of tidal flats to paddy soils reshuffles the soil microbiomes along a 53-year reclamation chronosequence: Evidence from assembly processes, co-occurrence patterns and multifunctionality. *Environ. Int.* **2023**, *179*, 108151. [CrossRef]
78. Cui, J.; Meng, H.; Nie, M.; Chen, X.; Li, Z.; Bu, N.; Li, B.; Chen, J.; Quan, Z.; Fang, C. Bacterial succession during 500 years of soil development under agricultural use. *Ecol. Res.* **2012**, *27*, 793–807. [CrossRef]

79. Rasche, F.; Musyoki, M.K.; Röhl, C.; Muema, E.K.; Vanlauwe, B.; Cadisch, G. Lasting influence of biochemically contrasting organic inputs on abundance and community structure of total and proteolytic bacteria in tropical soils. *Soil Biol Biochem.* **2014**, *74*, 204–213. [CrossRef]
80. Wekesa, C.S.; Furch, A.C.U.; Oelmüller, R. Isolation and characterization of high-efficiency rhizobia from western kenya nodulating with common bean. *Front. Microbiol.* **2021**, *12*, 697567. [CrossRef]
81. Muema, E.K.; Cadisch, G.; Röhl, C.; Vanlauwe, B.; Rasche, F. Response of ammonia-oxidizing bacteria and archaea to biochemical quality of organic inputs combined with mineral nitrogen fertilizer in an arable soil. *Appl. Soil Ecol.* **2015**, *95*, 128–139. [CrossRef]
82. Muema, E.K.; Steenkamp, E.T.; Venter, S.N. Rhizosphere Diazotrophs and other bacteria associated with native and encroaching legumes in the Succulent Karoo Biome in South Africa. *Microorganisms* **2022**, *10*, 216. [CrossRef] [PubMed]
83. Chen, L.M.; Zhang, G.L.; Effland, W.R. Soil characteristic response times and pedogenic thresholds during the 1000-year evolution of a paddy soil chronosequence. *Soil Sci. Soc. Am. J.* **2011**, *75*, 1807–1820. [CrossRef]
84. Hanke, A.; Cerli, C.; Muhr, J.; Borken, W.; Kalbitz, K. Redox control on carbon mineralization and dissolved organic matter along a chronosequence of paddy soils. *Eur. J. Soil Sci.* **2013**, *64*, 476–487. [CrossRef]
85. Huang, L.M.; Zhang, G.L.; Thompson, A.; Rossiter, D.G. Pedogenic transformation of phosphorus during paddy soil development on calcareous and acid parent materials. *Soil Sci. Soc. Am. J.* **2013**, *77*, 2078–2088. [CrossRef]
86. Wissing, L.; Kölbl, A.; Schad, P.; Bräuer, T.; Cao, Z.H.; Kögel-Knabner, I. Organic carbon accumulation on soil mineral surfaces in paddy soils derived from tidal wetlands. *Geoderma* **2014**, *228*, 90–103. [CrossRef]
87. Liu, Y.; Dong, Y.; Ge, T.; Hussain, Q.; Wang, P.; Wang, J.; Li, Y.; Guggenberger, G.; Wu, J. Impact of prolonged rice cultivation on coupling relationship among C, Fe, and Fe-reducing bacteria over a 1000-year paddy soil chronosequence. *Biol. Fertil. Soils* **2019**, *55*, 589–602. [CrossRef]
88. Wang, F.; Peng, W.; Zhang, B.; Cao, Y.; Zhao, J.; Cao, H. Succession of bacterial community composition in coastal agricultural soils along a 1000-year reclamation chronosequence in Hangzhou Bay, China. *Ecol. Indic.* **2021**, *121*, 106972. [CrossRef]
89. Ding, L.J.; An, X.L.; Li, S.; Zhang, G.L.; Zhu, Y.G. Nitrogen loss through anaerobic ammonium oxidation coupled to iron reduction from paddy soils in a chronosequence. *Environ. Sci. Technol.* **2014**, *48*, 10641–10647. [CrossRef]

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