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前瞻与评论

# 基于文献计量学的连作对土壤微生物群落影响研究的可视化分析

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杨阳, 王鸿, 张雪冰, 张帆, 郝兰兰. 基于文献计量学的连作对土壤微生物群落影响研究的可视化分析[J]. 微生物学通报, 2025, 52(1): 426-444.
YANG Yang, WANG Hong, ZHANG Xuebing, ZHANG Fan, HAO Lanlan. Visual analysis of studies on effects of continuous cropping on soil microbial communities based on bibliometrics[J]. Microbiology China, 2025, 52(1): 426-444.

**摘 要：**【背景】作物长期连作会导致土壤环境恶化，破坏土壤微生物群落之间的平衡，影响土壤生态系统的健康。【目的】基于文献计量学方法探讨了作物连作对土壤微生物群落影响相关研究领域的研究现状、热点和发展趋势。【方法】本文利用 CiteSpace 软件，对 Web of Science (WOS)核心数据库中 2003−2023 年间所收录的连作对土壤微生物群落影响的研究文献进行了可视化分析，分析内容包括了发文国家/地区、机构、作者和关键词等。【结果】通过筛选共获得相关文献 1 652 篇，出版物数量总体呈上升趋势。结果表明中国在该研究领域发文量逐年增加，2003−2023 年间总发文量位居全球首位。发文量最大的机构为中国科学院。以学者 LIANG Aizhen 为核心的研究团队在该研究领域具有较高的影响力。期刊 *Applied and Environmental Microbiology* 是该研究领域的核心期刊。在研究内容方面，连作过程中微生物群落与土壤碳氮循环的互作机制是目前的研究热点，土壤微生物群落对耕作措施的响应为该研究领域的重点内容。【结论】文献计量学分析结果表明，综合利用多种微生物学研究方法探究土壤微生物群落在连作过程中介导土壤环境变化对土壤食物网的影响机制是未来研究的主要潜在趋势，今后的研究重点则是关注于连作过程中农业管理方式对土壤微生物群落的调节和改善。

**关键词：**连作；微生物；CiteSpace；文献计量学

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# Visual analysis of studies on effects of continuous cropping on soil microbial communities based on bibliometrics

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**Abstract: [Background]** Long-term continuous cropping deteriorates the soil environment, disrupts the soil microbial community balance, and impacts soil ecosystem health. **[Objective]** This paper employed a bibliometric approach to explore the current research status, hotspots, and development trends related to the effects of continuous cropping on soil microbial communities. **[Methods]** CiteSpace was used for the visual analysis of the studies on the effects of continuous cropping on soil microbial communities that were published from 2003 to 2023 in the Web of Science (WOS) core collection. The analysis involved publishing countries/regions, institutions, authors, and keywords. **[Results]** A total of 1 652 publications were screened out. The annual number of publications showed a general increasing trend. China's annual publications in this research field kept growing, with the number of total publications during 2003–2023 ranking first globally. The Chinese Academy of Sciences was the institution with the largest number of publications. The research team led by LIANG Aizhen was highly influential. The *Applied and Environmental Microbiology* was deemed as the core journal in this field. The research hotspots in this field included the interaction mechanisms between microbial communities and the soil carbon and nitrogen cycling during continuous cropping. The responses of soil microbial communities to tillage measures were also a key research area. **[Conclusion]** The bibliometric analysis suggests that future research should focus on the integrated use of multiple microbiological methods to investigate how soil microbial communities mediate changes in soil environments and food webs during continuous cropping. Additionally, the regulation and improvement of soil microbial communities by agricultural management practices should be a primary focus in the future studies.

**Keywords:** continuous cropping; microorganisms; CiteSpace; bibliometrics

连作(continuous cropping)指一年内或连续多年在同一块田地上连续种植同一种作物的种植方式。作物连作通常会导致土壤退化、病害积累和作物产量下降等问题，这一现象被称为连作障碍(continuous cropping obstacle)[1]。近年来，随着分子生物学技术及系统生物学方法的发展,研究者们逐渐认识到土壤微生物群落在连作中对于维持土壤生态系统健康的重要性[2]。土壤微生物群落在维持土壤健康方面具有重要作用，微生物生物量、代谢活动和群落组成等是影响土壤中养分分解和物质代谢循环的关键因素[3-4]。研究表明土壤微生物群落不仅能够参与土壤中矿物分解，释放养分，还能参与 $N_2$ 的固定和土壤团聚体的形成，改善土壤的通气性和保水性等[5]。此外，丰富的微生物类群能够缩小有害微生物的生态位，减少植物土传病害。植物残体和根系分泌物为微生物群落提供了生长材料，而微生物群落通过分解和转化将养分

返还给土壤和植物，植物与土壤之间的反馈作用构成了微生物群落演替和土壤生态恢复建设的核心驱动力[6-7]。

连作改变了土壤的理化特征，也改变了土壤微生物的群落特征。作物在长期连作过程中，以植物代谢物为主要碳源的微生物群落特征会随着土壤中代谢物的积累发生相应的变化，土壤中细菌和真菌的相对丰度随着连作年限的增加而增加或者降低[8-9]。作物连作会导致土壤中重要功能菌群的相对丰度下降，如固氮菌属(*Azotobacter*)、芽孢杆菌属(*Bacillus*)和放线菌属(*Actinomyces*)等有益细菌类群，以及一些重要的真菌类群如粘帚霉属(*Gliocladium*)、青霉属(*Penicillium*)和木霉属(*Trichoderma*)等，而有害菌如镰刀菌属(*Fusarium*)和炭疽菌属(*Colletotrichum*)等的相对丰度则显著增加，导致土壤微环境恶化，影响作物生长，从而引发一系列负面效应[10-11]。因此，明确连作对土壤微生物群落的影响和土壤微生物群落对连作的响应机制对于缓解连作的负面效应具有重要的意义。

本文利用 CiteSpace 软件对 Web of Science (WOS)核心数据库中 2003−2023 年间所收录的连作对土壤微生物群落影响的研究文献进行了可视化分析，以阐明连作对土壤微生物群落的影响研究现状和未来的发展趋势，以期为该研究领域提供一定的参考。

# 1 数据的采集和分析方法

## 1.1 数据的采集

本文中文献数据为 Web of Science (WOS)核心数据库中 2003−2023 年间相关研究主题的文献，所使用检索式为：TS=((continuous cropping AND microorganism) OR(continuous cropping AND germ) OR (continuous cropping AND microbes) OR (continuous cropping AND microbial) OR (continuous cropping AND bacteria) OR (continuous cropping AND fungi) OR (succession cropping AND microorganism) OR (succession cropping AND germ) OR (succession cropping AND microbes) OR (succession cropping AND microbial) OR (succession cropping AND bacteria) OR (succession cropping AND fungi))，语种为“English”，文献类型为“article”，检索时间范围为 2003−2023 年，共检索出相关文献 2 056 篇。

## 1.2 数据分析方法

为确保分析结果的准确度和可信度，本文中在文献数据分析前使用 UltraEdit v25.10 软件剔除与主题内容不符的文献记录。通过筛选获得相关文献 1 652 篇，使用 CiteSpace 6.1.R3 软件对相关研究文献数据的国家/地区、机构、作者和关键词等进行可视化分析。本文中 CiteSpace 软件参数分别为：时间段(time slicing)为 2000−2023，时间切片(years per slice)为 1 年，阈值参数 G-index、Top N 和 Top N%分别为 25、50 和 100，其他参数为默认值。

利用 CiteSpace 软件对文献数据进行统计和分析，并绘制知识图谱，计算图谱中各节点中心值(centrality)。中心值指在网络图谱中通过节点的最短路径条数，主要用于衡量某个节点在整个网络中的重要性和影响力。其计算公式如下[12]。

$$\mathrm{BC_i} = \sum_{s\neq i\neq t} \frac{\mathrm{n}_{\mathrm{st}}^{\mathrm{i}}}{g_{\mathrm{st}}}$$

式中，$BC_\mathrm{i}$ 表示节点中心值，$g_{\mathrm{st}}$ 表示节点 s 到节点 t 的最短路径数目，$\mathrm{n}_{\mathrm{st}}^{\mathrm{i}}$ 表示从节点 s 到节点 t 的 $g_{\mathrm{st}}$ 条最短路径中经过节点 i 的最短路径数目。

# 2 结果与分析

## 2.1 发文数量分析

通过对 2003−2023 年各国发表的关于连作对土壤微生物群落影响的文献进行分析，发文量排名前 5 的国家如图 1 所示。2003−2023 年

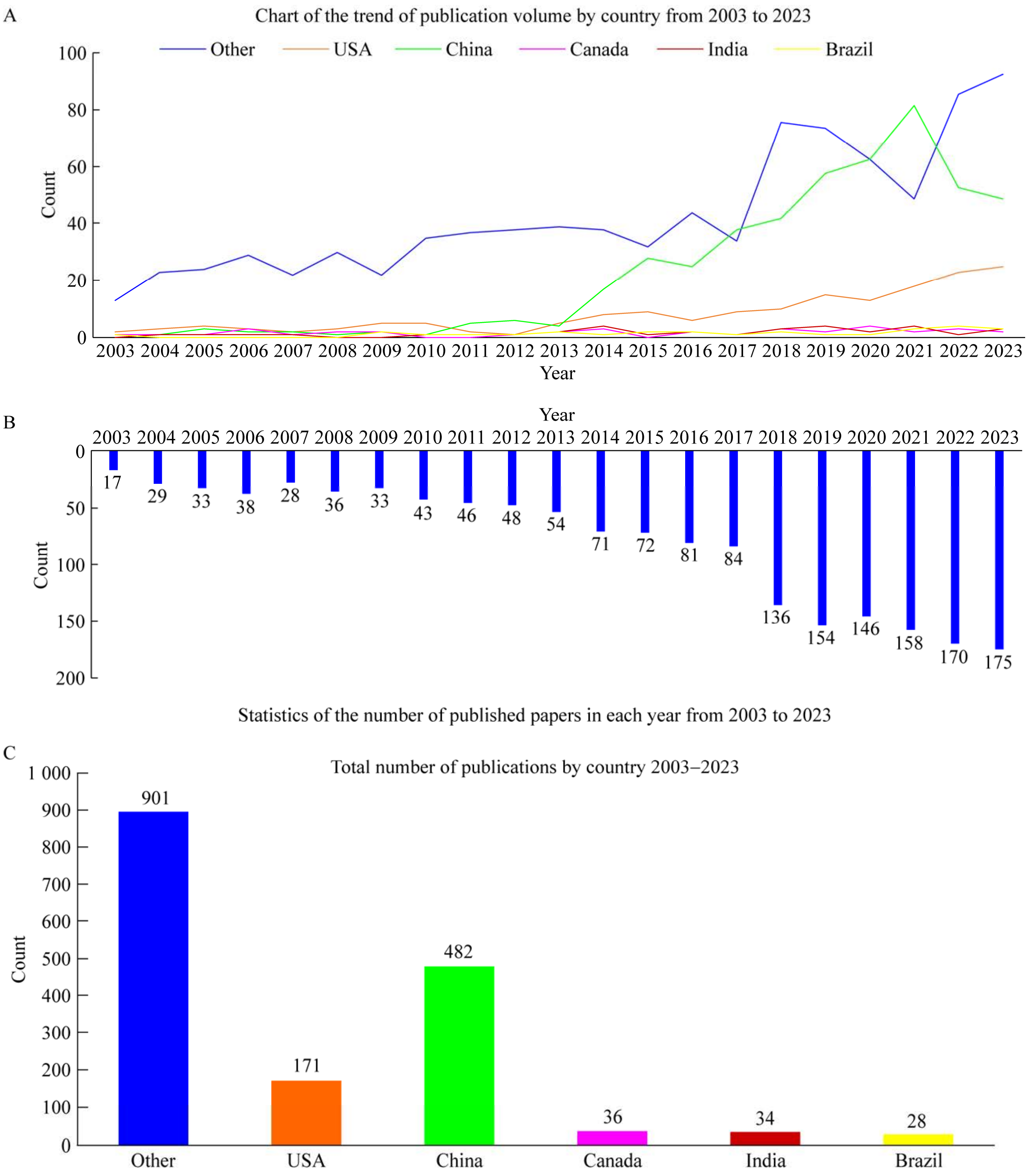

**图 1　2003–2023 年各国发文量趋势变化统计**　A：各国每年发文量统计；B：该研究领域每年发文量统计；C：各国发文总量统计。

Figure 1　Statistics on the trend of national publications from 2003 to 2023. A: Statistics on the annual publications of each country; B: Statistics on the annual number of publications in this research field; C: Total number of publications by country.

该研究领域发文量达到了 1 652 篇，其中中国发文量位居首位(482 篇)，占总发文量 29.18%。总体上，该研究领域的发文量呈逐年增加的趋势。2003−2013 年间，美国发文量最高，而在 2013−2023年间中国在该领域发文量跃居第一，特别是在 2014−2023 年间中国在这一研究领域的发文量急剧增加，表明中国的研究者对该研究领域的关注度逐年提高。

## 2.2 国家/地区和机构合作分布

连作对土壤微生物群落影响相关研究领域发文量较大的前 15 个国家/地区(共 48 个)和机构(共 512 个)如表 1 所示，国家/地区和机构分布知识图谱如图 2 所示。从表 1 可知该研究领域发文量最大的国家为中国(China) (482)，其次为美国(USA) (171)、加拿大(Canada) (36)、印度(India) (34)和巴西(Brazil) (28)等。知识图谱中节点的中心值与其对应国家/地区影响力呈正相关关系[13]。由图 2A 可知中国(1.04)在知识图谱中具有较高的中心值，表明中国在该研究领域中与其他国家合作较为密切，具有较高的影响力，其次为美国。加拿大发文量大于印度和巴西，但其在知识图谱中的中心值低于印度(0.13)和巴西(0.13)。

该研究领域发文量较大的机构为中国科学院(Chinese Academy of Sciences) (87)、美国农业部农业科学研究院(Agricultural Research Service U.S. Department of Agriculture Agricultural Research Service) (40)和中国农业科学院(Chinese Academy of Agricultural Sciences) (38) (表 1)。其中中国科学院在知识图谱中具有较高的中心值(0.29) (图 2B)，表明中国科学院与其他研究机构合作较为密切，具有较高的影响力，其次为美国农业部农业科学研究院(0.11)和中国农业大学(0.09)。

## 2.3 作者和共被引作者分析

该研究领域发文作者共 662 位，发文量前 15 的作者如表 2 所示。其中，发文量较大的作者为 CAI Baiyan (12)、WU Fengzhi (9)、DAI

**表 1 发文量前 15 的国家/地区和机构**

Table 1 Top 15 countries/regions and institutions

| Ranking | Country/Region | Count | Centrality | Institution | Count | Centrality |
|---|---|---|---|---|---|---|
| 1 | China | 482 | 1.04 | Chinese Academy of Sciences | 87 | 0.29 |
| 2 | USA | 171 | 0.46 | Agricultural Research Service U.S. Department of Agriculture Agricultural Research Service | 40 | 0.11 |
| 3 | Canada | 36 | 0.00 | Chinese Academy of Agricultural Sciences | 38 | 0.07 |
| 4 | India | 34 | 0.13 | University of Chinese Academy of Sciences | 31 | 0.01 |
| 5 | Brazil | 28 | 0.13 | China Agricultural University | 30 | 0.09 |
| 6 | Germany | 24 | 0.11 | Northwest A&F University | 27 | 0.02 |
| 7 | Australia | 22 | 0.13 | Nanjing Agricultural University | 25 | 0.01 |
| 8 | France | 20 | 0.00 | Shenyang Agricultural University | 24 | 0.01 |
| 9 | Pakistan | 19 | 0.09 | Heilongjiang University | 19 | 0.02 |
| 10 | Kenya | 14 | 0.08 | Gansu Agricultural University | 19 | 0.02 |
| 11 | Argentina | 11 | 0.02 | Heilongjiang Academy of Agricultural Sciences | 18 | 0.02 |
| 12 | Switzerland | 10 | 0.03 | Fujian Agriculture and Forestry University | 17 | 0.03 |
| 13 | England | 9 | 0.03 | Northeast Agricultural University | 16 | 0.00 |
| 14 | Italy | 8 | 0.03 | Agriculture and Agri-Food Canada | 16 | 0.02 |
| 15 | Spain | 8 | 0.00 | Huazhong Agricultural University | 15 | 0.02 |

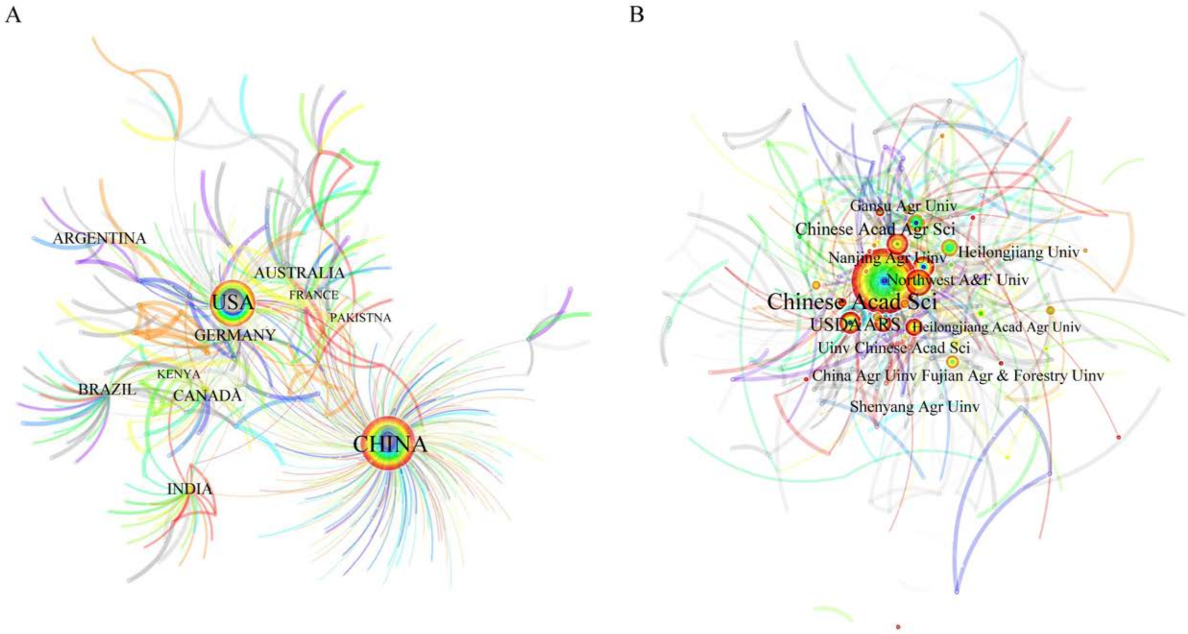

**图 2　发文国家/地区(A)和机构(B)合作知识图谱**　图中相同颜色的连线代表了相关节点之间的合作关系，连线越多表明该节点的共现性越强，其中心值越高。下同。

Figure 2　Knowledge graph of cooperation between countries/regions (A) and institutions (B). The lines of the same color in the figure represent the cooperative relationship between the related nodes, the more lines, the stronger the co-occurrence of the node, and the higher its center value. The same below.

**表 2　频数排名前 15 的作者和共被引作者**

Table 2　Top 15 authors and co-cited authors in frequency

| Ranking | Authors | Count | Centrality | Co-cited authors | Count | Centrality |
|---|---|---|---|---|---|---|
| 1 | CAI Baiyan | 12 | 0.02 | EDGAR RC | 177 | 0.02 |
| 2 | WU Fengzhi | 9 | 0.01 | CAPORASO JG | 141 | 0.02 |
| 3 | DAI Chuanchao | 9 | 0.01 | ZHOU XG | 136 | 0.06 |
| 4 | ALI Ahmad | 7 | 0.01 | FIERER N | 130 | 0.06 |
| 5 | YAO Qin | 7 | 0.01 | XIONG W | 119 | 0.04 |
| 6 | LIU Junjie | 7 | 0.02 | LI XG | 109 | 0.02 |
| 7 | LIANG Aizhen | 7 | 0.05 | VANCG ED | 100 | 0.05 |
| 8 | WANG Guanghua | 7 | 0.00 | ACOSTA-MARTINEZ V | 88 | 0.24 |
| 9 | JIE Weiguang | 6 | 0.00 | MAGOC T | 85 | 0.01 |
| 10 | SHEN Qirong | 5 | 0.01 | WANG Q | 78 | 0.02 |
| 11 | WRIGHT Alan L. | 5 | 0.01 | ZHAO J | 74 | 0.02 |
| 12 | LARKIN Robert P. | 4 | 0.02 | LIU X | 74 | 0.02 |
| 13 | WANG Mei | 4 | 0.02 | ROUSK J | 74 | 0.02 |
| 14 | ZHANG Yan | 4 | 0.01 | GARBEVA P | 72 | 0.10 |
| 15 | LIN Wenxiong | 4 | 0.01 | BERENDSEN RL | 69 | 0.03 |

Chuanchao (9)和 ALI Ahmad (7) (表 2)。本文结果表明发文量较高的作者在知识图谱中不一定具有较高的中心值(图 3A)，如 CAI Baiyan 具有高的发文量，但其中心值低于 LIANG Aizhen (0.05)，该作者来自中国科学院东北地理与农业生态研究所，主要研究方向为农田黑土地力提升机制、土壤生物生态过程和保护性耕作技术等。此外，作者 WANG Guanghua 和 JIE Weiguang 在知识图谱中的中心值较低(0.00)。表明该作者与其他研究者合作较少。发文量前 15 的作者中来自中国的研究者占总量的 86.67%，表明国内研究者对连作对土壤微生物群落影响的研究具有较高的关注度。

共被引作者分析结果表明涉及该研究领域的共被引作者共 934 位，其中共被引频次较高的作者如表 2 所示。其中 EDGAR RC 具有较高的共被引频次(177)，其次为 CAPORASO JG (141)、ZHOU XG (136)和 FIERER N (130)。ACOSTA-MARTINEZ V 虽共被引频次较低(88)，但其在知识图谱中具有较高的中心值(0.24) (图 3B)，表明该作者在该研究领域具有较高的影响力。以 ACOSTA-MARTINEZ V 为主要节点的研究团队主要来自美国农业部农业科学研究院，其主要的研究方向为极端环境与土壤微生物群落的互作机制。其次为 GARBEVA P (0.10)。

## 2.4　期刊共被引分析

该研究领域涉及的发文期刊共 718 个，共被引频数较高的期刊如表 3 所示。其中创刊于 1969 年的期刊 *Soil Biology and Biochemistry* 具有较高的共被引频次(776)，该期刊属于农林科学和土壤科学研究领域的权威期刊。其次为 *Plant and Soil* (650)、*Applied Soil Ecology* (607)和 *Biology and Fertility of Soils* (552)。*Applied and Environmental Microbiology* 期刊的引用频次不高，但其中心值较高(0.05)，表明该期刊在

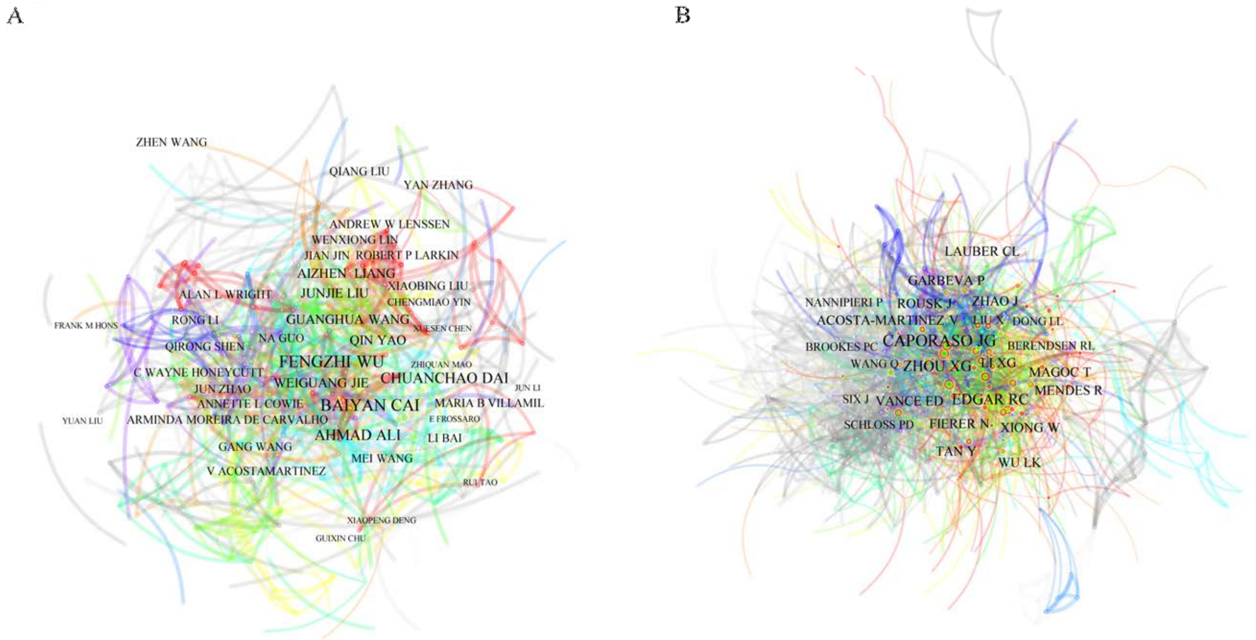

**图 3　发文作者(A)和共被引作者(B)知识图谱**

Figure 3　Knowledge graph of published authors (A) and co-cited authors (B).

**表 3 发文量前 15 的期刊及相关信息**

Table 3 The information of the top 15 journals

| Ranking | Journal | Count | Centrality | Publishing country/region | Impact Factor |
|---|---|---|---|---|---|
| 1 | *Soil Biology and Biochemistry* | 776 | 0.01 | England | 9.7 |
| 2 | *Plant and Soil* | 650 | 0.02 | Netherlands | 4.9 |
| 3 | *Applied Soil Ecology* | 607 | 0.02 | Netherlands | 4.8 |
| 4 | *Biology and Fertility of Soils* | 552 | 0.01 | Germany | 6.5 |
| 5 | *Applied and Environmental Microbiology* | 500 | 0.05 | United States | 4.4 |
| 6 | *PLoS One* | 462 | 0.01 | United States | 3.7 |
| 7 | *Soil and Tillage Research* | 417 | 0.02 | Netherlands | 6.5 |
| 8 | *Agriculture Ecosystems and Environment* | 399 | 0.03 | Netherlands | 6.6 |
| 9 | *Soil Science Society of America Journal* | 380 | 0.01 | United States | 2.9 |
| 10 | *Frontiers in Microbiology* | 356 | 0.02 | Switzerland | 5.2 |
| 11 | *Scientific Reports* | 338 | 0.01 | England | 4.6 |
| 12 | *FEMS Microbiology Ecology* | 335 | 0.03 | Netherlands | 4.2 |
| 13 | *ISME Journal* | 322 | 0.01 | United States | 11.2 |
| 14 | *Microbial Ecology* | 302 | 0.02 | United States | 3.6 |
| 15 | *Nature* | 281 | 0.03 | England | 64.8 |

该研究领域中具有较高的影响力，属于该研究领域的“核心期刊” (图 4A)。

## 2.5 共被引文献分析

文献共被引分析可以反映某一研究领域的知识结构组成，通过文献共被引分析，研究者可以了解某一领域内文献之间的引用关系，揭示出关键的研究成果、研究热点以及学科间的交叉关系。

本文中，通过文献共被引分析共得共被引文献 936 篇，其中共被引频次较高的文献[14-28]如表 4 所示。本文中该研究领域共被引频数较高的文献为 Liu 等[14]于 2020 年发表在 *Soil and Tillage Research* 期刊上的题为“Long-term continuous cropping of soybean is comparable to crop rotation in mediating microbial abundance, diversity and community composition”一文，该研究中作者通过对比不同连作年限的大豆根际土壤中微生物的相对丰度和群落组成，系统地探讨了连作对土壤微生物群落及多样性的影响，研究发现大豆短期连作降低了土壤细菌的丰度，增加了真菌的丰度；而长期连作过程中土壤有益菌属增加，有害菌属降低，论证了大豆长期连作的可能性，为大豆实际生产提供了一定的理论基础。其次是发表在 *Microbiological Research* 上的“Rhizospheric soil and root endogenous fungal diversity and composition in response to continuous *Panax notoginseng* cropping practices”一文，该研究分析了连作过程中三七根际土壤真菌和根内真菌群落的变化特征，研究表明随着连作年限的增加，三七根内真菌及根际土壤的真菌多样性显著增加，*Leotiomycetes*、*Cydrocarpon*、*Fusarium* 和 *Mycocentrospora* 是造成三七连作障碍的潜在病原菌[15]。此外，2018 年发表于 *Scientific Reports* 上的“Long-term coffee monoculture alters soil chemical properties and microbial communities”一文在知识图谱中具有较高的中心值，表明该文在该研究领域具有较高的影响力，该研究发现咖啡长期单一种植会导致土壤中细菌和真菌的相对丰度下降，且随着连作年限的增加土壤 pH 和有机质含量呈下降的趋势，此外连作导致土壤次生盐碱化情况加剧[16] (图 4B)。

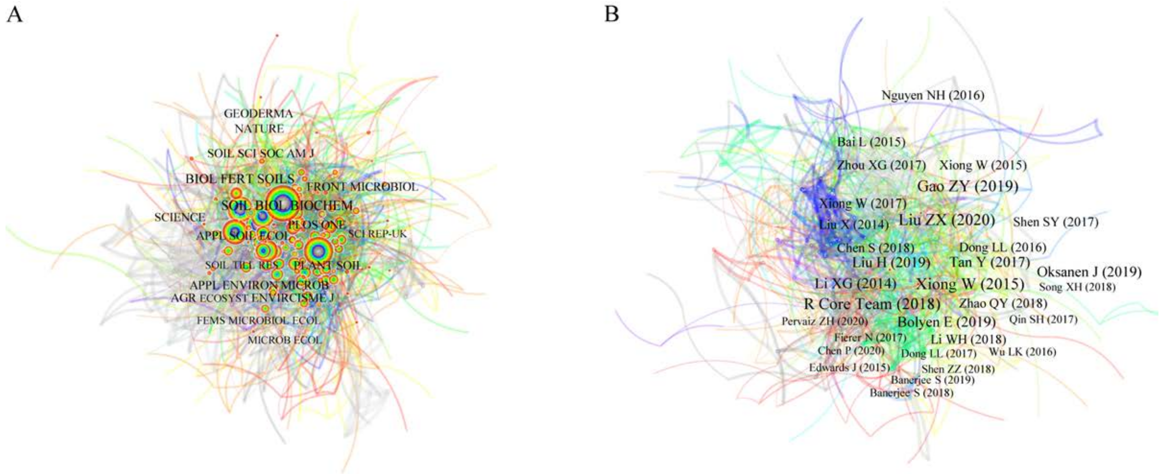

**图 4** 发文期刊(A)和引用文献(B)知识图谱

Figure 4 Knowledge graph of published journals (A) and cited literatures (B).

**表 4** 被引频次最高的 15 篇共被引文献

Table 4 Top 15 cited references and the importance index

| Ranking | Literatures | Journals | Count | Centrality |
|---|---|---|---|---|
| 1 | Long-term continuous cropping of soybean is comparable to crop rotation in mediating microbial abundance, diversity and community composition[14] | *Soil and Tillage Research* | 43 | 0.02 |
| 2 | Rhizospheric soil and root endogenous fungal diversity and composition in response to continuous *Panax notoginseng* cropping practices[15] | *Microbiological Research* | 38 | 0.05 |
| 3 | Different continuous cropping spans significantly affect microbial community membership and structure in a vanilla-grown soil as revealed by deep Pyrosequencing[17] | *Microbial Ecology* | 35 | 0.02 |
| 4 | Effects of continuous cropping of sweet potato on the fungal community structure in rhizospheric soil[18] | *Frontiers in Microbiology* | 34 | 0.04 |
| 5 | Response of soil fungal community structure to long-term continuous soybean cropping[19] | *Frontiers in Microbiology* | 34 | 0.02 |
| 6 | Continuous-cropping tobacco caused variance of chemical properties and structure of bacterial network in soils[20] | *Land Degradation and Development* | 33 | 0.04 |
| 7 | Significant relationship between soil bacterial community structure and incidence of bacterial wilt disease under continuous cropping system[21] | *Archives of Microbiology* | 30 | 0.03 |
| 8 | Analysis of the community compositions of rhizosphere fungi in soybeans continuous cropping fields[22] | *Microbiological Research* | 28 | 0.05 |
| 9 | Fungal pathogen accumulation at the expense of plant-beneficial fungi as a consequence of consecutive peanut monoculturing[23] | *Soil Biology and Biochemistry* | 28 | 0.04 |
| 10 | The effect of long-term continuous cropping of black pepper on soil bacterial communities as determined by 454 Pyrosequencing[24] | *PLoS One* | 27 | 0.01 |
| 11 | Long-term coffee monoculture alters soil chemical properties and microbial communities[16] | *Scientific Reports* | 24 | 0.12 |
| 12 | Soil microbial communities in cucumber monoculture and rotation systems and their feedback effects on cucumber seedling growth[25] | *Plant and Soil* | 23 | 0.03 |
| 13 | High-throughput sequencing technology reveals that continuous cropping of American ginseng results in changes in the microbial community in arable soil[26] | *Chinese Medicine* | 22 | 0.01 |
| 14 | Soil bacterial and fungal community dynamics in relation to *Panax notoginseng* death rate in a continuous cropping system[27] | *Scientific Reports* | 21 | 0.01 |
| 15 | Breaking continuous potato cropping with legumes improves soil microbial communities, enzyme activities and tuber yield[28] | *PLoS One* | 20 | 0.02 |

## 2.6 学科突现分析

学科突现分析用于研究某一研究领域所涉及学科的演化和发展趋势，它有助于研究者明晰某一研究领域相关学科的时间演替变化特征，通过学科突现分析，研究者可以明确特定时间段内出现频率显著增加的学科，从而揭示出某一研究领域的学科发展趋势和变化特征[29]。本文中，通过学科突现分析共得突现学科 5 个，其中土壤学(Soil Science) (13.42)在 2003−2023 年范围内的暴发强度较高且暴发期最长，其次是农学(Agriculture) (6.64) (表 5)。从突现知识图谱的学科时间演替变化来看，该研究领域早期主要侧重于土壤学，随着时间的推移，该研究领域研究重点逐渐转向了化学、园艺学和分析化学等学科。

土壤作为自然界中微生物的主要活动场所，提供了微生物生长所需的各种营养物质和外部条件[30]。土壤中的微生物形成了复杂而多样的群落，研究表明一些微生物群落成员生态位的构建可以改变其周围的环境条件，从而影响其周围其他生物的适应性。如微生物的生态位构建可导致物种间竞争或合作的变化，这种变化是由微生物介导环境条件的变化引起的间接反馈作用[31]。作物连作导致土壤中某些微生物种群过度富集，而其他微生物种群的数量减少，导致微生物生态位的改变。这种不平衡可能会改变土壤中物质的循环和分布，如影响有机物的降解和土壤中的氮和磷等元素的含量，进而影响作物的生长条件[32]。此外，作物连作会破坏土壤微生物的生存环境，增加微生物群落内部的竞争作用，进而导致土壤环境的恶化，成为诱发作物连作障碍主要原因[33]。因此，研究者对作物连作过程中土壤微生物群落的变化机制给予了高度关注。

早期关于连作对土壤微生物影响机制的研究主要集中在大田作物，后期逐渐转向中药材、蔬菜和果树等作物的连作障碍研究。设施栽培作物连作障碍现象是当前园艺学科主要的研究热点内容之一。由于设施栽培是一种高度集约化的生产方式，长期种植单一作物容易引起连作障碍，表现为土壤质量退化、土传病害加重和自毒物质累积等问题[34-35]。土壤微生物是土壤养分代谢和土壤化学循环的主要参与者，因此土壤微生物群落的改变所引起土壤化学机制的变化成为了未来研究的重要方向之一。

**表 5 学科突发性检测知识图谱**

Table 5 Network map of category burst detection

| Subject | Year | Strength | Begin | End | 2003−2023 |
|---|---|---|---|---|---|
| Soil Science | 2003 | 13.42 | 2003 | 2023 | ▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| Agriculture | 2003 | 6.64 | 2003 | 2023 | ▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| Chemistry | 2003 | 3.64 | 2007 | 2023 | ▂▂▂▂▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| Horticulture | 2003 | 3.21 | 2008 | 2023 | ▂▂▂▂▂▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| Chemistry, Analytical | 2003 | 3.17 | 2011 | 2023 | ▂▂▂▂▂▂▂▂▬▬▬▬▬▬▬▬▬▬▬▬▬ |

每个条块代表 1 年，较细的条块表示其他年份，较粗的条块表示关键词突现的时间，“begin”和“end”分别表示关键词突现的开始时间和结束时间，“strength”表示关键词突现强度，强度越大表示关键词在文章中出现的频次越高、其重要程度和被关注度就越大，下同。

Each bar represents a year, the thinner bar represents other years, the thicker bar represents the time of keyword emergence, “begin” and “end” represent the start time and end time of keyword emergence, and “strength” represents the strength of keyword emergence. The greater the intensity is, the higher the frequency of the keyword in the article, the greater its importance and attention, the same as below.

## 2.7 关键词共现分析

关键词是一篇论文核心内容的体现，通过对文章的关键词进行共现分析，有助于研究者明晰该研究领域的研究热点及其变化趋势[36]。本文通过关键词共现分析得共现关键词 512 个，共现频次较高的关键词如表 6 所示。多样性(diversity)、微生物群落(microbial community)、氮(nitrogen)、碳(carbon)、管理(management)、微生物生物量(microbial biomass)和耕作(tillage)等是构成关键词知识图谱的核心节点(图 5)，表明目前该研究领域的研究热点主要集中在以下方面。

(1) 微生物群落特征与土壤碳氮循环。研究表明微生物群落结构通过与植物和土壤的相互作用影响土壤碳氮循环。土壤碳积累受土壤微生物生物量的增加与微生物分解之间平衡的影响，而微生物的分解过程受微生物生物量、微生物群落结构和土壤性质等因素的影响[37-38]。Six 等[39]和 Bastida 等[40]研究发现土壤真菌的生物量周转率和微生物代谢熵均低于细菌，因此土壤真菌与细菌的比值及总生物量的变化均能显著地影响土壤中的碳和氮的储存和通量，长期连作过程中，土壤细菌的生物量减少，真菌的生物量增加，土壤细菌/真菌比降低，导致碳氮循环受阻。土壤碳是微生物生命活动重要的碳源，其含量对微生物的丰度和群落结构具有显著的影响。Liu 等[41]研究表明土壤碳组分是影响真菌和细菌生物量的主要因素，其中土壤易氧化有机碳是真菌和细菌生物量的主要来源。Wang 等[42]研究发现随着连作年限的增加，根际土壤中微生物群落的多样性和丰度发生了显著的变化，土壤中需氧菌和固氮菌等功能菌株的数量显著减少。

**图 5 关键词共现知识图谱**

Figure 5 Knowledge graph of keyword co-occurrence.

**表 6 频次排名前 15 的关键词**

Table 6 Top 15 keywords in terms of citation count

| Ranking | Keywords | Count | Centrality |
|---|---|---|---|
| 1 | Diversity | 255 | 0.07 |
| 2 | Microbial community | 187 | 0.06 |
| 3 | Nitrogen | 136 | 0.07 |
| 4 | Carbon | 131 | 0.07 |
| 5 | Management | 125 | 0.08 |
| 6 | Rhizosphere | 120 | 0.04 |
| 7 | Plant | 109 | 0.03 |
| 8 | Growth | 106 | 0.03 |
| 9 | Microbial biomass | 102 | 0.06 |
| 10 | Tillage | 99 | 0.07 |
| 11 | Soil | 99 | 0.04 |
| 12 | Bacterial community | 96 | 0.04 |
| 13 | Enzyme activity | 92 | 0.04 |
| 14 | Organic matter | 91 | 0.03 |
| 15 | Crop rotation | 85 | 0.04 |

(2) 耕作管理对土壤微生物群落的影响。研究表明通过改变现有的种植制度，进行合理的轮作或间作可以改善连作所引起的土壤环境质

量的恶化[43]。此外，作物种类的变化导致作物根系分泌物种类发生变化，促使能够利用新分泌物作为碳源的微生物相对丰度的增加，从而改变了微生物的群落特征[44]。如 Wang 等[45]研究发现不同作物与三七轮作后土壤中有益微生物的丰度显著增加，潜在致病菌的丰度降低，尤其是薏米与三七轮作对于缓解连作障碍的效果最为显著。Dang 等[46]研究发现谷类作物与豆科植物间作有助于土壤微生物群落结构和多样性的提高，细菌 α 多样性显著高于真菌 α 多样性，固氮微生物的相对丰度显著增加，这显著提高了土壤中氮的有效性和植物氮素的积累，促进了土壤氮素的转化。此外，适宜的轮作或间作对缓解连作障碍具有重要的意义[47]。

## 2.8 关键词突现分析

关键词突现分析有助于分析某一研究领域的研究热点演替。通过关键词突现分析可以识别出在特定时间段内频繁出现的关键词，这些关键词反映了该领域当前的研究热点与趋势[36]。本文中，通过关键词突现分析得突现关键词 43 个，其中突现强度较高的关键词包括微生物量(microbial biomass) (20.76)、氮(nitrogen) (10.47)、芳基硫酸酯酶(arylsulfatase activity) (8.31)、管理(management) (8.26)和耕作(tillage) (8.13)等(表 7)。

由表 7 可知，作物连作过程中微生物群落介导的土壤养分循环方面的研究为该研究领域的热点之一。微生物生物量在土壤生态系统中起着重要的作用，能够维持土壤的健康和生态系统的功能稳定性。因此，保护和促进微生物生物量的增加及其多样性对于维护土壤生态系统的健康至关重要[48]。土壤微生物生物量的降低不仅减少了土壤中有益微生物类群的丰度，还导致土壤功能的下降，如养分转化功能等[49]。作物长期连作过程中，土壤中真菌的丰度随着连作年限的增加而增加，而细菌的丰度呈下降的趋势，特别是有益菌如固氮菌的丰度显著降低[50]。微生物作为土壤中氮素转化主要的参与者，通过微生物固氮作用转化的氮素占自然固氮的 90%，而连作过程中土壤中固氮菌生物量

**表 7　关键词突发性检测知识图谱**

Table 7　Network map of keywords burst detection

| Keyword | Year | Strength | Begin | End | 2003−2023 |
|---|---|---|---|---|---|
| Microbial biomass | 2003 | 20.76 | 2003 | 2023 | ▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| Nitrogen | 2003 | 10.47 | 2003 | 2023 | ▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| Crop rotation | 2003 | 6.03 | 2003 | 2023 | ▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| Arylsulfatase activity | 2003 | 8.31 | 2003 | 2023 | ▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| Organic matter | 2003 | 4.1 | 2004 | 2023 | ▂▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| Phosphorus | 2003 | 4.77 | 2004 | 2023 | ▂▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| Tillage | 2003 | 8.13 | 2005 | 2023 | ▂▂▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| Management | 2003 | 8.26 | 2005 | 2023 | ▂▂▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| Carbon sequestration | 2003 | 5.16 | 2005 | 2023 | ▂▂▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| System | 2003 | 4.46 | 2006 | 2023 | ▂▂▂▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| Intercropping | 2003 | 3.49 | 2006 | 2023 | ▂▂▂▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| Cotton | 2003 | 4.65 | 2007 | 2023 | ▂▂▂▂▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| Fatty acid | 2003 | 3.63 | 2007 | 2023 | ▂▂▂▂▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| 16S rRNA | 2003 | 4.13 | 2009 | 2023 | ▂▂▂▂▂▂▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬ |
| Temperature | 2003 | 4.83 | 2011 | 2023 | ▂▂▂▂▂▂▂▂▬▬▬▬▬▬▬▬▬▬▬▬▬ |

的减少导致土壤中氮素的固定和转化受阻，进而影响了植物对氮素的吸收[51-52]。

随着研究的深入，研究者开始关注连作对土壤中其他养分元素如碳、硫和磷等循环与转化的影响，如目前关注度较高且在短期内出现频率较高的关键词如土壤芳基硫酸酯酶。土壤中芳基硫酸酯酶主要来源于土壤微生物的一类重要的水解酶，芳基硫酸酯酶能够催化芳香族硫酸酯的水解反应，将其分解为硫酸盐类化合物和相应的芳香族化合物[53]。这一过程对于土壤中的硫素循环具有重要意义，因为硫酸盐是植物吸收硫元素的主要形式[54]。其次，土壤有机物分解过程中会产生大量芳香族硫酸酯，如果不能被有效分解，会导致土壤中有机质积累。芳基硫酸酯酶在有机质的分解和循环中发挥着关键作用，有助于维持土壤的有机质平衡[55]。此外，芳基硫酸酯酶的活性与土壤健康密切相关。高活性的芳基硫酸酯酶有助于土壤中有机质的分解。因此，近年来，研究者对芳基硫酸酯酶在土壤中的作用关注度逐渐增高。通过提高芳基硫酸酯酶活性，可以增强土壤微生物的代谢活动，提高土壤酶活性，进而促进土壤养分的转化和利用，这对于缓解农业生产中的连作障碍具有重要的应用价值[56]。

### 2.9 关键词聚类分析

关键词聚类分析有助于研究者发现在该领域中频繁出现的关键词之间的关联性，揭示出该研究领域的热点和主题[29]。本文利用 CiteSpace 软件进行关键词聚类分析，结果如图 6 所示，图中相同颜色的连线和节点表示为一个聚类，聚类模块值 $Q$ 值为 0.701 9，平均轮廓值为 0.848 1，表明聚类结构显著且结果可信度高。本文根据每个聚类的含义将 9 个聚类划分为以下两方面。

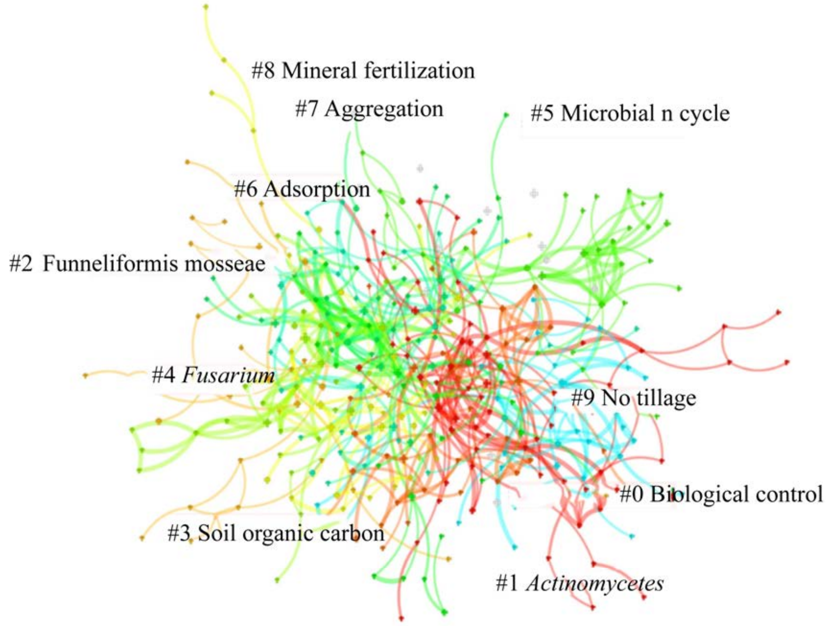

图 **6** 关键词聚类分析
Figure 6 Keyword cluster analysis.

(1) 连作的影响效应：相关的聚类包括土壤有机碳(soil organic carbon)、镰刀菌属(*Fusarium*)、聚合(aggregation)和微生物氮循环(microbial N cycle)。土壤碳含量是评价土壤健康的重要指标之一，在土壤肥力方面发挥着重要作用，研究表明作物连作主要影响土壤中碳的组成和化学成分[57]。此外，连作对土壤有机碳含量也有一定的影响，这种影响主要取决于土壤性质和种植的作物类型[58]。如棉花连作过程中，棉花残茬和有毒的代谢产物的积累限制了作物残体的降解，从而导致土壤中有机碳含量的降低[59]。作物连作对土壤氮矿化特征的影响主要受土壤质地、团聚结构及肥料的影响，研究表明黏土较沙土对土壤养分的结合能力更强[60]，然而长期连作过程中氮肥的施用导致氮的矿化速率降低，影响了土壤养分的循环，导致土壤肥力降低[61-62]。此外，作物连作过程中土壤微生物群落特征的改变如土壤中有害微生物的积累也是诱发作物连作障碍发生的主要原因之一[63]。其中镰刀菌为一种典型的植物致病菌，能够诱发多种植物病害，如党参根腐病、黄瓜枯萎病和玉米穗腐病等。作物连作容易导致镰刀菌等植物致病菌在土壤中的积累，进而引起植物病害的发生[64]。

(2) 连作障碍的缓解：相关聚类包括生物防治(biological control)、放线菌(*Actinomycetes*)、摩西管柄囊霉(*Funneliformis mosseae*)、吸附作用(adsorption)、矿物培肥(mineral fertilization)和免耕(no tillage)。连作障碍的发生是多种因素综合作用的结果，因此防治连作障碍需从多方面着手。目前，生物防治技术在连作障碍缓解中应用较为广泛，多采用以菌治菌的方法[65]，生物防治通过引入有益微生物，抢夺病原微生物的生存空间和养分来源，从而抑制有害微生物的生长[66]。此外，一些微生物的代谢产物在植物根际表面形成生物屏障，阻止了病原微生物的入侵，从而抑制了病害的发生[67]。如 Li 等[68]研究发现施用放线菌肥能显著提高土壤中有益菌的相对丰度，增加微生物群落的稳定性和抗逆性。摩西管柄囊霉菌属于丛枝菌根真菌(Arbuscular mycorrhiza fungi)的一类，研究表明 AMF 真菌可以促进作物对养分的吸收，也可以调节植物根际土壤微生物的群落平衡，从而改善土壤微环境的养分循环[69]。Guo 等[70]研究发现大豆连作过程中土壤中接种摩西管柄囊霉菌降低了土壤中真菌的多样性，并且土壤中镰刀菌等有害菌属的丰度显著降低。

此外，通过施肥及耕作措施的改变也可以在一定程度上缓解作物的连作障碍。Shi 等[71]研究发现施用有机肥能够显著增加土壤中重氮营养的微生物的多样性，形成稳定的氮素转化营养网络，从而提高土壤的肥力。Sainju 等[72]研究发现与常规管理措施相比，作物连作过程中免耕减少了土壤扰动，促进了作物残茬进入土壤，从而保持土壤肥力和作物的产量。土壤中施加生物质炭，利用其吸附作用，可以有效缓解土壤过度施肥和土壤污染所造成的负面影响，对连作障碍具有一定的缓解作用[73]。

## 2.10 关键词时间线图分析

关键词时间线分析有助于理解相关研究领域内关键词的演替和变化趋势(图 7)。本文根据关键词聚类的时间分布，将研究主题分为 3 个时间段。

起始阶段(2003−2007 年)。涉及的关键词有：生物量(biomass)、碳储存(C storage)、聚合(aggregation)、分解(decomposition)、α(β)-半乳糖苷酶(alpha and bate-galactosidase)、牛粪(cattle slurry)、三磷酸腺苷(adenosine triphosphate)、纤维素(cellulose)、氨基糖(amino sugar)、覆盖(cover)、碳(carbon)、杂草(bindweed)和作物生

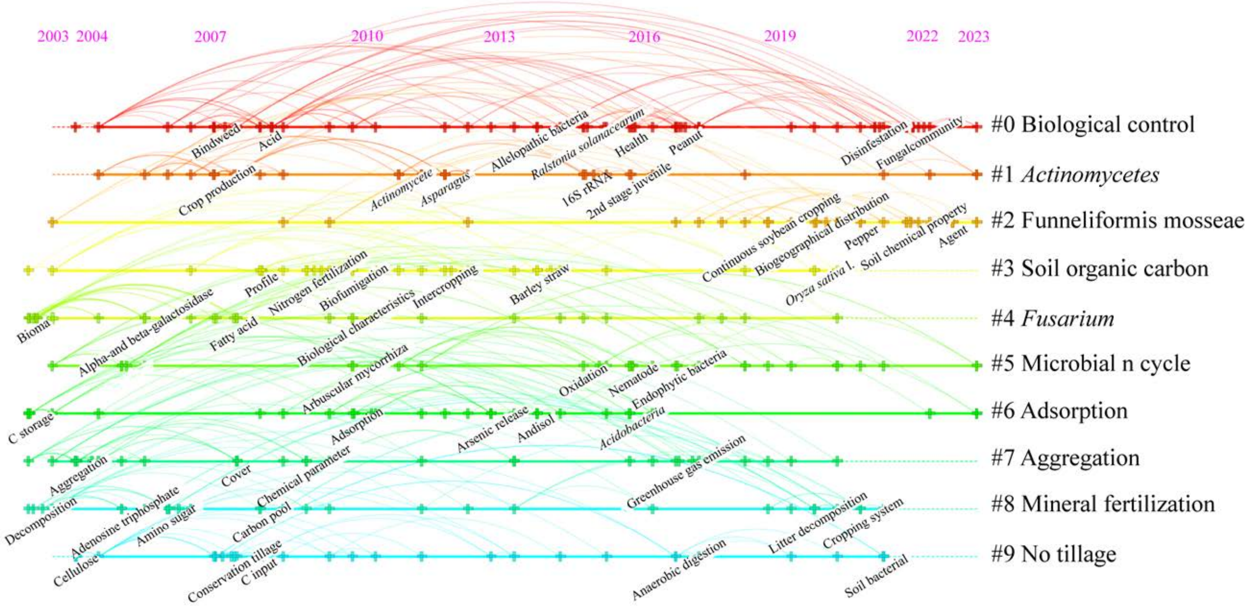

**图 7 关键词时间线图分析**

Figure 7 Time plot analysis of keywords.

产(crop production)。这一阶段的研究主要集中在连作对土壤理化性质的影响方面，通过采取不同的耕作措施以缓解作物连作障碍，研究重点侧重在耕作措施对土壤养分循环和酶活性的影响。

发展阶段(2007−2019 年)。涉及的关键词有：剖面(profile)、脂肪酸(fatty acid)、碳库(carbon pool)、保护性耕作(conservation tillage)、碳输入(C input)、施氮(nitrogen fertilization)、生物熏蒸(biofumigation)、生物学特征(biological characteristic)、间作(intercropping)、丛枝菌根(arbuscular mycorrhiza)、吸附(adsorption)、生化参数(chemical parameter)、放线菌(*Actinomycete*)、化感作用细菌(allelopathic bacteria)、青枯病(ralstonia solanacearum)、植物内生菌(endophytic bacteria)和酸杆菌门(*Acidobacteria*)等。这一阶段的研究主要集中在土壤微生物群落对连作及其对连作障碍缓解措施的响应，侧重于采用生物防治措施调控土壤微生物群落的结构。

成熟阶段(2019−2023 年)：涉及的关键词有：灭菌(disinfestation)、真菌群落(fungal community)、生物地理分布(biogeographical distribution)、土壤化学性质(soil chemical property)、凋落物分解(litter decomposition)、耕作制度(cropping system)和土壤细菌(soil bacterial)等。目前的研究主要集中在通过调控土壤养分分布以调节土壤微生物群落结构特征从而缓解连作障碍的影响。

## 3 讨论与结论

本文利用 CiteSpace 软件对近 20 年国际上关于连作对土壤微生物群落影响的研究文献进行了可视化分析，结果表明我国研究者对该研究领域具有较高的关注度和较高的发文量，在该研究领域具有较高的影响力。其中，发文量最高的研究机构为中国科学院。土壤微生物介导的土壤养分循环特征对作物连作的响应机制为目前研究的重点内容，通过耕作措施和田间

管理措施的改良缓解和防治连作障碍是潜在的研究热点。目前的研究表明，采取措施增加土壤微生物群落的多样性对于维持和改善土壤生态系统的物质循环以及缓解作物连作障碍具有重要作用，这些措施包括了轮作、间作、合理施肥和有机物添加等，通过调节土壤微生物群落的结构以提高土壤生态系统的稳定性和健康水平。

连作对土壤微生物群落影响主要表现为土壤微生物群落组成和稳定性的改变，通常呈现出负面效应。连作导致土壤环境恶化，影响微生物群落的食物供给和生存条件，间接改变了土壤微生物群落的组成和多样性，增加了微生物群落之间的竞争作用。为适应生存环境的变化，微生物群落会重新构建新的生态位，进而改变了其周围的土壤环境，这种改变会间接影响其他生物的适应能力，对土壤食物网的结构和功能产生了消极影响。目前，连作对土壤中其他生物如土壤原生生物和病毒等的群落结构和功能影响方面的研究较少，研究者应关注这些生物类群，以全面理解作物连作对土壤食物网结构和功能的影响。

此外，该研究领域未来的研究趋势是通过综合运用多种研究方法如跨组学数据整合，利用系统生物学方法，整合基因组学、转录组学、蛋白质组学和代谢组学数据，全面解析连作过程中土壤微生物群落功能和行为变化。通过建立微生物生态系统的动态模型，预测连作过程中土壤环境变化对微生物群落及其功能的影响机制。

## REFERENCES

[1] LI CW, CHEN GZ, ZHANG JL, ZHU P, BAI XF, HOU YP, ZHANG XX. The comprehensive changes in soil properties are continuous cropping obstacles associated with American ginseng (*Panax quinquefolius*) cultivation[J]. Scientific Reports, 2021, 11: 5068.

[2] ZHOU M, LIU CZ, WANG J, MENG QF, YUAN Y, MA XF, LIU XB, ZHU YX, DING GW, ZHANG JZ, ZENG XN, DU WL. Soil aggregates stability and storage of soil organic carbon respond to cropping systems on black soils of northeast China[J]. Scientific Reports, 2020, 10: 265.

[3] TAN G, LIU YJ, PENG SG, YIN HQ, MENG DL, TAO JM, GU YB, LI J, YANG S, XIAO NW, LIU DM, XIANG XW, ZHOU ZC. Soil potentials to resist continuous cropping obstacle: three field cases[J]. Environmental Research, 2021, 200: 111319.

[4] MO AS, QIU ZQ, HE Q, WU HY, ZHOU XB. Effect of continuous monocropping of tomato on soil microorganism and microbial biomass carbon[J]. Communications in Soil Science and Plant Analysis, 2016, 47(9): 1069-1077.

[5] XIA Q, RUFTY T, SHI W. Soil microbial diversity and composition: links to soil texture and associated properties[J]. Soil Biology and Biochemistry, 2020, 149: 107953.

[6] JIAO S, PENG ZH, QI JJ, GAO JM, WEI GH. Linking bacterial-fungal relationships to microbial diversity and soil nutrient cycling[J]. mSystems, 2021, 6(2): e01052-20.

[7] ZHAO J, ZHANG D, YANG YQ, PAN Y, ZHAO DM, ZHU JH, ZHANG LK, YANG ZH. Dissecting the effect of continuous cropping of potato on soil bacterial communities as revealed by high-throughput sequencing[J]. PLoS One, 2020, 15(5): e0233356.

[8] LIU WB, WANG N, YAO XD, HE DX, SUN HX, AO X, WANG HY, ZHANG HJ, ST MARTIN S, XIE FT, WANG JK. Continuous-cropping-tolerant soybean cultivars alleviate continuous cropping obstacles by improving structure and function of rhizosphere microorganisms[J]. Frontiers in Microbiology, 2023, 13: 1048747.

[9] PANG ZQ, DONG F, LIU Q, LIN WX, HU CH, YUAN ZN. Soil metagenomics reveals effects of continuous sugarcane cropping on the structure and functional pathway of rhizospheric microbial community[J]. Frontiers in Microbiology, 2021, 12: 627569.

[10] MA ZM, GUAN ZJ, LIU QC, HU YY, LIU LF, WANG BQ, HUANG LF, LI HF, YANG YF, HAN MK, GAO ZY, SALEEM M. Obstacles in continuous cropping: mechanisms and control measures[J]. Advances in Agronomy, 2023, 179: 205-256.

[11] PERVAIZ ZH, IQBAL J, ZHANG QM, CHEN DM, WEI H, SALEEM M. Continuous cropping alters multiple biotic and abiotic indicators of soil health[J]. Soil Systems, 2020, 4(4): 59.

[12] FREEMAN LC, ROEDER D, MULHOLLAND RR. Centrality in social networks: ii. experimental results[J]. Social Networks, 1979, 2(2): 119-141.

[13] DING X, YANG Z. Knowledge mapping of platform research: a visual analysis using VOSviewer and CiteSpace[J]. Electronic Commerce Research, 2022, 22(3): 787-809.

[14] LIU ZX, LIU JJ, YU ZH, YAO Q, LI YS, LIANG AZ, ZHANG W, MI G, JIN J, LIU XB, WANG GH. Long-term continuous cropping of soybean is

comparable to crop rotation in mediating microbial abundance, diversity and community composition[J]. Soil and Tillage Research, 2020, 197: 104503.

[15] TAN Y, CUI YS, LI HY, KUANG AX, LI XR, WEI YL, JI XL. Rhizospheric soil and root endogenous fungal diversity and composition in response to continuous *Panax notoginseng* cropping practices[J]. Microbiological Research, 2017, 194: 10-19.

[16] ZHAO QY, XIONG W, XING YZ, SUN Y, LIN XJ, DONG YP. Long-term coffee monoculture alters soil chemical properties and microbial communities[J]. Scientific Reports, 2018, 8: 6116.

[17] XIONG W, ZHAO QY, ZHAO J, XUN WB, LI R, ZHANG RF, WU HS, SHEN QR. Different continuous cropping spans significantly affect microbial community membership and structure in a vanilla-grown soil as revealed by deep Pyrosequencing[J]. Microbial Ecology, 2015, 70: 209-218.

[18] GAO Z, HAN M, HU Y, LI Z, LIU C, WANG X, MA Z. Effects of continuous cropping of sweet potato on the fungal community structure in rhizospheric soil[J]. Frontiers in Microbiology, 2019, 10: 2269.

[19] LIU H, PAN F, HAN X, SONG F, ZHANG Z, YAN J, XU Y. Response of soil fungal community structure to long-term continuous soybean crop**[J]. Frontiers in Microbiology, 2019, 9: 3316.

[20] CHEN S, QI G, LUO T, ZHANG H, JIANG Q, WANG R, ZHAO X. Continuous-cropping tobacco caused variance of chemical properties and structure of bacterial network in soils[J]. Land Degradation & Development, 2018, 29(11): 4106-4120.

[21] SHE S, NIU J, ZHANG C, XIAO YH, CHEN W, DAI LJ, LIU XD, YIN HQ. Significant relationship between soil bacterial community structure and incidence of bacterial wilt disease under continuous cropping system[J]. Archives of Microbiology, 2017, 199: 267-275.

[22] BAI L, CUI JQ, JIE WG, CAI BY. Analysis of the community compositions of rhizosphere fungi in soybeans continuous cropping fields[J]. Microbiological Research, 2015, 180: 49-56.

[23] LI XG, DING CF, ZHANG TL, WANG XX. Fungal pathogen accumulation at the expense of plant-beneficial fungi as a consequence of consecutive peanut monoculturing[J]. Soil Biology and Biochemistry, 2014, 72: 11-18.

[24] XIONG W, LI ZG, LIU HJ, XUE C, ZHANG RF, WU HS, LI R, SHEN QR. The effect of long-term continuous cropping of black pepper on soil bacterial communities as determined by 454 Pyrosequencing[J]. PLoS One, 2015, 10(8): e0136946.

[25] ZHOU XG, LIU J, WU FZ. Soil microbial communities in cucumber monoculture and rotation systems and their feedback effects on cucumber seedling growth[J]. Plant and Soil, 2017, 415: 507-520.

[26] DONG LL, XU J, ZHANG LJ, YANG J, LIAO BS, LI XW, CHEN SL. High-throughput sequencing technology reveals that continuous cropping of American ginseng results in changes in the microbial community in arable soil[J]. Chinese Medicine, 2017, 12: 1-11.

[27] DONG LL, XU J, FENG GQ, LI XW, CHEN SL. Soil bacterial and fungal community dynamics in relation to Panax notoginseng death rate in a continuous cropping system[J]. Scientific Reports, 2016, 6(1): 31802.

[28] QIN SH, YEBOAH S, CAO L, ZHANG JL, SHI SL, LIU YH. Breaking continuous potato cropping with legumes improves soil microbial communities, enzyme activities and tuber yield[J]. PLoS One, 2017, 12(5): e0175934.

[29] LI H, C. CRABBE M J, CHEN H. History and trends in ecological stoichiometry research from 1992 to 2019: A scientometric analysis[J]. Sustainability, 2020, 12(21): 8909.

[30] GAO ZY, HU YY, HAN MK, XU JJ, WANG X, LIU LF, TANG ZH, JIAO WJ, JIN R, LIU M, GUAN ZJ, MA ZM. Effects of continuous cropping of sweet potatoes on the bacterial community structure in rhizospheric soil[J]. BMC Microbiology, 2021, 21(1): 102.

[31] MACIAS-BENITEZ S, GARCIA-MARTINEZ AM, JIMENEZ PC, GONZALEZ JM, MORAL MT, RUBIO JP. Rhizospheric organic acids as biostimulants: monitoring feedbacks on soil microorganisms and biochemical properties[J]. Frontiers in Plant Science, 2020, 11: 633.

[32] CHEN Y, DU J, LI Y, TANG H, YIN Z, YANG L, DING X. Evolutions and managements of soil microbial community structure drove by continuous cropping[J]. Frontiers in Microbiology, 2022, 13: 839494.

[33] LIU ZX, LIU JJ, YU ZH, YAO Q, LI YS, LIANG AZ, ZHANG W, MI G, JIN J, LIU XB, WANG GH. Long-term continuous cropping of soybean is comparable to crop rotation in mediating microbial abundance, diversity and community composition[J]. Soil and Tillage Research, 2020, 197: 104503.

[34] LYU J, JIN L, JIN N, XIE JM, XIAO XM, HU LL, TANG ZQ, WU Y, NIU LJ, YU JH. Effects of different vegetable rotations on fungal community structure in continuous tomato cropping matrix in greenhouse[J]. Frontiers in Microbiology, 2020, 11: 829.

[35] SHEN WS, HU MC, QIAN D, XUE HW, GAO N, LIN XG. Microbial deterioration and restoration in greenhouse-based intensive vegetable production systems[J]. Plant and Soil, 2021, 463(1): 1-18.

[36] XU Y, LYU J, LIU H, XUE Y. A bibliometric and visualized analysis of the global literature on black soil conservation from 1983–2022 based on CiteSpace and VOSviewer[J]. Agronomy, 2022, 12(10): 2432.

[37] LIU N, SHAO C, SUN H, LIU ZB, GUAN YM, WU LJ, ZHANG LL, PAN XX, ZHANG ZH, ZHANG YY, ZHANG B. Arbuscular mycorrhizal fungi biofertilizer improves American ginseng (*Panax quinquefolius* L.) growth under the continuous cropping regime[J]. Geoderma, 2020, 363: 114155.

[38] LIU YY, BAO LM, SUN WW, CUI YS, LI XR, JI XL, WEI YL, TAN Y. Diversity and composition of active and total bacteria in rhizospheric soil in response to

continuous cropping years of *Panax notoginseng*[J]. Folia Microbiologica, 2023: 1-13.

[39] SIX J, FREY SD, THIET RK, BATTEN KM. Bacterial and fungal contributions to carbon sequestration in agroecosystems[J]. Soil Science Society of America Journal, 2006, 70(2): 555-569.

[40] BASTIDA F, ELDRIDGE DJ, GARCÍA C, KENNY PNG G, BARDGETT RD, DELGADO-BAQUERIZO M. Soil microbial diversity-biomass relationships are driven by soil carbon content across global biomes[J]. The ISME Journal, 2021, 15(7): 2081-2091.

[41] LIU MH, SUI X, HU YB, FENG FJ. Microbial community structure and the relationship with soil carbon and nitrogen in an original Korean pine forest of Changbai Mountain, China[J]. BMC Microbiology, 2019, 19(1): 218.

[42] WANG Y, ZHANG Y, LI ZZ, ZHAO Q, HUANG XY, HUANG KF. Effect of continuous cropping on the rhizosphere soil and growth of common buckwheat[J]. Plant Production Science, 2020, 23(1): 81-90.

[43] MUPANGWA W, NYAGUMBO I, LIBEN F, CHIPINDU L, CRAUFURD P, MKUHLANI S. Maize yields from rotation and intercropping systems with different legumes under conservation agriculture in contrasting agro-ecologies[J]. Agriculture, Ecosystems & Environment, 2021, 306: 107170.

[44] HARTMANN M, SIX J. Soil structure and microbiome functions in agroecosystems[J]. Nature Reviews Earth & Environment, 2023, 4: 4-18.

[45] WANG FY, ZHANG XM, WEI MT, WANG Y, LIANG ZS, XIA PG. Appropriate crop rotation alleviates continuous cropping barriers by changing rhizosphere microorganisms in *Panax notoginseng*[J]. Rhizosphere, 2022, 23: 100568.

[46] DANG K, GONG XW, ZHAO G, WANG HL, IVANISTAU A, FENG BL. Intercropping alters the soil microbial diversity and community to facilitate nitrogen assimilation: a potential mechanism for increasing proso millet grain yield[J]. Frontiers in Microbiology, 2020, 11: 601054.

[47] HAQ MZU, YU J, YAO GL, YANG HG, IQBAL HA, TAHIR H, CUI HG, LIU Y, WU YG. A systematic review on the continuous cropping obstacles and control strategies in medicinal plants[J]. International Journal of Molecular Sciences, 2023, 24(15): 12470.

[48] KASCHUK G, ALBERTON O, HUNGRIA M. Three decades of soil microbial biomass studies in Brazilian ecosystems: lessons learned about soil quality and indications for improving sustainability[J]. Soil Biology and Biochemistry, 2010, 42(1): 1-13.

[49] SINGH JS, GUPTA VK. Soil microbial biomass: a key soil driver in management of ecosystem functioning[J]. The Science of the Total Environment, 2018, 634: 497-500.

[50] HU HY, LI H, HAO MM, REN YN, ZHANG MK, LIU RY, ZHANG Y, LI G, CHEN JS, NING TY, KUZYAKOV Y. Nitrogen fixation and crop productivity enhancements co-driven by intercrop root exudates and key rhizosphere bacteria[J]. Journal of Applied Ecology, 2021, 58(10): 2243-2255.

[51] SOUMARE A, DIEDHIOU AG, THUITA M, HAFIDI M, OUHDOUCH Y, GOPALAKRISHNAN S, KOUISNI L. Exploiting biological nitrogen fixation: a route towards a sustainable agriculture[J]. Plants, 2020, 9(8): 1011.

[52] KUNITO T, KURITA H, KUMORI M, SAKAGUCHI K, NISHIZAWA S, FUJITA K, ISHIKAWA Y. Microbial synthesis of arylsulfatase depends on the soluble and adsorbed sulfate concentration in soils[J]. European Journal of Soil Biology, 2022, 111: 103418.

[53] LAI HL, GAO FY, SU H, ZHENG P, LI YY, YAO HY. Nitrogen distribution and soil microbial community characteristics in a legume-cereal intercropping system: a review[J]. Agronomy, 2022, 12(8): 1900.

[54] XUE YT, MISHRA P, EIVAZI F, AFRASIABI Z. Effects of silver nanoparticle size, concentration and coating on soil quality as indicated by arylsulfatase and sulfite oxidase activities[J]. Pedosphere, 2022, 32(5): 733-743.

[55] YU MJ, WU MX, SECUNDO F, LIU Z. Detection, production, modification, and application of arylsulfatases[J]. Biotechnology Advances, 2023, 67: 108207.

[56] ZHANG XH, SONG YL, YANG X, HU C, WANG KQ. Regulation of soil enzyme activity and bacterial communities by food waste compost application during field tobacco cultivation cycle[J]. Applied Soil Ecology, 2023, 192: 105016.

[57] JONES AR, ORTON TG, DALAL RC. The legacy of cropping history reduces the recovery of soil carbon and nitrogen after conversion from continuous cropping to permanent pasture[J]. Agriculture, Ecosystems & Environment, 2016, 216: 166-176.

[58] SEMMARTIN M, COSENTINO D, POGGIO SL, BENEDIT B, BIGANZOLI F, PEPER A. Soil carbon accumulation in continuous cropping systems of the rolling *Pampa* (*Argentina*): the role of crop sequence, cover cropping and agronomic technology[J]. Agriculture, Ecosystems & Environment, 2023, 347: 108368.

[59] ASHWORTH AJ, OWENS PR, ALLEN FL. Long-term cropping systems management influences soil strength and nutrient cycling[J]. Geoderma, 2020, 361: 114062.

[60] LI HY, LI CH, SONG X, LIU Y, GAO QX, ZHENG R, LI JT, ZHANG PC, LIU XL. Impacts of continuous and rotational cropping practices on soil chemical properties and microbial communities during peanut cultivation[J]. Scientific Reports, 2022, 12: 2758.

[61] DONG NQ, LIN HX. Higher yield with less nitrogen fertilizer[J]. Nature Plants, 2020, 6: 1078-1079.

[62] RAO DM, MENG FG, YAN XY, ZHANG MH, YAO XD, KIM KS, ZHAO J, QIU Q, XIE FT, ZHANG W. Changes in soil microbial activity, bacterial community composition and function in a long-term continuous soybean cropping system after corn insertion and fertilization[J]. Frontiers in Microbiology, 2021, 12: 638326.

[63] CHEN YD, DU JF, LI Y, TANG H, YIN ZY, YANG L, DING XH. Evolutions and managements of soil microbial community structure drove by continuous cropping[J]. Frontiers in Microbiology, 2022, 13:

839494.

[64] LÓPEZ-CORIA M, GUZMÁN-CHÁVEZ F, CARVENTE-GARCÍA R, MUÑOZ-CHAPUL D, SÁNCHEZ-SÁNCHEZ T, ARCINIEGA-RUÍZ JM, KING-DÍAZ B, SÁNCHEZ-NIETO S. Maize plant expresses SWEET transporters differently when interacting with *Trichoderma asperellum* and *Fusarium verticillioides*, two fungi with different lifestyles[J]. Frontiers in Plant Science, 2023, 14: 1253741.

[65] COLLINGE DB, JENSEN DF, RABIEY M, SARROCCO S, SHAW MW, SHAW RH. Biological control of plant diseases: what has been achieved and what is the direction?[J]. Plant Pathology, 2022, 71(5): 1024-1047.

[66] CHEN W, MODI DX, PICOT A. Soil and phytomicrobiome for plant disease suppression and management under climate change: a review[J]. Plants, 2023, 12(14): 2736.

[67] MENDES R, GARBEVA P, RAAIJMAKERS JM. The rhizosphere microbiome: significance of plant beneficial, plant pathogenic, and human pathogenic microorganisms[J]. FEMS Microbiology Reviews, 2013, 37(5): 634-663.

[68] LI YL, LI HY, HAN X, HAN G, XI J, LIU YT, ZHANG YJ, XUE QH, GUO Q, LAI HX. Actinobacterial biofertilizer improves the yields of different plants and alters the assembly processes of rhizosphere microbial communities[J]. Applied Soil Ecology, 2022, 171: 104345.

[69] KIM K, NEUBERGER P, DALY EJ, GORZELAK M, HERNANDEZ-RAMIREZ G. Arbuscular mycorrhizal fungi community linkages to soil nutrient availability across contrasting agroecosystems[J]. Applied Soil Ecology, 2022, 176: 104464.

[70] GUO N, LI L, CUI JQ, CAI BY. Effects of *Funneliformis mosseae* on the fungal community in and soil properties of a continuously cropped soybean system[J]. Applied Soil Ecology, 2021, 164: 103930.

[71] SHI W, ZHAO HY, CHEN Y, WANG JS, HAN B, LI CP, LU JY, ZHANG LM. Organic manure rather than phosphorus fertilization primarily determined asymbiotic nitrogen fixation rate and the stability of diazotrophic community in an upland red soil[J]. Agriculture, Ecosystems & Environment, 2021, 319: 107535.

[72] SAINJU UM, GHIMIRE R, PRADHAN GP. Improving dryland cropping system nitrogen balance with no-tillage and nitrogen fertilization[J]. Journal of Plant Nutrition and Soil Science, 2019, 182(3): 374-384.

[73] YUAN M, YU TB, SHI QH, HAN DW, YU KC, WANG LX, WANG SR, XIANG H, WEN RH, NIAN H, LIAN TX. Rhizosphere soil bacterial communities of continuous cropping-tolerant and sensitive soybean genotypes respond differently to long-term continuous cropping in mollisols[J]. Frontiers in Microbiology, 2021, 12: 729047.