

还田秸秆碳在土壤中的转化分配及对土壤有机碳库影响的研究进展

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摘要 农田土壤有机碳库是全球碳循环的重要组成部分.随着秸秆还田技术的广泛应用,作物秸秆成为土壤外源碳的主要来源.秸秆碳在土壤中的转化与分配直接影响土壤有机碳组成与含量,进而改变土壤养分循环.基于近年来的相关研究,本文探讨了还田秸秆碳转化与分配过程的影响因子,详细介绍了参与秸秆碳同化过程的土壤微生物组成,归纳与阐述了秸秆碳对土壤有机碳组成、含量及其周转的影响.同时,就非生物因子对秸秆碳的生物转化效应的影响、秸秆碳转化过程中的生物和非生物因子的互作、秸秆碳氮和土壤碳氮循环的耦合作用、秸秆碳向土壤活性有机碳库或稳定性有机碳库转化的有效调控技术等主要研究方向进行了展望,以期为准确揭示秸秆还田条件下各类土壤有机碳的变化特征,进而为实现秸秆还田的高效培肥与固碳效应提供理论依据和技术支撑.

关键词 秸秆还田; 土壤有机碳; 秸秆碳转化; 秸秆碳分配; 秸秆碳同化微生物

Transformation and distribution of straw-derived carbon in soil and the effects on soil organic carbon pool: A review. YANG Yan-hua^{1,2}, SU Yao^{2*}, HE Zhen-chao², YU Man², CHEN Xi-jing², SHEN A-lin² (¹*College of Environment and Resources, Zhejiang A & F University, Hangzhou 311300, China*; ²*Environmental Resources and Soil Fertilizer Research Institute, Zhejiang Academy of Agricultural Sciences, Hangzhou 310021, China*).

Abstract: Farmland soil organic carbon (SOC) pool is a crucial component of global carbon cycle. Due to the widely-implemented straw returning, crop straws have become the primary exogenous carbon source for agricultural soils. The conversion and distribution of straw-derived carbon in soil directly affect the composition and contents of SOC, with further influence on soil nutrient cycling. Based on recent studies, this review investigated the factors impacting the transformation and distribution of straw-carbon; introduced the microbial composition that contributes to the assimilation of carbon from straw; and summarized the effects of straw-carbon on the composition, content, and turnover of SOC. Additionally, we proposed the future research regarding the effects of abiotic factors on the bio-transformation of straw-carbon; the interaction between biotic and abiotic factors during the straw carbon transformation processes; the coupling of carbon and nitrogen from straws into the soil carbon and nitrogen cycles; and the effective control over the transformation of straw-carbon that enters the active or stable soil organic carbon pool. The purpose was to reveal variation characteristics of SOC during straw returning, and provide theoretical basis and technical support for the efficient fertilization and carbon sequestration of straw returning.

Key words: straw return; soil organic carbon; straw-C conversion; straw-C distribution; assimilating straw-C microbes.

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我国秸秆年产达 7 亿~8 亿 t,居世界首位^[1-2]。秸秆中富含有机物,是重要的生物质资源^[3-4],可通过肥料化、饲料化、基质化等技术加以利用^[5]。秸秆还田是我国目前主要的资源化利用方式^[6],但不同省份的还田比例存在差异,在 7%~67.1%^[7]。随着国家相关部委关于秸秆禁烧和综合利用政策的相继颁布,以秸秆还田为优先方式的秸秆利用模式得到快速发展。

还田进入土壤的秸秆在微生物的作用下大部分被转化为 CO₂ 释放至大气中^[8],剩余的碳组分经微生物同化后进入土壤有机碳库,使土壤有机质含量和总碳储量得以维持或增加^[9]。根据土壤有机碳(soil organic carbon, SOC)的存在方式及其稳定性,可将其划分为活性有机碳、缓效性有机碳和稳定性有机碳。从土壤肥力角度考虑,活性有机碳含量高则有利于矿化分解,从而提高土壤养分含量,但从土壤固碳角度考虑,稳定性有机碳含量的增加会更有利于土壤有机碳固定^[10-11]。因此,秸秆碳的转化及其分配过程与秸秆还田后土壤肥力和固碳能力的变化密切相关。近年来,国内外学者从不同的时间尺度、还田方式、土壤类型和肥力水平等角度探究了秸秆碳的转化分配及其对土壤有机碳库的影响,秸秆还田条件下的农田土壤变化已成为研究热点。有关参与秸秆碳同化的微生物群落特征的研究工作也相继开展并取得了较大进展。秸秆碳在土壤中的转化与分配同时受外界环境因子和内在生物因子的共同影响。然而,目前还未有报道对这两部分内容进行系统的归纳总结。

鉴于此,本文对秸秆碳在土壤中的转化与分配及其影响因素、秸秆碳同化微生物组成以及秸秆还田下土壤有机碳库的变化等国内外相关研究进行综述,以期为进一步解析秸秆还田条件下土壤有机碳库的动态变化机制及其微生物机理提供参考,为实现对秸秆碳转化过程的有效调控提供理论支撑,进而实现秸秆资源的高效利用。

1 土壤有机碳库组成及分类概述

SOC 是土壤有机质的化学度量,与土壤质量和土壤肥力密切相关,对于调节碳元素的地球生物化学循环有着重要作用^[12]。SOC 不同组分间存在高度异质性,可表征土壤的不同性状。随着国内外相关研究的深入,对于 SOC 组分的分类方法也在不断的改进和完善。早期的 SOC 组分分类主要根据其单一特性的差异进行,较难反映其综合特征,如依据化学浸

提剂不同^[13],将 SOC 分为水溶解性有机碳(dissolved organic carbon, DOC)、酸水解有机碳和易氧化有机碳(labile organic carbon, LOC);依据其物理特性^[14],如密度的不同,分为轻组有机碳和重组有机碳;对于 SOC 组分中的颗粒性有机碳(particulate organic carbon, POC),根据其结合的团聚体大小和性质的不同,又分为大团聚体有机碳、微团聚体有机碳、矿物结合有机碳(mineral-incorporated organic carbon, MOC)等^[15-17]。依据其生物特性,可分为微生物生物量碳(microbial biomass carbon, MBC)和可矿化碳^[14]。Stewart 等^[18-19]根据不同有机碳组分的特性,提出物理-化学联合分组方法,将 SOC 分为 4 大类,即游离活性有机碳库、物理保护有机碳库、化学保护有机碳库和生物化学保护有机碳库。该类分组方式可综合表征 SOC 的物理化学特性,亦可在一定程度上反映 SOC 的固碳潜力。近年来,多数学者根据 SOC 生物稳定性和周转期的不同,将 SOC 组分归类为活性有机碳、慢性(缓效性)有机碳和惰性(稳定性)有机碳^[20-22]。其中,活性有机碳组分主要包括 LOC、DOC 和 MBC,因其转化周期短、易被微生物分解利用,常用作土壤碳循环和有效养分变化周转的敏感指标^[23-25]。慢性(缓效性)有机碳,主要指 POC,是介于动植物残体和腐殖化有机物之间的有机碳形态,是活性向惰性有机碳转化的过渡性有机碳,可反映土壤有机碳的固定趋势^[26],也有学者将其归为活性有机碳组分^[27]。惰性(稳定性)有机碳多指与细粒矿物质紧密结合,不易被微生物分解或植物利用的碳量^[28-29]。该类分组方法可更好地反映 SOC 的转化分配与固碳潜力,是目前应用较为广泛的一类分组方法。

2 还田秸秆碳的转化分配及相关微生物组成

2.1 还田秸秆碳的转化与分配

早在 1963 年,¹⁴C 同位素示踪技术就被用来研究有机碳在土壤汇中的周转^[30],与之相比,¹³C 具有标记均匀、无放射性、无污染,且适用于短期培养和长期定位试验等优点^[31-34],在 20 世纪 80 年代后被越来越多的研究者采用。通过向土壤中添加¹³C 标记的玉米、小麦、水稻等作物秸秆,对秸秆¹³C 在 CO₂ 和 SOC 中的转化进行了研究,这些研究结果表明不同类型作物秸秆碳的转化总体上均呈现先快后慢的规律。对于玉米秸秆而言,添加后 12~14 d 秸秆碳的分解转化率可达最大,CO₂ 累积释放碳量占 50% 以上,此后,秸秆碳转化速率逐渐下降并趋于稳定^[35-36]。

小麦秸秆施入土壤后的前2~3周为其快速分解转化期,约有半数以上的秸秆碳以 CO_2 释放形式损失^[37-38].相较于玉米和小麦秸秆,水稻在淹水土壤中秸秆碳的快速分解期略有滞后,在18~21 d碳释放量才达到最大值^[39-40],但其分解转化更为完全.

秸秆碳在土壤中的转化快慢和转化程度除了与还田环境有关外,还与秸秆自身有机碳组成密切相关.秸秆中不同含碳组分的分子量和结构稳定性的不同,造成微生物对其分解转化能力有所差异.Wang等^[41]研究结果显示,不同气候条件下同一类型土壤中的玉米和小麦秸秆随分解转化的进行,秸秆碳组分中二氧烷基C和O/N烷基C含量减少,而烷基碳、芳香碳、芳香C-O基团和COO/N-CO基团增加.这些变化反映了分解过程中蛋白质等易分解碳化合物的损失,而含有高比例芳香碳的难分解有机质相对含量有所积累.一般而言,作物秸秆中的易分解碳组分,如淀粉、蔗糖、低聚糖、果糖和氨基酸等,能在短期内被土壤微生物矿化分解,约占秸秆总有机碳的51%~63%;而秸秆中的慢分解碳组分,如半纤维素、纤维素、木质素和多酚类等,所占比例为16%~35%,这些碳组分虽也能被微生物代谢利用,但在较短时间内无法实现矿化,大多仍以秸秆碳形式残留于土壤中^[3,21,42].相较于小麦秸秆,玉米秸秆中易分解的水溶性物质和粗蛋白质含量高、难分解的纤维素和木质素含量较低,因此能在更短时间内被微生物分解利用和腐殖化^[41].

现有的秸秆碳在土壤不同有机碳库中的转化分配比例的研究结果显示,秸秆碳转化过程中42%~79%的秸秆碳被转化为 CO_2 进入大气,1.9%~13.9%的秸秆碳可转化为土壤活性有机碳,其中1.9%~10.6%进入土壤MBC,0.01%~3.3%进入土壤DOC,另有约10%的秸秆碳可转化为土壤POC^[21,43-45],而进入土壤POC中的秸秆碳将在不同粒级的土壤团聚体中进一步分配,转化为更稳定的SOC组分,实现土壤固碳效应^[40].相较于大团聚体,进入微团聚体中的秸秆碳的稳定性更高,且分配比例随秸秆添加时间的延长而逐渐增加^[46-49].刘哲等^[50]研究显示,水稻秸秆碳在粒径250~53、<53、>2000、250~2000 μm 的砂姜黑土团聚体中的分配比例分别为37.5%、29.2%、22.4%、10.9%.综上,仅不足40%的秸秆碳经转化分配后进入土壤碳库,并以活性有机碳为主,稳定性较弱,对土壤培肥与碳固持的贡献有限.未来,需深入研究不同条件下秸秆碳的转化分配机制,明确影响秸秆碳向不同碳库转化的关键因子,

为合理有效调控秸秆碳向土壤活性或稳定性有机碳库的转化,实现秸秆还田的持续增碳培肥效果提供理论依据.

2.2 还田秸秆碳转化与分配的影响因素

秸秆碳在土壤各有机碳库中的分配除了受自身化学组分性质的影响外,还与土壤类型、土壤肥力、土壤含水量及耕作制度等密切相关.秸秆碳转化过程中存在对土壤微生物种群的选择性差异^[45,51],而不同类型土壤由于其土著微生物群落组成本身存在差异,从而影响秸秆碳在不同类型土壤中的转化与分配.秸秆施入棕壤后60 d, MBC升至最高;黑土中,其最高MBC出现在秸秆添加后360 d;相较于棕壤,秸秆碳在黑土中更容易转化为DOC^[21].此外,成土母质类型和特点的差异也会造成不同类型土壤间秸秆碳在SOC中的转化分配差异.相较于以2:1型蒙脱石黏土矿物为主的砂姜黑土,黏土矿物主要为1:1型高岭石的红壤对秸秆碳的保护较弱,因此,更有利于秸秆碳在前期的分解转化^[39].

同类型土壤在不同肥力水平下秸秆碳的转化与分配也存在差异.相较于中、高肥力土壤,虽然秸秆碳在低肥力土壤中的转化速率较慢,但其对SOC的贡献比例却更高.王旭东等^[52]研究了玉米秸秆碳在不同肥力壤土中的动态变化,结果显示,秸秆碳在中、高肥力水平下的分解转化率分别为90%和85%,高于低肥力壤土的82%.Pei等^[9]通过 ^{13}C 标记玉米秸秆探究了秸秆碳在不同肥力土壤中的动态转化与分配,结果表明,秸秆碳对棕壤和黑土SOC的贡献均呈现低肥力(36.3%~62.8%)大于高肥力(11.6%~53.2%)趋势.An等^[45]研究表明,秸秆碳对MBC的贡献在低肥力黑土中达75%以上,中、高肥力黑土中秸秆碳的贡献率仅为50%~60%.这主要是由于高肥力土壤中微生物生物量和活性相对较高,保障了秸秆碳的快速转化分解;但该过程中形成的DOC和MBC,进一步增强了土壤微生物的数量和活性,进而有效促进了土壤原SOC的矿化^[45,53-54].因此,秸秆碳对高肥力土壤SOC的贡献比例低于低肥力土壤.Poirier等^[55]研究发现,相较于有机质含量较高的表层土壤(0~20 cm),秸秆碳转化形成的稳定性有机碳组分在有机质含量较低的底层土壤(30~70 cm)中积累更多,表明低肥力的底层土壤更有利于秸秆碳的固定.这主要是由于秸秆碳在低肥力土壤中转化分解缓慢,而这部分还未来得及被微生物利用的秸秆碳,可被土壤细矿物颗粒包裹,以稳定的形式积累于土壤中.由此可推测,采

用秸秆深层还田(20~40 cm)的方式有利于固定更多的秸秆碳,若同时合理配施养分,将进一步促进秸秆碳向土壤有机碳库的转化,更有利于土壤培肥与固碳^[56-57],但这还需要未来更多的相关研究为实际应用提供数据支撑。

土壤含水量直接影响土壤透气性、微生物数量及活性,进而影响秸秆碳的分解转化速率,尤其是秸秆碳分解与转化的前期阶段。左玉萍等^[58-59]采用模拟培养法探究土壤含水量对玉米秸秆分解的影响,结果显示,第10天土壤含水量为20.0%的秸秆碳转化率是15.0%含水量条件下的2倍,此后分解转化率的差异逐渐减小,这与不同含水量条件下形成的可被微生物利用的有机碳含量及土壤微生物活性有关。土壤含水量还影响秸秆碳在不同深度土层中的分配。Poll等^[44]研究表明,秸秆碳转化形成DOC后,在不同土壤深度的迁移随土壤含水量的增加而加剧,进而增加了秸秆碳在深层土壤MBC中的分配比例。此外,耕种制度也会影响秸秆碳在土壤中的转化与分配。相较于免耕,常规耕作对土壤扰动频繁,破坏土壤团聚化过程造成有机碳损失。Chen等^[60]研究结果显示,相较于常规除茬耕作,麦秸覆盖浅耕和覆盖免耕条件下,土壤活性有机碳(DOC、MBC和POC)增加更为显著。

秸秆碳的转化分配过程受到以上各个影响因素的共同作用,需要较系统地研究来量化各影响因素与秸秆碳转化分配比例间的关系,进而指导农田管理措施的制定和调整,使秸秆还田技术能在满足作物养分需求、保障作物产量的同时,实现土壤肥力和土壤固碳能力提升的目标。

2.3 秸秆碳同化微生物

土壤微生物直接参与还田秸秆的碳转化与分配过程,秸秆碳同化微生物的组成、多样性及活性是驱动秸秆碳转化的内在动力^[61]。过去,人们通过传统的分离、培养方法对少数可培养的具备秸秆腐解功能的微生物类群做了大量的研究。近年来,随着稳定性同位素探针技术(stable isotope probing, SIP)和现代分子生物学技术的发展,国内外学者通过¹³C标记作物秸秆,结合DNA-SIP、RNA-SIP等技术更全面准确地揭示了秸秆碳同化微生物的群落组成、多样性及其动态变化规律,本文主要针对这部分研究内容进行概述。

参与秸秆碳同化过程的土壤微生物组成随秸秆腐解周期在动态变化,同时与作物类型和还田环境密切相关。Bernard等^[62]于2007年首次采用DNA-

SIP和RNA-SIP技术对参与小麦秸秆碳同化的土壤微生物群落组成及其动态变化进行了分析,结果显示,在小麦秸秆碳转化初期,以紫色杆菌属(*Janthinobacterium*)、马赛菌属(*Massilia*)、贪噬菌属(*Variovorax*)、黄单胞菌属(*Xanthomonas*)和假单胞菌属(*Pseudomonas*)为主;随着秸秆碳组分中易分解有机质被大量转化为有机酸、腐殖酸等DOC,参与秸秆碳同化的微生物群落的多样性显著降低,以变形菌门(Proteobacteria)、拟杆菌门(Bacteroidetes)和酸杆菌门(Acidobacteria)为主。此后,菌群多样性逐渐回升,群落组成与无秸秆添加组的差异也逐渐缩小。针对玉米秸秆碳同化微生物组成的研究显示,放线菌门(Actinobacteria)、硬壁菌门(Firmicutes)、芽单胞菌门(Gemmatimonadetes)和变形菌门中的酸热菌属(*Acidothermus*)、壤霉菌属(*Agromyces*)、节杆菌属(*Arthrobacter*)、芽球菌属(*Blastococcus*)、链霉菌属(*Streptomyces*)、芽孢杆菌属(*Bacillus*)、热气单胞菌属(*Thermacetogenium*)、芽单胞菌属(*Gemmatimonas*)、溶杆菌属(*Lysobacter*)、李斯特氏菌属(*Na-tronocella*)、根瘤菌属(*Rhizobium*)、堆囊粘细菌属(*Sorangium*)和马赛菌属(*Steroidobacter*)为同化玉米秸秆碳的主要土壤微生物^[63]。其中,除节杆菌属(*Arthrobacter*)^[64]、链霉菌属(*Streptomyces*)^[65]、芽孢杆菌属(*Bacillus*)^[66]和根瘤菌属(*Rhizobium*)^[67]外,其余发现的菌属均未曾报道具有纤维素、半纤维素或木质素降解功能,这些细菌大多与秸秆次生代谢产物的转化有关。相似的,玉米秸秆碳快速转化阶段之后,秸秆碳同化微生物群落多样性同样有所回升,表现为拟杆菌门(Bacteroidetes)和软壁菌门(Tenericutes)的相对丰度有所增加。Shrestha等^[68]发现,变形菌门(Proteobacteria)、芽孢杆菌纲(Bacilli)、放线菌门(Actinobacteria)、拟杆菌门(Bacteroidetes)和绿硫菌门(Chlorobi)是参与水稻秸秆碳同化的主要细菌,甲烷八叠球菌属(*Methanosarcina*)和甲烷杆菌科(Methanobacteriaceae)是根际土壤中利用秸秆碳代谢的主要古菌,这与水稻田厌氧环境下产CH₄过程有关。然而,由于这些研究采用的土壤不同,其微生物群落组成本身就存在差异,因此难以判断这些微生物种群是否特定参与某一类型的作物秸秆碳同化。此外,由于土壤微生物的组成、多样性受到土壤其他各项因子(包括土壤pH、养分、碳组分含量等)的影响,因此,需要将秸秆碳同化过程中的生物与非生物因子的动态变化相结合,才能进一步揭示秸秆碳转化与分配的微生物机制。

现有研究还发现,可同化秸秆碳的微生物中还包括了部分异养固氮微生物和反硝化微生物,如慢生根瘤菌属(*Bradyrhizobium*)、伯克氏菌属(*Burkholderia*)、嗜糖精胞单胞菌(*Pelomonas*)、伯克氏菌目(*Burkholderiales*)、根瘤菌(*Rhizobia*/*Sinorhizobia*)和胶状红长命菌(*Rubrivivax gelatinosus*)、假单胞菌属(*Pseudomonas*)、陶厄氏菌属(*Thauera*)、考克氏菌属(*Kocuria*)以及固氮螺菌属(*Azospirillum*)等,表明部分土壤微生物在转化秸秆碳的过程中,同时参与了秸秆氮和/或土壤氮的转化^[63],进而可引起土壤氮素水平,主要是有效氮水平的变化,而这种变化又将进一步影响秸秆碳的转化.目前,有关秸秆碳与土壤氮转化间的相互作用关系及其机制的研究还非常缺乏.而实际上,无论是秸秆还是土壤的碳氮转化都是一个相互耦合的过程^[69-70].因此,在探究秸秆碳转化机制过程中有必要同时对秸秆氮和土壤氮转化过程及该过程中的关键微生物群落特性展开研究.

3 秸秆还田对土壤有机碳库的影响

秸秆还田后,随着秸秆碳在土壤中的转化及其在土壤不同碳库中的分配,必将引起土壤各有机碳库含量的动态变化,同时将会改变土壤中老有机质的矿化分解进程.明晰秸秆还田对 SOC 组成、含量及其周转的影响,有助于理解秸秆还田对土壤增碳的作用机制.

3.1 秸秆还田对 SOC 含量及其组成的影响

不同时空尺度的试验结果表明,秸秆还田总体上可有效提升 SOC 含量,但增加幅度存在差异^[71-73],主要与秸秆还田量、还田时间和还田方式等因素密切相关.研究表明,SOC 含量与秸秆还田量呈显著正相关关系^[72,74].陈鲜妮等^[75]通过 21 年的田间定位试验研究表明,0~20 cm 耕层 SOC 随还田秸秆量的增加而成倍增加,高(37500 kg·hm⁻²)、中(18750 kg·hm⁻²)、低(9375 kg·hm⁻²)秸秆还田量下 SOC 年平均增加量分别为 413、265 和 155 kg·hm⁻².然而,当还田秸秆量过高时,可能因土壤中氧气和养分的供应不足,为保障快速增加的微生物的生长而限制秸秆碳的转化分解,进而影响 SOC 含量的提升.Zhu 等^[76]在稻麦轮作体系下进行了 2 年的田间试验结果显示,50% 秸秆还田量下耕层土壤(0~21 cm)中的 TOC、DOC 和 LOC 均高于 100% 秸秆还田量处理.

从时间尺度上分析,短期秸秆还田 SOC 变化不显著,中期还田 SOC 含量随还田时间的延长而显著

增加,长期连续秸秆还田条件下,平均约在 12 年后 SOC 趋于饱和状态,增幅平均为 12.8%^[74].王金洲^[42]对 10~30 年连续秸秆还田的统计分析表明,秸秆还田可使 SOC 含量平均增加 10.1%.Poeplau 等^[77]分析了瑞典 6 个长期定位试验点秸秆碳对 SOC 储量的影响,27~56 年时间尺度上的数据分析表明,平均约在 36 年后,各试验地秸秆还田引起 SOC 储量的变化趋于一致.

比较不同的秸秆还田方式发现,由于微生物主要分布在 0~10 cm 土层^[78],秸秆覆盖还田下秸秆与土壤接触混合较差,不利于微生物对秸秆碳的转化分解及土壤颗粒对有机碳保护作用的发挥.与翻压还田相比,虽然秸秆覆盖还田下耕层 TOC、MOC 提升量均较低,但有利于土壤墒情的保持和温度的稳定,使其犁底层土壤 POC、MOC 和 TOC 均高于翻压还田^[17].然而相较于秸秆覆盖或翻压还田,秸秆深层还田(还田深度 20~40 cm)条件下分解率有所降低,但能改善腐殖质组成,使胡敏酸缩合度变大,进而使土壤亚表层有机碳含量提高 10%~15%^[56,79].这与深层土壤肥力较低、土壤通气较差不利于秸秆分解,但有利于秸秆碳固定有关.

3.2 秸秆还田对 SOC 矿化的影响

秸秆还田对 SOC 矿化的影响主要包括 3 个方面:1) 促进分解^[80-81](正激发效应);2) 抑制分解^[42,72,74](负激发效应);3) 无显著影响^[82-84].多数室内培养试验结果表明,因土壤中添加了秸秆,改善了土壤团聚体结构,增加了土壤养分,有效促进了土壤微生物的生长和代谢,进而增强了其对土壤原 SOC 的分解,即发生正激发效应.伊云锋等^[85]研究指出,添加玉米秸秆明显地促进了红壤原有有机碳和重组有机碳的分解,且土壤原有有机碳分解速率随秸秆施用量的增多而加快.王志明等^[53]研究结果显示,黄棕壤中 MB¹²C 的周转速率随秸秆量的增加而加快,从而加速了秸秆碳和土壤原 SOC 的分解. Blagodatskaya 等^[86]指出,当秸秆碳占微生物生物量碳的 4%~9% 时,激发效应强度最高,但随秸秆量的增加,活性有机碳量大于微生物生物量碳的 50% 时,激发效应呈指数下降,这主要与土壤养分是否足以保障微生物生长与代谢密切相关^[54,69].相反地,还田秸秆在土壤微生物的作用下同时进行的矿化和腐殖质化过程增加了 SOC 含量,而源于秸秆碳新形成的 SOC,主要是形成的活性有机碳,更易被微生物利用^[45,74],从而降低土壤原 SOC 的分解. Pei 等^[9]研究发现,高肥力黑土对添加秸秆的响应呈负激发效应,

而添加玉米秸秆的高、低肥力棕壤和低肥力黑土在前两个月产生了正激发效应,但随着秸秆中活性有机质的消耗,微生物生物量及其活性因土壤有效养分的减少而降低,后期秸秆残余有机碳缓慢分解并在土壤中不断积累,补充了前期正激发效应引起的土壤原 SOC 损失.由此表明,秸秆还田量和土壤养分含量是影响秸秆还田激发效应的关键因子.因此,在秸秆还田量一定的条件下,如何通过合理施肥调整土壤养分来有效调控秸秆还田的激发效应,实现秸秆还田条件下的土壤固碳,是当前需进一步研究的重要内容.

4 总结与展望

还田秸秆碳在微生物作用下虽然大部分被转化为 CO_2 , 且转化为 SOC 的部分也多为活性有机碳,但是秸秆还田对土壤固碳的贡献有限,且还受还田数量与年限、环境因素以及耕作、施肥等农事活动的影响,但可以明确的是秸秆还田确实可以有效增加 SOC 储量.因此,在现有基础上继续加强和深化时间尺度、环境因子、土壤类型、土壤结构与理化性状等非生物因子对秸秆碳的生物转化效应研究,以揭示秸秆还田下各类土壤的固碳机制,显得尤为重要.

随着秸秆碳的转化及养分的释放,土壤环境发生改变而对土壤微生物组成、多样性和活性等产生影响,进一步影响秸秆碳的转化与分配过程.由于参与秸秆碳同化的微生物群落组成与结构的变化是驱动秸秆碳转化的重要内在因子,近年来有关参与秸秆碳同化的微生物群落特征的研究工作得到了明显加强,但现有研究所覆盖的土壤类型和范围有限,而且研究多集中于某单一影响因素下的情况,对其他农田生态系统的研究应用和生产实践的指导意义存在局限性.因此,未来应加强对秸秆碳转化过程中的生物和非生物因子进行系统研究和综合分析,以了解秸秆碳转化与分配的微生物驱动机制.

此外,土壤中 SOC 和其他养分(如氮、磷、硫等)存在密切的耦合关系,作物秸秆 C/N 较高的情况下,养分供应不足可能限制秸秆有机碳向 SOC 转化.秸秆碳、SOC 矿化均与土壤养分转化,尤其是氮素转化存在耦合效应.因而,为全面准确把握秸秆还田对土壤增碳培肥的作用机制,还需要深入探究秸秆还田条件下秸秆碳、氮和土壤碳、氮循环的耦合作用,以准确揭示秸秆还田条件下土壤 SOC 的变化特征,特别是加强对不同条件下秸秆碳转化分配机制及其与影响因子间的定量关系研究,可为有效调控

秸秆碳向土壤活性有机碳库或稳定性有机碳库的转化提供技术手段,为实现秸秆还田的持续增碳培肥效果提供理论基础和数据支撑.

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