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Review 综述

合成菌群在促进农业可持续发展中的研究进展

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摘　要：目前，全球农业可持续发展面临土壤退化、资源限制和环境污染等多重压力。随着人口持续增长，以及对粮食品质需求的不断提高，提升土壤健康水平已成为保障粮食安全的重要基础。虽然化肥在保障植物高产优质方面发挥着重要作用，但其过量或不合理使用会造成土壤酸化、水体富营养化等环境问题。植物根际有益微生物在宿主养分吸收、胁迫耐受性以及适应环境变化过程中发挥着重要作用。其中，合成菌群(synthetic microbial communities, SynComs)是通过定向设计功能明确、遗传背景清晰的多个微生物组合，从而实现单一菌株无法完成的复杂功能。它是破解植物-土壤-微生物关键界面互作机制的有力工具，在植物养分高效利用、抗逆性提升和化肥减量增效等方面发挥着关键作用。本文分析了 SynComs 的概念演化以及当前的研究态势，系统阐述了其构建原则、方法及技术工具，并从促进植物生长、抵抗生物和非生物胁迫、改善和恢复土壤健康等方面，概述了 SynComs 在农业可持续发展中的作用。最后，展望了未来的研究方向，应重视靶向型菌剂的研发、人工智能(artificial intelligence, AI)技术在群落构建中的应用，以及提高 SynComs 在田间应用的效果，为利用近自然微生物手段解决粮食安全、资源高效利用和环境保护的多目标协同发展问题提供支撑，进而推动我国农业绿色发展。

关键词：合成菌群；菌株相互作用；植物-土壤系统健康；农业可持续发展

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Research progress on synthetic microbial communities in promoting sustainable agriculture development

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Abstract: Currently, the sustainable development of global agriculture is facing multiple challenges, including soil degradation, resource constraints, and environmental pollution. With the continuous growth of the population and the increasing demand for food quality, improving soil health has become a crucial foundation for ensuring food security. Although chemical fertilizers play an important role in maintaining the high yields and high quality of plants, their excessive or unreasonable use can cause environmental problems, such as soil acidification and water eutrophication. Rhizosphere microbial communities play an essential role in plant nutrient acquisition, tolerance to environmental stress, and adaptation to environmental changes. Among them, synthetic microbial communities (SynComs) are designed *via* the targeted assembly of multiple microorganisms with well-defined functions and clear genetic backgrounds, enabling the achievement of complex functionalities that cannot be accomplished by single strains. They are powerful tools for deciphering the key interface interaction mechanisms among plants, soil, and microorganisms and play a vital role in promoting efficient utilization of plant nutrients, enhancing plant stress resistance, and increasing the efficiency and reducing the application of fertilizers. This study reviews the conceptual evolution, current research trends, and construction principles, methods, and tools of SynComs, and summarizes the role of SynComs in the sustainable development of agriculture from the aspects of promoting plant growth, inhibiting biotic and abiotic stresses, and improving and restoring soil health. Furthermore, this paper makes an outlook on the future research directions and emphasizes the research and development of targeted microbial agents, the application of artificial intelligence (AI) in community assembly, and the performance improvement of SynComs in field applications, aiming to support the coordinated and multi-objective development of food security, efficient resource utilization, and environmental protection through near-natural microbial means, thereby facilitating the green agricultural development of China.

Keywords: synthetic microbial communities; microbial interactions; health of plant-soil systems; sustainable development of agriculture

随着人类社会对优质农产品需求的持续增长，我国耕地质量正面临急剧退化的严峻挑战。据农业农村部《2019 年全国耕地质量等级情况公报》数据，我国存在突出障碍因子的农田土壤面积占耕地总面积的 21.95%[1]。其中，土壤盐渍化和酸化进程加速，致使耕作层理化性质发生改变；同时，传统耕作制度与重型农业机械的高频作业导致土壤机械压实程度不断加剧[2]。土壤结构性障碍限制了土壤的透气性和保水保肥能力，使土壤有机质含量和养分有效性显著降低，引发土地退化、草地贫瘠化和林地沙化等一系列问题，最终造成因土壤功能性衰退而严重制约植物生长和产量的情况[3-5]。预计到 2050 年，全球人口将接近百亿，人类对粮食的刚性需求将增加 70%[6]。因此在全球人口增长、资源与环境复合压力的背景下，确保全球粮食安全已成为亟待解决的难题。

虽然化肥被誉为现代农业的“营养针”，在保障粮食安全方面发挥着至关重要的作用，但过量和集约化施肥导致大量资源浪费、土壤质量下降、土壤酸化等问题，严重制约了农业可持续发展[6-9]。因此在保障粮食安全的同时，如何实现资源高效利用与生态保护是当前农业可持续发展的核心目标。

根际是植物根系吸收养分和水分的门户，是根系-土壤-微生物相互作用的微区域，定殖于该微环境中的微生物被称为根际微生物[10]。在自然环境中，它们会大量富集在植物根系内部和周围，这些微生物构成根际微生物组，根际微生物组通过活跃的物质转化和相互作用直接影响宿主植物的营养和健康，对于推动我国化肥减施、农药减量，促进农业绿色发展具有重要意义，因此根际微生物组也被视为植物的“第二基因组”[11-15]。然而，由于自然环境的异质性和复杂性，将单一优良微生物应用到土壤后，其会与土著微生物发生复杂的相互作用(竞争拮抗或协同共存)，因此激发单个土壤微生物发挥功能仍存在一定限制[13-16]。合成菌群(synthetic microbial communities, SynComs)是由多个功能菌种组成的复合体，能够实现单一菌株无法完成的复杂功能，从而弥补单一菌株功能受限的不足。大量研究表明，合成菌群在促进植物养分高效利用和提高植物抗逆性等方面展现出巨大潜力。例如，固氮菌与解磷菌的协同作用可显著提高氮磷利用率[16]；添加 SynComs 能修复酸化土壤的微生物网络结构[17]；由具有重金属抗性的细菌组成的 SynComs 能促进不同重金属污染土壤中植物的生长，降低重金属向植物地上部的转移，从而阻断重金属进入食物链的风险[18]。此外，研究表明 SynComs 技术可实现化肥减施、提高作物养分效率的目的，并且到 2030 年，全球对生物肥料的需求将达 50.2 亿美元，表明以 SynComs 为核心的生物肥料是支撑农业绿色发展、保障国家粮食安全的重要途径[19]。

目前，关于 SynComs 的研究虽进展迅速，但在其研究态势、构建工具及农业应用等方面仍存在诸多难题和挑战。本文采用 CiteSpace 等工具，基于 Web of Science (WOS)核心合集数据库对其进行相关文献的可视化分析以总结其研究态势，阐述 SynComs 的构建原则、方法与工具，以及 SynComs 在农业可持续发展中的应用，以期为合成菌群在农业可持续发展中的应用提供理论参考。

1 合成菌群的概念及研究态势

1.1 合成菌群的概念

合成菌群起源于医学研究中的合成生物学技术。Burlage 等[20]于 1994 年首次发现，将工程菌株引入微生物群落可形成共生微生物联盟，该联盟能够有效抑制病原菌的定殖，同时延长有益微生物的定殖时间，为微生物群落定向调控的相关研究开辟了新纪元[20-21]。随后，Brenner 等[22]在整合合成生物学领域的研究中提出了“工程微生物菌落(engineering microbial consortia)”的概念，这被视为合成菌群的前身，为合成菌群的形成与发展奠定了基础。随着相关研究的不断深入，De Roy 等[23]对合成菌群进行了明确定义：在特定受控条件下，由 2 种或多种已知微生物所构成的共培养体系。韦中等[24]基于合成生物学和生态学基本理论将合成菌群的概念扩充为：将分类地位明确、功能特性清晰的 2 个或多个不同微生物在特定可控条件下按预设比例进行混合培养，经定向进化最终获得一种高效、功能强、可控性好、易保存且便于应用的有机微生物群体[24-27]。这些优良特性使其在微生物组功能和生态机制的解析、农业生物技术等方面展现出巨大的研究价值和应用潜力[25]。

1.2 研究态势

SynComs 属于合成生物学、微生物学和微生物组学的交叉领域，是新兴的研究方向[22,25]。本文以“synthetic microbial consorti or synthetic microbial consortium or microbiota or microbiome or microbial community”和“soil”为关键词，根据 Web of Science 核心数据库检索结果和统计分析发现，近 10 年来 SynComs 相关研究呈快速增长趋势(图 1A)，其跨学科研究特征显著。2015−2025 年期间的学科分布数据显示，环境科学与生态学(38.86%)、农业(28.90%)、微生物学(18.11%)、植物科学(8.60%)是 SynComs 研究所涉及的主要领域(图 1B)。此外，SynComs 的相关研究也呈现地域分布特征(图 1C)，中国学者以 22 163 篇的发文量位居全球首位；美国次之(8 301 篇)；随后是德国(3 242 篇)、澳大利亚(2 333 篇)和西班牙(1 901 篇)等国家。这表明 SynComs 在环境安全与农业生产应用中发挥关键作用，其调控植物-土壤-微生物关键互作界面的复杂机制是目前学术界关注的焦点[28]，这为“破译”根际微生物菌群调控生态安全和植物健康的机制，科学指导根际菌群应用，保障农业可持续发展、粮食安全和生态健康提供科学依据和技术支持。

2 SynComs 的构建

构建 SynComs 是探究和利用复杂自然微生物群落的有效途径之一。其中，SynComs 的构建原则是确保其稳定性、功能性和可重复性的关键。然而，关于合成菌群的构建原则学术界存在诸多见解与观点。基于生态位过程理论的研究表明，群落的结构和代谢功能主要由确定性因素驱动，这些因素包括物种的固有特征、物种间的相互作用以及环境条件的影响。具体而言，微生物群落的组装过程被认为是由生物因素(如物种间的竞争、捕食等相互作用)和非生物因素(如 pH、温度等环境条件)共同塑造的；这种确定性过程的核心在于微生物对不同栖息地的偏好及其适应性策略存在差异，即不同物种在特定环境条件下的生存能力和功能表达决定了它们在群落中的分布和丰度，这种观点强调环境过滤和物种相互作用在群落构建中的主导作用[29-30]。有学者则认为，遗传进化在 SynComs 的种间相互作用中扮演核心角色。群落内各成员通过基因水平转移、突变和自然选择等进化机制不断适应环境变化并优化其功能，导致群落内物种间形成协同或竞争关系，从而使整个生态系统逐渐趋近一种功能最优的稳定状态[31-32]。Lawson 等[33]提出了一种以设计-构建-测试-学习(design-build-test-learn)循环为核心的研究范式，为 SynComs 的设计与优化提供了系统化框架。该方法要求首先根据目标设计并构建具有特定结构和功能的 SynComs，随后通过高通量测序、代谢组学等手段测试其功能，并利用机器学习(machine learning, ML)算法和数据分析工具总结规律，为下一轮设计-构建-测试-学习循环提供理论依据和实践指导[21,33]。SynComs 的构建融合了生态学、合成生物学与系统生物学等基本原理，其核心在于通过设计实现微生物间的功能分工与协同作用。目前，对 SynComs 构建方法的研究多聚焦于基于功能的“自上而下(top-down)”或基于相互作用的“自

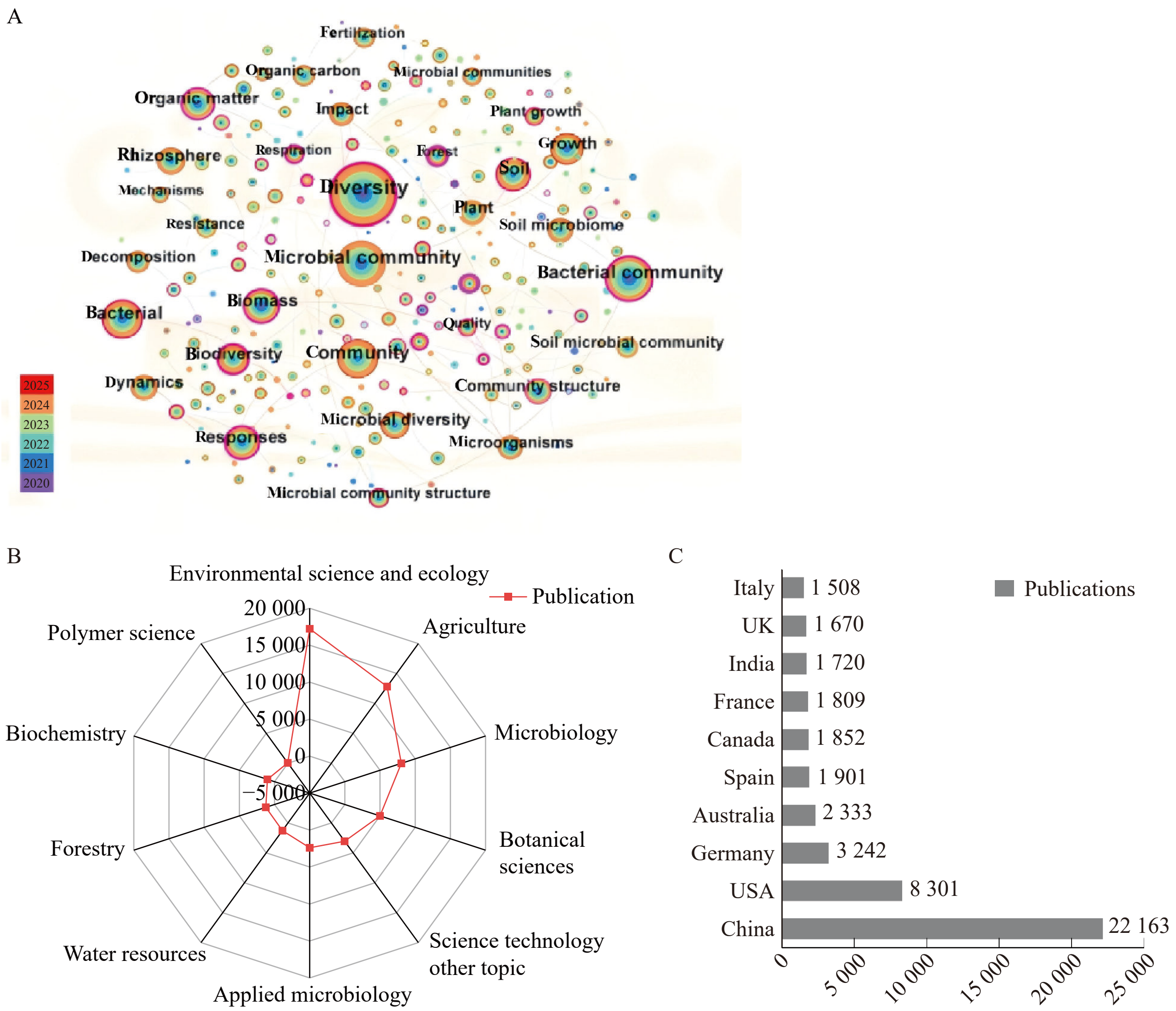


图1　合成菌群相关文献可视化分析。A：关键词共现图；B：近10年SynComs相关研究所涉及学科的占比图；C：近10年SynComs研究领域发文量排名前10国家的文献分布情况。

Figure 1　Visualization analysis of literature related to synthetic microbial communities. A: Co-occurrence map of keywords; B: Proportion of disciplines involved in SynComs research areas in the past 10 years; C: The distribution map of the top ten countries in terms of published papers in the SynComs research field in the past decade.

下而上(bottom-up)”，而忽略了微生物的进化关系与功能特征、生物间潜在的代谢互作关系等。本文将对以上 4 种构建方法进行较为全面的分析。

2.1　SynComs 的构建方法

2.1.1　基于分类学或系统发育的构建方法

基于分类学或系统发育的构建方法是指通过整合微生物的进化关系与功能特征来构建 SynComs，从而为高效稳定的功能群落组装提供理论基础。在以分类学为导向的组装中，研究者通常基于自然微生物的组成差异来筛选核心功能类群，这类方法主要依赖于自然群落的生态位分化规律。例如，Zhuang 等[34]通过分析不同农业实践下的根际微生物丰度差异，筛选出

与植物生长显著相关的菌株构建 SynComs，并通过试验证实其可显著提高植物生物量。系统发育驱动的组装策略则更关注微生物的进化关联与功能协同性。通过宏基因组和代谢组数据关联分析发现糖用甜菜根际中壳多糖酶编码(chitinase-encoding)基因的富集特征，据此构建的小型 SynComs 可有效抑制土传病害[35]。尽管分类学和系统发育组装方法各有侧重点，然而未来的研究趋势将更加强调对分类和系统发育数据的多维整合，从而进一步解决功能冗余和生态位竞争之间的平衡问题。

2.1.2 基于交叉喂养的代谢互作构建方法

基于表型互作的组装策略聚焦于菌株的代谢能力，通过筛选具有明确功能特征的菌株实现目标驱动的群落设计；交叉喂养(cross-feeding)正是以此为基础，通过设计微生物间的代谢互补关系以实现微生物群落稳定共存的基本方法；这种方法模拟了自然界中普遍存在的现象：大多数微生物无法合成自身所需的全部营养物质，而是通过与邻近微生物进行代谢物的交换，从而实现资源的互补与共享；此外，微生物群落通过代谢交叉喂养策略维持了从单一个体到复杂群落的功能完整性与生物多样性间的平衡[36-37]。研究表明群体感应(quorum sensing, QS)是这些微生物间相互作用的核心调控机制，其通过协调营养物质的摄取与代谢过程使微生物群落能够精确响应并适应不断变化的环境[38-39]。Ma 等[17]研究发现，红城红球菌(*Rhodococcus erythropolis*)和铜绿假单胞菌(*Pseudomonas aeruginosa*)组成的功能菌群对铝的耐受性优于单个菌株，并揭示了基于交叉喂养的微生物铝耐受性机制，为设计 SynComs 以支持酸性土壤地区的粮食安全和可持续农业提供新见解。然而，微生物交叉喂养相互作用的探索尚处于起步阶段，其分子识别机制、代谢物交换阈值及环境扰动响应等关键科学问题亟待系统解析[40]。

2.1.3 基于功能的“自上而下”构建方法

基于功能的“自上而下”构建方法(图 2)应用多组学分析技术，从宏观微生物群落入手，解析其系统运行规律，进而揭示维持系统稳定的分子机制[41-43]，即通过简化天然土壤微生物群落，对天然存在的微生物群落进行定向改造，保留特定功能模块进行定向重建[33,44]。该方法首先从自然环境中分离原始微生物群落，然后利用稀释技术或调整环境参数来模拟微生物群落的动态变化、自然演替或生态恢复过程，经过一系列继代培养后，获得一个简化的微生物群落体系，进而通过对该体系的精准操控以实现预期的特定功能[45]。该策略可优先保留自然群落中已存在的微生物互作关系，规避人工组合菌株间的非自然竞争或拮抗效应。该策略在土壤修复应用中表现出良好的功能延续性，特别是在有机污染物降解方面展现出工程化群落难以比拟的优势[46]。研究表明芽孢杆菌门(*Bacillota*)和拟杆菌门(*Bacteroidota*)的菌群在磺胺降解过程中发挥重要作用，其中芽孢杆菌属(*Bacillus*)和黄杆菌属(*Flavobacterium*)是关键菌群，这些微生物群落在 1 周内降解磺胺类抗生素近 50%，4 周后降解率可达 78.3%[47]。然而，“自上而下”策略需通过稀释培养或梯度富集获得低复杂度群落，但据估算，每克土壤中约含数万个物种、100 亿左右微生物，其中仅有 1%的物种可通过分离培养进行研究，因此该策略存在一定局限性。

2.1.4 基于相互作用的“自下而上”构建方法

随着高通量测序技术和生物信息学分析工具的飞速发展，研究者可通过整合测序数据与表型分析结果，精确模拟并预测微生物间的相互作用及其调控网络，并以此为依据设计具有特定功能的 SynComs，这种方法被称为“自下而上”的构建方法，目前这类研究主要集中在模式微生物上[44]。Chen 等[48]通过代谢组学与高通量分析揭示了氰化物会显著影响花生微生物群落的结构组成，而重组的花生根际微生物群落可

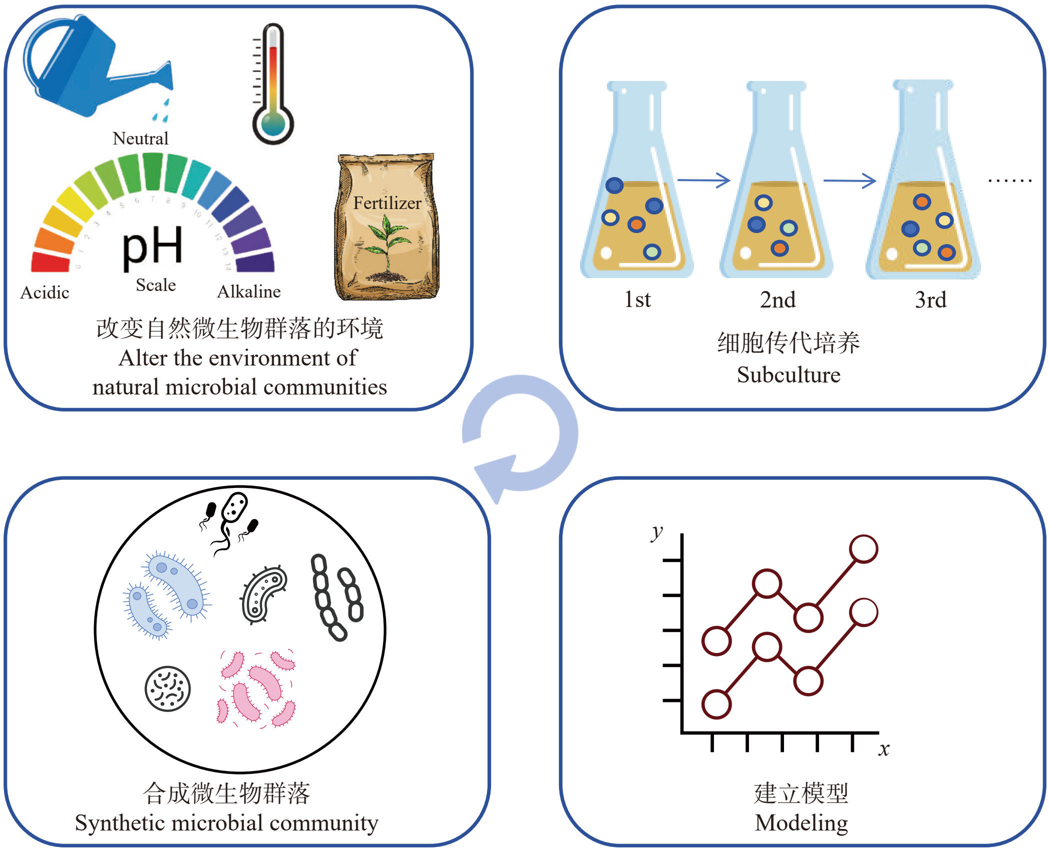


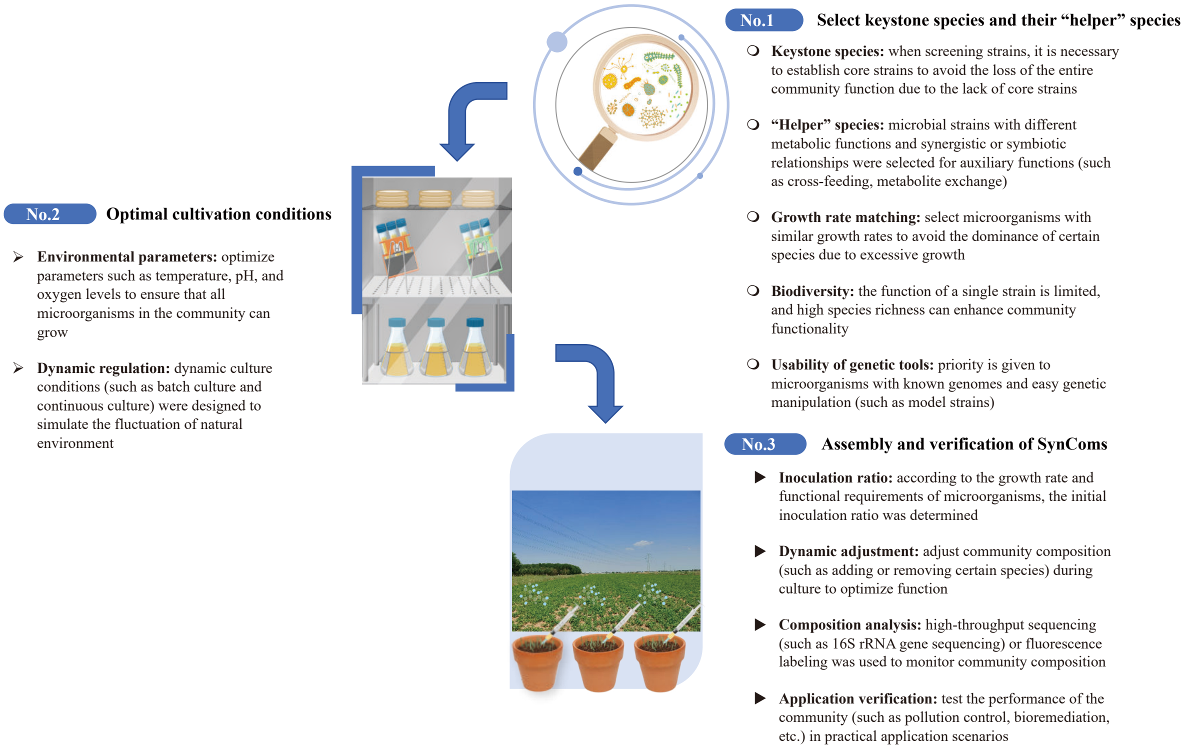
图2　SynComs的“自上而下”构建方法示意图

Figure 2　Schematic diagram of SynComs constructed by “top-down” method.

促进其根部对养分的吸收，进而提高植物产量。也有学者通过宏基因组数据分析和网络分析精准识别关键微生物类群及其功能特征，进而构建特定功能的 SynComs，实现对植物表型的定向调控[35]。然而，在自然微生物群落中不同物种对整体群落功能的贡献程度各不相同，因此从复杂的自然微生物群落中鉴别并筛选核心微生物是构建 SynComs 的关键。基于相对丰度、功能表达和微生物网络分析是目前常见的分离筛选核心微生物的标准[49]。然而，在实际研究中这 3 种筛选标准并非绝对孤立，而是相互补充、综合应用。通过结合相对丰度、功能表达和微生物网络分析等多方面信息可以更全面、深入地掌握微生物群落的结构和功能，从而更准确地筛选核心微生物。目前基于“自下而上”的 SynComs 的构建通常包括以下几个步骤：微生物的选择、培养条件的优化、群落的组装与验证(图 3)。

2.2　构建 SynComs 的工具与技术

在生物信息学与群落生态学模型取得突破性进展的驱动下，学者基于计算模拟和实验验证相结合的策略开发出多种 SynComs 构建工具，为环境修复、生物制造等领域的工程化应用提供技术支撑(表 1)。以广义 Lotka-Volterra 方程和消费者-资源动力学模型及代谢通量粗粒化模型为代表的群落生态模型，通过解析微生物群落内资源分配与代谢网络的耦合规律，建立了 SynComs 构建的定量调控框架[58]。代谢网络建模技术则是通过通量平衡分析(flux balance analysis, FBA)预测菌群代谢物转运路径，指导



No.1 Select keystone species and their “helper” species

- **Keystone species:** when screening strains, it is necessary to establish core strains to avoid the loss of the entire community function due to the lack of core strains
- **“Helper” species:** microbial strains with different metabolic functions and synergistic or symbiotic relationships were selected for auxiliary functions (such as cross-feeding, metabolite exchange)
- **Growth rate matching:** select microorganisms with similar growth rates to avoid the dominance of certain species due to excessive growth
- **Biodiversity:** the function of a single strain is limited, and high species richness can enhance community functionality
- **Usability of genetic tools:** priority is given to microorganisms with known genomes and easy genetic manipulation (such as model strains)

No.2 Optimal cultivation conditions

- **Environmental parameters:** optimize parameters such as temperature, pH, and oxygen levels to ensure that all microorganisms in the community can grow
- **Dynamic regulation:** dynamic culture conditions (such as batch culture and continuous culture) were designed to simulate the fluctuation of natural environment

No.3 Assembly and verification of SynComs

- **Inoculation ratio:** according to the growth rate and functional requirements of microorganisms, the initial inoculation ratio was determined
- **Dynamic adjustment:** adjust community composition (such as adding or removing certain species) during culture to optimize function
- **Composition analysis:** high-throughput sequencing (such as 16S rRNA gene sequencing) or fluorescence labeling was used to monitor community composition
- **Application verification:** test the performance of the community (such as pollution control, bioremediation, etc.) in practical application scenarios

图3　SynComs “自下而上”构建步骤与要点

Figure 3　Schematic diagram of SynComs constructed by the “down-top” method.

表1　构建合成菌群的相关模型

Table 1　Constructing relevant models of synthetic microbial communities

Model	Application	References
Lotka-Volterra model and consumer-resource model	The coupling law of resource allocation and metabolic network in microbial community was analyzed and the niche of microbial interaction was predicted	[50-51]
Coarse grained metabolic model	The response of the microbiota to interference was accurately predicted by simulating one-way, two-way, and multi-way cross-feeding	[52]
D-OptCom	It is used for multi-scale metabolic interaction simulation of microbial community and microbial community analysis	[53]
Genome-scale metabolic model	Systematically characterize the metabolic network of organisms, predict the exchange of metabolites between species (such as cross-feeding, electron transfer), and guide the optimization of strain combinations	[54-55]
Super community combinations	Simulating complex microbial community synergy for dynamic analysis of transmembrane metabolite exchange flux in microbial communities	[56]
Flux balance analysis	It is used to optimize the co-culture system, biological community metabolic network reconstruction and metabolic simulation	[57]

构建具有协同代谢功能的人工群落[59]。例如，通过多尺度代谢互作模拟动态代谢建模框架(dynamic OptCom, D-OptCom)预测微生物之间的代谢物交换，优化微生物群落[60]；基因组规模代谢模型(genome-scale metabolic model, GEM)的约束重建和分析(如 Cobra)方法，整合大量的生物学数据和数学方法，以研究混合微生物群落的代谢活动，为合理设计合成微生物群落提供

指导，并为生态修复提供有效策略[61]。

随着高通量基因组解析与多组学技术的快速发展，一些创新的计算模型和工具也应运而生，为处理大规模宏基因组数据集提供了便利，也为 SynComs 理性设计与功能优化提供了关键支撑[62]。例如，Hale 等[63]采用合成“长读长”序列和亲和力测序技术，深入探究了大豆根际微生物群落的组成与多样性，并据此探讨了其与环境因素和植物表型特征之间的关系。在功能基因组解析层面，病原与宿主互作数据库(pathogen host interactions database, PHI-base) (用于致病性鉴定)通过整合病原与宿主相互作用(pathogen host interactions, PHI)与表型突变数据，构建了基因型-表型关联网络图谱，为宿主-病原互作机制解析提供了基准数据库[64]；而 MacSyFinder 则基于蛋白结构域组成与基因簇排列规律，实现原核生物中大分子复合物的功能注释与进化解析[65]；AntiSMASH 则通过模块化算法精准注释次级代谢产物生物合成基因簇(biosynthetic gene cluster, BGC)，解析微生物化学多样性形成机制[66]。在群落代谢建模领域，超级群落组合(super community combinations, SuperCC)作为整合动态通量平衡分析与多组学数据同化的计算框架，通过构建多物种代谢网络的约束优化模型，用于微生物群落中跨膜代谢物交换通量的动态解析[56]。与其他模型相比，SuperCC 能更精准模拟复杂微生物群落的协同代谢网络，为设计和构建天然微生物组提供指导[56,67]。

随着人工智能(artificial intelligence, AI)技术的迅猛发展，机器学习算法已被成功应用于 SynComs 的理性设计与实验优化，通过高通量数据训练建立的预测模型，特别是在菌群组合预测、功能模块组装及生长参数优化等关键环节中，能够实现微生物群落组成-功能关系的精准预测(准确率>85%)，大幅提升菌群设计效率[62]。其中，机器学习和传统机器学习算法如线性回归、随机森林(random forest, RF)和支持向量机(support vector machine, SVM)通过监督式特征筛选与非线性模式识别能力，在微生物组数据解析中展现出显著效能($P<0.05$)，其预测精度与模型可解释性已通过多组学数据集验证[68-69]。此外，研究表明与传统随机分类方法与经验驱动的非建模预测相比，机器学习算法可显著提升分类精度与预测性能[70]。BacterAI (通过设计和使用实验平台生成成长数据，以便学者据此优化 SynComs 的模型设计)[71]和自动化合成微生物群落设计器(automated synthetic microbial community designer, AutoCD, 设计稳定稳态共培养物)[72]等均是机器学习算法的代表性技术。值得注意的是，深度学习(deep learning, DL)作为机器学习算法的重要分支，凭借其强大的特征提取能力已在多学科领域展现出卓越的适用性[73]。例如，在生态学中进行表型分析[74-75]，大规模监控的环境分析[76-77]等。随着合成生物学和生物信息学技术的协同快速发展，SynComs 构建的相关工具与技术在自动化程度和实用性方面不断优化，这将极大推动 SynComs 从实验室研究向产业应用的转化。

3 合成菌群在农业可持续发展中的应用

近年来，SynComs 在农业领域中的应用价值日益凸显，然而现代农业发展面临耕地资源锐减、气候变化加剧、土壤退化等多重挑战，这些挑战严重威胁农产品产量和安全，阻碍农业绿色发展。根际有益微生物作为植物微生态系统的关键成员，具有活化根区养分、促进植物生长、增强植物抗逆性、抑制土传病害等功能，已成为开发生物肥料和生物农药的重要资源，在推动化肥农药减量增效、实现农业绿色发展方面具有重要的价值[78]。本课题组前期从多种生境中分离鉴定了诸多植物根际促生菌(plant growth promoting rhizobacteria, PGPR) 菌株，并探究了这些菌株在促进植物生长、增强

植物抗逆性(特别是抵御盐碱、干旱等非生物胁迫)方面的潜力，为新型微生物肥料的研发利用提供菌种资源[79-83]。然而，单一微生物在实际应用中易受到自然环境的影响，当将其引入土壤环境后，这些外源微生物会与土著微生物建立复杂的生态关系(竞争抑制或协同共生等)，它们对植物-土壤系统的调控效果通常不稳定。因此，充分发挥单个土壤微生物的功能还存在一定限制。相比之下，基于生态位互补原理构建的 SynComs 通过多菌株的协同作用能够高效完成单一菌株难以实现的复杂生态功能，在促进植物养分高效利用和提高植物抗逆性方面具有巨大的应用前景[84]。Gou 等[84]基于荒漠优势植物梭梭根际挖掘的有益微生物资源，构建了一种由 4 株功能互补的 PGPR 菌株[*Bacillus* sp. WM13-24、假单胞菌属(*Pseudomonas* sp.) M30-35、解淀粉芽孢杆菌(*Bacillus amyloliquefaciens*) GB03 以及草木栖剑菌(*Sinorhizobium meliloti*) ACCC17578]组成的复合菌剂，其通过微生物互作网络显著改善了根际微生态环境，使土壤总氮含量提升 21.89%，活菌生物量增加 2.3 倍，并显著提高了微生物群落多样性，从而显著提升了辣椒植株的生长、果实产量和品质。这进一步表明通过精心设计、构建特定的微生物组合来优化土壤微生物群落结构能显著提高植物产量和品质。同时，SynComs 的应用对增强植物耐受性和抗病性、减少对化学肥料和农药的依赖等发挥重要作用，从而有力推动农业绿色发展(表 2)。

3.1 SynComs 在促进植物生长方面的应用

根际微生物作为植物的“第二基因组”，是植物生理调控的关键因子，在调节植物健康生长方面发挥重要作用，其群落结构与功能特征直接影响宿主植物的营养获取。研究表明 SynComs 的应用可显著提升长角豆(*Ceratonia siliqua* L.)中光合色素含量(如叶绿素 a/b、类胡萝卜素)，并通过增加根系水力传导率以提高水分及养分吸收效率，从而增强植物的光合作用[92]。将 8 种具有通过分泌有机酸来增溶土壤中难溶性无机磷能力的假单胞菌属的菌株构建成数量不同的 SynComs，可发现随着 SynComs 中菌株多样性的增加，假单胞菌属菌株的性能、番茄磷含量以及生物量的积累都显著增加[93]。此外，水稻氮转运和受体 *NRT1.1B* 基因在调控其根系微生物组中发挥关键作用。研究发现接种人工重组群落后籼稻根系比粳稻富集更多与氮循环相关的微生物，从而更好地改善有机氮条件下的水稻生长和氮素利用[94]。也有学者基于功能菌株筛选的方法从甘蔗根际筛选并构建了包含伯克霍尔德菌(*Burkholderia*)和假单胞菌(*Pseudomonas*)的 SynComs，该菌群能显著增加植物生物量(3.4 倍)[95]。在 SynComs 中引入固氮菌、解磷菌及有机质分解菌群，可显著提高养分利用效率，而且减少化肥和农药的使用[96-97]。以上研究也表明解析植物基因型-微生物功能-环境因子间的互作网络是实现根系微生物组精准调控的关键。

3.2 SynComs 在抵抗生物和非生物胁迫方面的应用

SynComs 在增强植物抵御胁迫方面扮演至关重要的角色。在应对生物胁迫方面，SynComs 通过调控微生物互作模式抑制病原菌入侵。例如，番茄根际微生物群落的竞争性互作(如营养争夺、生态位抢占)可显著降低病原菌定殖效率[98]；由枯草芽孢杆菌(*Bacillus subtilis*)构建的具有广谱抑菌性的 SynComs 可通过分泌多种抗菌物质、拮抗细胞活性物质及抑菌蛋白，破坏病原菌细胞膜完整性，使番茄青枯病发病延迟，显著降低病情指数[99]。在非生物胁迫响应方面，具有耐盐特性的细菌菌株所构成的 SynComs 可以有效提高植物耐盐性和产量[100]。同时，耐盐植物(如野大豆、田菁等)可通过根际招募具有促生功能及调节 Na^+浓度能力的微生物，形成盐胁

表2　合成菌群在农业生产中的应用

Table 2　Application of synthetic microbial communities in agricultural production

Plant	SynComs size & origin	Mechanism	Results	References
Solanum lycopersicum L.	15 strains (isolated from *Indigofera tinctoria* Linn. root of Jizan)	Differential expression of salt stress-related genes and ion accumulation in aboveground parts	Under salt stress and non-sterile conditions, SynComs has a strong growth-promoting effect on *Solanum lycopersicum* L.	[85]
Arabidopsis thaliana (L.) Heynh.	22 strains (symbiotic bacteria isolated from *Arabidopsis thaliana* (L.) Heynh. roots)	Redox-mediated mechanism of SynComs	The molecular mechanism was established to elucidate the composition of microbial communities derived from plants, and the functional diversity of plant rhizosphere-dependent specialized metabolites was analyzed	[86]
Zea mays L.	6 strains (*Bacillus* strains isolated from roots and leaves of *Zea mays* L.)	Endophytic microorganisms fight pathogens by competing, producing disease-resistant substances, or activating plant immune systems	Promote plant growth and significantly reduce the incidence of band-shaped leaf blight and sheath blight	[87]
Oryza sativa L.	4 strains (isolated from intercropping *Oryza sativa* L. roots)	Synergistic soil phosphorus activation, root architecture remodeling, and transporter gene regulation to regulate phosphorus use efficiency	It effectively regulates the distribution of P in the aboveground and underground parts of *Oryza sativa* L., promotes root growth and increases the yield of rice plants	[88]
Triticum aestivum L.	4 strains (isolated from *Triticum aestivum* L. rhizosphere)	Indole acetic acid producing bacteria and some volatile-releasing bacteria interact with fungi	Protecting *Triticum aestivum* L. from *Rhizoctonia solani* AG8 infection, reducing the occurrence of *Triticum aestivum* L. root rot and affecting plant characteristics	[89]
Cucumis sativus L.	2 strains (*Bacillus* strains isolated from *Cucumis sativus* L. rhizosphere soil and native *Pseudomonas* strains beneficial to plants)	Synergistic metabolic promotion between strains	Synergistically promote the growth of *Cucumis sativus* L., significantly increased the plant branch height, dry weight, and chlorophyll content	[90]
Glycine max	12 strains (isolated from *Glycine max* rhizosphere)	To systematically regulate the N and P signal transduction network at the transcriptional level and enhance the growth pathway related to auxin response	It significantly increased the nodulation rate and nitrogenase activity, and increased the field yield of *Glycine max* by approximately 20%−30%	[91]

迫适应性微生物组[101-102]。此外，功能微生物还可通过直接拮抗病原菌或诱导系统抗性这一双重机制来增强植物抵抗非生物胁迫的能力[103-104]。例如，Castrillo 等[105]通过分析野生型植物与突变株的微生物群落揭示了植物磷胁迫响应与其共生微生物的互作关系，在磷胁迫下植物通常容易被微生物群落中潜在的机会主义竞争者定殖，从而加剧植物的磷饥饿(phosphate starvation response, PSR)。SynComs 能够激活低磷胁迫下植物 PSR 应答核心调控因子——植物免疫系统基因 PHR1 的活性，这种协同效应不仅促进了正常植物根际微生物组的组装，还可构建由共生生物主导的生物防御屏障，从而抑制病原菌的入侵[105-106]。这些研究可为利用微生物群落调控策略增强植物对生物和非生物胁迫的抵御能力提供支撑。

3.3 SynComs 在改善与恢复土壤健康方面的应用

SynComs 通过多维度调控机制在改善土壤生物组成部分、理化性质以及增强生态修复效能等方面展现出独特优势，有助于提升土壤肥力和健康水平。Sun 等[90]研究发现，将有益芽孢杆菌菌肥接种到土壤中可定向富集有益微生物类群，并通过代谢互作增强本土微生物群落的丰度和抑菌功能。Qiao 等[107]通过构建对苹果病原菌具有显著拮抗作用的 SynComs，发现经 SynComs 处理后的植物根际有益菌丰度增加，病原真菌丰度降低，并且微生物网络复杂度(边数、平均度)显著提升，负相互作用减少(竞争比例从 47% 降至 36%)。此外，Song 等[108]研究证实了在盐碱地改良中 SynComs 与有机改良剂协同施用可提升土壤碳储量 9%–40%。其中，微生物分泌的类蛋白黏合剂可通过桥接作用促进土壤形成团粒结构，该过程可显著改善土壤三相结构比例，使水肥保持效率显著提升[109]。在生物修复方面，20 世纪 80 年代便有学者提出利用功能微生物解决重金属污染土壤的问题。通过微生物的生物化学过程可有效固定土壤中的重金属离子，并将其中有害的重金属离子转化为无害或毒性大幅降低的形态[110]，为重金属污染土壤的生物修复开辟了新途径。SynComs 可通过构建多级代谢网络实现污染物定向转化：(1) 在重金属修复方面，PGPR 间的协同作用不仅能增强宿主植物应对各类环境胁迫的能力，还能调节植物对重金属的耐受性，并影响土壤中重金属的活化、稳定、迁移及转化过程[111]；此外，土壤改良剂联合丛枝菌根真菌(arbuscular mycorrhizal fungi, AMF)、腐生丝状真菌 *Aspergillus terreus* 通过调控金属转运蛋白表达及氧化还原酶活性，将 Cr(Ⅵ)还原为低毒态 Cr(Ⅲ)，同时抑制重金属向植物地上部迁移[112]；(2) 在有机污染物治理方面，高秀荣[113]发现与传统单一菌株的修复技术相比，构建的多环芳烃(polycyclic aromatic hydrocarbons, PAHs)降解菌群可显著提高 PAHs 修复效果，土壤 PAHs 总去除率可达 45.7%。上述结果表明，SynComs 在土壤健康管理中发挥重要作用。

4 总结与展望

SynComs 作为一种新兴的交叉学科方向，其通过微生物成员间的功能互补和代谢互作在多变的环境中展现出比传统单一菌株更为独特的优势。这种多菌株协同体系不仅能够有效调节土壤微生态平衡，促进植物健康生长，提升植物抗逆性，还蕴含着巨大的生态修复潜力，为应对传统农业中病害频发、营养失衡及土壤退化等难题提供了近自然的微生物解决方案。然而，构建并应用稳定且功能强大的 SynComs 仍面临诸多难题。

如何突破“微生物暗物质”培养瓶颈，以及如何高效筛选和组合这些微生物菌株，是 SynComs 构建所面临的首要难题。因为自然环境具有时空异质性，研究者难以准确识别在特定环境或功能中发挥关键作用的核心微生物。加之目前分离方法的局限性，环境中绝大部分微生物仍不能被纯培养，这严重阻碍了对微生物生命活动规律的探究及其利用，可能会导致部分优良功能微生物尚未被发掘。因此，应结合各种先进的技术或手段，改进培养措施、开发新型培养技术或多维度筛选技术等，以充分挖掘潜在的功能微生物。

微生物在植物根际动态定殖过程中，SynComs 成员与宿主发育阶段、组织微环境存

在时空特异性互作，其表型调控的关键基因元件(如群体感应基因、抗生素合成基因)与代谢途径(如铁载体、植物激素合成)的精准解析仍需系统研究。然而，现有 SynComs 的构建通常局限于单一营养级的菌群组合，忽视了自然土壤微环境中微生物之间跨营养级的复杂互作。即在自然土壤微环境中细菌-真菌-原生生物-线虫形成的跨营养级互作网络，在实验室条件下常被简化为单一营养级菌群组合。这种策略难以模拟根际真实生态位，可能导致菌群田间应用存在“水土不服”现象。因此，今后在 SynComs 的研究中需构建跨营养级复合菌群系统，通过引入捕食者(如原生生物)与分解者(如真菌)形成生态闭环，从而提升 SynComs 的生态位适应能力，并全面解析复杂群落间的多层次互作关系。

需重视 SynComs 的中试、生产与示范，以精准评估其稳定性与效果，研发靶向型菌剂，最终实现 SynComs 在农业可持续发展中的精准应用。结合 AI 在农业生产、环境监测、微生物群落优化等实践中的应用，需通过多源数据融合与智能分析技术、AI 驱动的微生物-植物互作研究平台构建、基于 AI 的微生物群落优化算法开发这三大核心路径，提高 SynComs 在植物健康中的应用效能，最终推动生态友好型农业体系的可持续发展。

作者贡献声明

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作者利益冲突公开声明

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