



•综述•

尿素对土壤细菌与真菌多样性影响的研究进展

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摘要: 土壤微生物组在养分循环和土壤生态系统功能的维持中具有至关重要的作用。氮素是植物生长过程中关键的限制性营养元素, 而大气中的非活性氮却无法被植物直接吸收利用。我国农业主要通过施加尿素补充土壤氮素营养, 提升作物产量。细菌和真菌是土壤微生物组的重要类群, 土壤细菌与真菌群落结构对尿素添加的响应近年来备受重视并被深入研究, 本文综述了施用尿素对土壤细菌与真菌多样性的影响及其机理的研究进展。大量研究表明, 施用尿素通过影响土壤和植物调节土壤细菌与真菌多样性和组成; 施用尿素降低农田(除水稻田、水稻-小麦田)土壤细菌多样性的阈值为 $200 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$, 小麦田土壤真菌多样性降低的阈值低于细菌多样性阈值, 水稻田或水稻-小麦轮作田土壤细菌多样性对尿素响应的阈值要高于其他农田类型; 施用尿素增加富营养类群细菌, 减少寡营养细菌类群, 增加腐生真菌与病原真菌的相对多度, 降低菌根真菌的相对多度。展望土壤微生物组的进一步研究, 强调未来研究要多关注土壤中食物网的重要性, 并指出设计平行引物及利用多组学方法研究土壤微生物是未来研究的重点之一。

关键词: 土壤微生物多样性; 群落结构; 有机氮素; 细菌; 真菌

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Research progress on the effect of urea on bacterial and fungal diversity in soil

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ABSTRACT

Background & Aim: Soil microbiome plays a crucial role in nutrient cycling and maintenance of soil ecosystem function. Nitrogen is a key limiting nutrient in plant growth, while the inactive nitrogen in the atmosphere cannot be directly absorbed and utilized by plants. Soil nutrition is supplemented mainly by applying urea to sustain and elevate crop yields in our country. In recent years, with the rapid development of high-throughput sequencing techniques and bioinformatics, the response of soil microbiome structure to urea application has been thoroughly studied. This study intends to review the pattern and mechanism of effects of urea application on soil microbial diversity and composition.

Progress: Urea application regulates soil microbial diversity and composition by affecting soil and plants. The threshold value of applying urea to reduce soil bacterial diversity in farmland (excluding rice and rice-wheat fields) is $200 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$, and the threshold for reducing fungal diversity in wheat fields is lower than the threshold for bacterial diversity. The threshold value of urea response in rice field or rice-wheat rotation farmland is higher than that in other farmland types; fertilization increases the number of eutrophic bacteria and decreases the number of oligotrophic bacteria; urea application increases the relative abundance of saprophytic fungi and pathogenic fungi, and reduces the relative abundance of mycorrhizal fungi.

Prospects: We suggest that the food web in soil should be paid more attention in future research, and point out that the

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design of parallel primers and the use of multi-omics methods to study soil microorganisms are necessary.

Key words: soil microbial diversity; community structure; organic nitrogen; bacteria; fungi

氮素是植物生长过程中所必需的大量元素之一,是构成核酸、蛋白质和有机代谢物等生物大分子的重要组成部分(de Bang et al, 2021)。虽然在大气中氮素的含量最高,但主要以惰性氮气的形式存在,无法直接被植物吸收利用,因而氮素往往是植物生长过程中关键的限制性营养元素(鲁显楷等, 2019)。农田土壤中氮素的补充主要依靠施加氮肥,解除植物生长时的氮限制,进而实现粮食或蔬菜等农作物的增产。与其他氮肥相比,尿素含氮量较高,质量稳定,是我国主要施用的氮肥。然而,我国农业生产中普遍过量施用尿素,这些过量施加到土壤中的尿素容易通过挥发、径流、淋溶等方式迁移到空气和水生系统中,不仅造成重大的经济损失,还带来严重的环境问题:土壤、淡水和海洋污染及农田生物多样性减少,并影响土壤微生物的多样性与生物量(Rojas et al, 2013; Zhang et al, 2016; Liao et al, 2021)。

土壤中栖息的大量微生物(如细菌、真菌、原生动物、古菌和病毒等)以及它们的组成成分(如基因组、转录组、蛋白组)、功能成分(如信号分子、代谢产物等)和周围环境一起被统称为土壤微生物组(Marchesi & Ravel, 2015; Berg et al, 2020)。土壤微生物在调控土壤元素循环、有机质分解、促进植物养分获取与吸收等土壤生态过程,帮助植物抵抗病原菌入侵和非生物胁迫中具有重要作用(Santos et al, 2021; Wu et al, 2022)。植物处于生物或非生物胁迫时也会招募土壤有益微生物来抵抗病原体侵害(Liu HW et al, 2021a)。

土壤微生物多样性和组成是保证作物健康生长和维持作物产量的基础。前人的研究发现,作物根部和体内的微生物主要来源于土壤(Zhang et al, 2022),土壤中微生物多样性越高,土壤越能表现出更多的生态功能和更高的生产能力(Chen et al, 2019)。

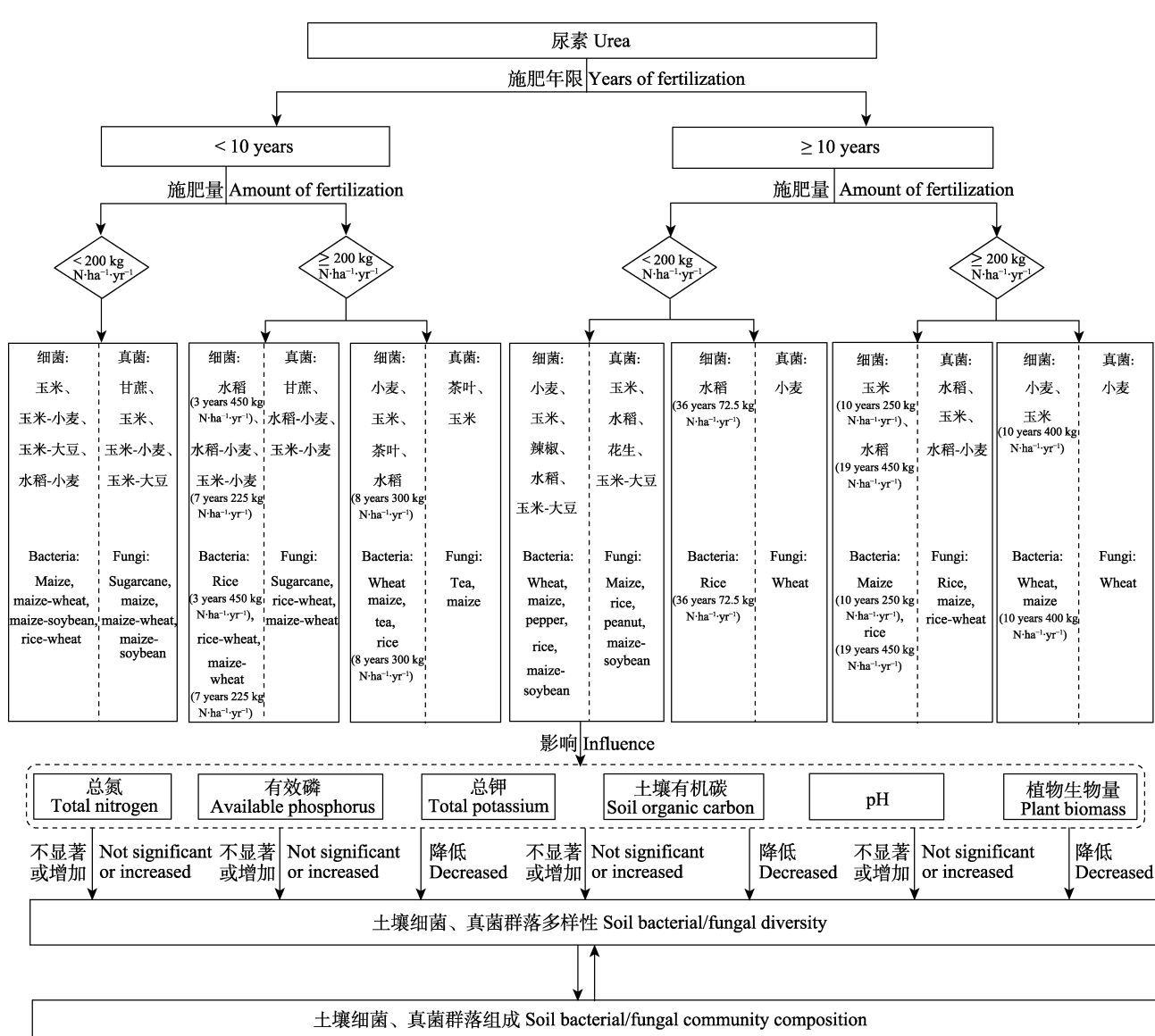
随着高通量测序技术及生物信息学的发展和应用,施用氮肥对土壤细菌与真菌多样性影响的研究取得了长足进展。但不同实验受到诸多因素的影响,研究结果不尽一致(图1)。同样施用10年尿素,

小麦田($210 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$, 尿素施用量)土壤中细菌群落显著降低,而水稻田($216 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$, 尿素施用量)则无显著变化(Zhong et al, 2015; Wang & Huang, 2021, 图1)。这可能是由于水稻田厌氧环境下细菌群落多样性降低的阈值要高于其他农田类型(Dai et al, 2018)。此外,施肥年限同样影响土壤细菌、真菌对施用尿素的响应。短时间的施肥增加或不影响玉米田和小麦田中土壤细菌、真菌群落的多样性,长时间的施肥则会降低这些农田土壤细菌、真菌的多样性(Luo et al, 2015; Yu et al, 2019)。本文综述了近些年施用尿素影响土壤细菌与真菌多样性的研究进展,以期在未来加强相关研究,探索减少尿素使用,重构农田微生物组,实现未来绿色健康农业可持续发展提供有效路径。

1 施用尿素对土壤细菌群落多样性的影响

施用尿素对农田土壤细菌多样性的影响取决于施肥量、施肥年限及作物类型。而对除水稻、水稻-小麦以外其他作物类型的农田土壤细菌多样性的影响主要取决于施肥量,其临界值在 $200 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$ 左右(Liang et al, 2020; Xu et al, 2020, 图1),这与以前研究报道的 $180 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$ 的临界值相当(Zhong et al, 2015)。适量施肥(小于 $200 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$)增加或不影响这些农田的土壤细菌多样性,而过高的施肥量(大于 $200 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$)则会降低其土壤细菌多样性(图1)。不过,在连续施用7年尿素($225 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$)的玉米-小麦轮作田和施用10年尿素($250 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$)的玉米田,土壤细菌多样性均无显著变化(Ullah et al, 2020; Liu JL et al, 2021, 图1)。在这两项研究中,尿素被分次施用,除开始的基础供给外,在作物生长关键时期也被施用。施肥制度可能是土壤细菌多样性对施用尿素响应与其他相关研究不一致的原因。此外,研究结果不一致也可能与土壤本身的异质性(如通气性)、采样时间以及采样季节的降水量和温度有关(Berg & Smalla, 2009)。

尿素降低水稻田土壤细菌多样性的施肥量临界值通常比其他作物类型的农田高(图1)。低剂量或



2019, 19年, $225 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$, $450 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$)。原因可能是不同水稻田的施肥制度和水管理制度不同, 水稻田中的水可以冲刷部分尿素, 降低盐度, 减轻高剂量尿素对作物生长和产量的影响(Singh et al, 2010)。然而, 更长时间施用尿素, 尽管低剂量, 也会降低土壤细菌多样性。如施用36年尿素($72.5 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$)的水稻田土壤细菌多样性降低(Cui et al, 2018)。尿素对水稻田土壤细菌群落多样性的影响相比其他农田似乎更加复杂, 需要更深入细致的研究。

施用尿素导致土壤有机质、有效氮和有效磷的增加, 是土壤细菌多样性增加的主要原因。无论是水稻田还是其他作物类型的农田, 施用尿素导致细菌多样性的增加往往都伴随着土壤有机质、有效磷和总氮的增加。此外, 施用尿素还可引起不同养分之间比例的变化, 可能是细菌多样性增加的另一原因。Delgado-Baquerizo等(2017)通过综合179个位点6类生态系统类型的数据发现, 土壤养分化学计量改变是影响土壤细菌多样性最主要的因素。

施用尿素量过高或年限过长可以通过多种途径降低细菌多样性, 包括直接途径和间接途径(图2)。一些研究显示过高的氮输入通过改变土壤氮的可利用性, 导致一些寡营养细菌的多样性降低(Cui et al, 2018)。此外, 施用尿素还可通过改变土壤理化性质间接影响细菌多样性。例如尿素通过降低土壤pH值, 导致土壤酸化, 使得土壤中的钙镁流失、铝离子活化, 降低了土壤缓冲能力并积累重金属, 对土壤微生物活性和多样性产生负面影响(Yao et al, 2021), 最终导致土壤微生物组系统稳定性下降(Lucas et al, 2011; Yu et al, 2019)。施用尿素还会改变植物的生物量, 降低土壤微生物活性, 进而对细菌群落多样性产生间接负面影响(Meier & Bowman, 2008)。施用尿素还会抑制分解顽固性碳的胞外酶活性, 导致微生物从对顽固性碳的分解转向对不稳定性碳的分解, 从而影响寡营养类群细菌的生长, 造成土壤细菌群落多样性下降(Ramirez et al, 2012; Chen et al, 2018)。氮素富集还会刺激与碳获取相关的水解酶, 降低氧化酶活性, 通过改变土壤有机碳含量进而影响细菌群落多样性(Jian et al, 2016)。施用尿素可通过影响其他土壤微生物类群调节细菌群落多样性。比如, 一项持续8年的田间实验显示高粱根际中原生生物的Shannon指数与细菌多样性呈

显著正相关, 施用尿素($225 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$)会降低原生动物多样性, 而原生动物会通过食物网的流动自上而下地控制细菌群落(Sun et al, 2021)。

2 施用尿素对土壤真菌群落多样性的影响

土壤真菌群落多样性对施用尿素的响应趋势也因作物类型、施肥年限及施肥量不同而表现出不变化、增加或降低。在水稻田、水稻-小麦轮作田及玉米、玉米-小麦轮作等农田中, 施用尿素通常不影响或增加土壤真菌的多样性(图1), 而在小麦田中, 尿素添加倾向于降低土壤真菌多样性。这可能是因为轮作改善了土壤孔隙度和水渗透, 增加了真菌的活性和多样性(Lal, 2011; Zhang et al, 2021)。此外, 轮作通过增加土壤有机碳和微生物生物量碳含量, 进而增加土壤真菌多样性(McDaniel et al, 2014)。土壤真菌多样性对尿素添加负响应的阈值比细菌低。比如, 在一项持续10年的施肥实验中, 施用尿素降低小麦土壤真菌多样性的阈值为 $90 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$, 而降低细菌多样性的阈值为 $180 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$ (Zhong et al, 2015)。

施用尿素并不显著影响土壤真菌多样性, 可能是由于施加的尿素被作物吸收或因施加量较少, 尚不足以改变真菌多样性。比如, 在玉米-大豆轮作田中, 连续施用3年 $112\text{--}168 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$ 的尿素未改变土壤真菌多样性(Castle et al, 2021)。相比细菌, 真菌通常具有更宽泛的最佳生长pH值, 这可能是尿素添加不影响土壤真菌多样性的另一个原因(Rousk et al, 2010a)。此外, 相对于细菌, 真菌对土壤酸化等环境胁迫的适应能力更强(Xiao et al, 2018; Ullah et al, 2019)。花生田间实验表明, 在pH值 < 6 的酸性土壤中施用26年尿素($120 \text{ kg N} \cdot \text{ha}^{-1} \cdot \text{yr}^{-1}$)后, 土壤真菌多样性未发生明显变化(Ye et al, 2020)。

施用尿素增加或降低真菌多样性可能与植物对尿素添加的响应有关(图2)。相对于细菌所需4:1的碳氮比, 真菌营养所需的碳氮比在10:1左右, 这意味着真菌对碳的需求更高(Wang C et al, 2018)。而植物作为农田生态系统的主要初级生产者, 是土壤中碳的主要来源。所以, 如果施用尿素能增加作物的地下生物量和根系分泌物, 则能增加土壤真菌的多样性; 而如果尿素添加减少作物向地下的碳分配, 则土壤真菌多样性也会下降。再者, 施用尿素

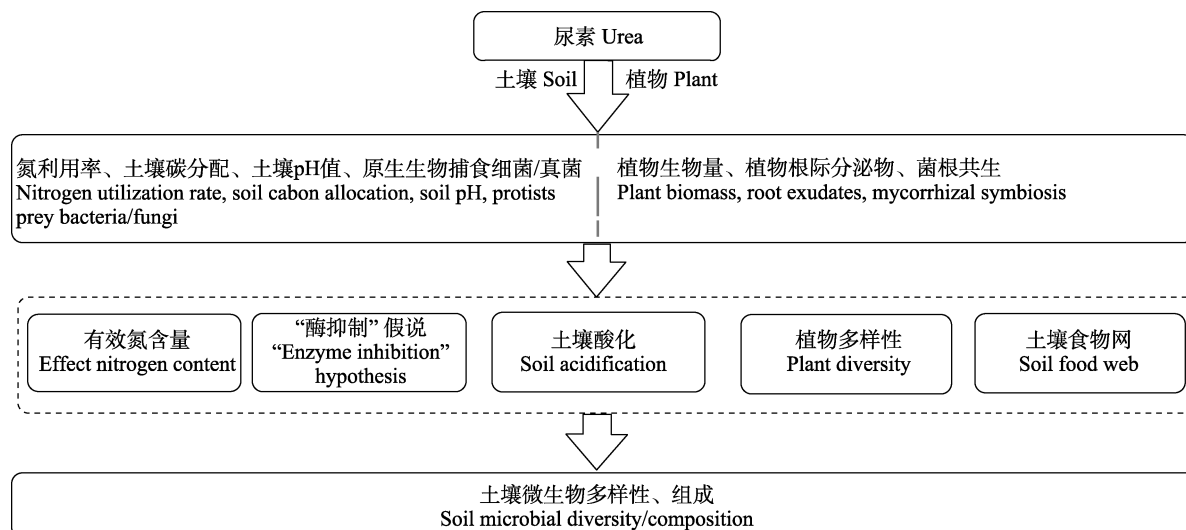


图2 施用尿素改变土壤微生物组多样性与组成的作用机制。数据源自Meier和Bowman (2008)、Lucas等(2011)、Yoneyama等(2013)、Jian等(2016)、Nguyen等(2016)、Delgado-Baquerizo等(2017)、Cui等(2018)、Wang JC等(2018)、Yu等(2019)、Huang等(2021)、Sun等(2021)、Yao等(2021)、Babalola等(2022)。

Fig. 2 Mechanisms of effects of urea application on soil microbiome diversity and structure. Data derived from Meier & Bowman (2008), Lucas et al (2011), Yoneyama et al (2013), Jian et al (2016), Nguyen et al (2016), Delgado-Baquerizo et al (2017), Cui et al (2018), Wang JC et al (2018), Yu et al (2019), Huang et al (2021), Sun et al (2021), Yao et al (2021), and Babalola et al (2022).

还可以通过降低土壤有机质的碳氮比从而减少土壤真菌多样性(Huang et al, 2021)。此外,施用尿素还可通过影响农作物代谢产物的产生影响真菌多样性。一项室内实验发现,添加氮素抑制高粱根部独角金内脂(strigolactones, SLs)的释放(Yoneyama et al, 2013)。而SLs已被证明是从枝菌根与宿主共生的识别信号,SLs的减少会降低丛枝菌根真菌以及土壤真菌多样性(Wright et al, 2009; Wei et al, 2013; Paungfoo-Lonhienne et al, 2015; Gao et al, 2022)。

3 施用尿素对土壤细菌群落组成的影响

施用尿素引起环境的富营养化是改变细菌群落组成的重要因素。施用33年尿素(300 kg N·ha⁻¹·yr⁻¹)导致小麦田土壤有效氮增加,从而显著降低了一些硝化细菌如硝化螺旋菌门的相对多度(Zhou et al, 2015)。施用尿素造成的富营养化有利于芽单孢菌门和变形菌门等富营养类群的生长,它们可以在富营养的环境下利用更多的不稳定碳(微生物生物量碳、土壤有机碳)生长繁殖,而诸如酸杆菌门等寡营养类群的生长速率很难在养分充足的条件下超过富营养类群(Ahn et al, 2012)。因此,在添加尿素后,土壤中富营养细菌类群的相对多度增加,寡营养类群及一些参与氮循环的细菌(固氮螺菌属

*Azospirillum*和硝化螺旋菌门)的相对多度降低。但也有研究结果相反的报道,例如,在一项10年的小麦田研究中发现,施用尿素(180 kg N·ha⁻¹·yr⁻¹)显著增加了硝化细菌的相对多度(Zhong et al, 2015)。这些不一致的响应结果可能是由于土壤的pH值、总氮、有机碳及有机氮等理化性质存在差异(Qiu et al, 2014; Tian et al, 2015; Liang et al, 2020; Yao et al, 2021)。土壤pH值也是添加尿素影响细菌群落组成的良好预测因子(Rousk et al, 2010b, 图2)。施用尿素造成土壤pH值降低,放线菌门、变形菌门、芽单孢菌门和拟杆菌门的相对多度随之增加(Rousk et al, 2010b; Cederlund et al, 2014; Xu et al, 2020)。

4 施用尿素对土壤真菌群落组成的影响

真菌按其生活方式可分为腐生菌、共生菌和寄生菌(Zhao et al, 2019)。这三类菌群通常对添加尿素有不同的响应。大多数田间实验表明,施加尿素显著增加腐生真菌(如粪壳菌纲、座囊菌纲)和病原真菌(如链格孢属*Alternaria*)的相对多度(Nguyen et al, 2016; Liao et al, 2021),而降低共生菌的相对多度(Paungfoo-Lonhienne et al, 2015)。

Paungfoo-Lonhienne等(2015)发现施用尿素(200 kg N·ha⁻¹·yr⁻¹)增加甘蔗土壤中子囊菌门螺旋

聚孢霉属(*Clonostachys*)和担子菌门树脂霉属(*Resinicium*)及致病真菌属(如丝核菌属*Rhizoctonia*和黑孢霉属*Nigrospora*)的相对多度,而降低丛枝菌根真菌的相对多度。可能的原因是腐生菌参与土壤中的碳分解,氮素的添加可在一定程度上促进碳的分解,刺激腐生真菌的生长(Hanson et al, 2008; Paungfoo-Lonhienne et al, 2015)。而大多数腐生菌如担子菌门和子囊菌门真菌是土壤碳、氮循环的重要调节者,参与土壤中化合物分解的过程,且他们的增长率与氮的可用性有关(Fontaine et al, 2011; Xiong et al, 2014)。链格孢属、镰刀菌属(*Fusarium*)等潜在病原菌的增加可能是由于施加尿素增加了植物生物量以及土壤有机碳含量(Nguyen et al, 2016),刺激了这些病原菌的生长。

共生菌如丛枝菌根真菌,可从宿主植物中获取营养,并作为交换向宿主植物提供矿物质营养(Wang JC et al, 2018)。氮素富集时,植物会将更多的资源用于自身生长,减少对共生菌的碳分配,进而降低菌根真菌的相对多度(Lin et al, 2012; Wei et al, 2013; Sterkenburg et al, 2015; Babalola et al, 2022)。菌根真菌中包括许多潜在病原菌的拮抗剂类群,丛枝菌根的菌丝和孢子可与其他微生物生成聚集体,这种聚集体可保护宿主植物免受一些根际病原体的侵害(Cruz & Ishii, 2012)。因此,未来的农田施肥管理中应注重发挥菌根真菌的作用,以保证作物健康和产量。

5 施用尿素对作物产量-微生物-土壤生态功能的影响

近几十年来,农作物产量的增加高度依赖尿素的投入。研究表明,施用尿素增添了农田土壤肥力,增加了作物干物质以及产量(高雪健等, 2022; 邹奇芳等, 2022)。然而,长期施用尿素导致土壤中存在大量的铵态氮和硝态氮,对农田生态系统和土壤微生物多样性造成显著的负面影响(Eo & Park, 2016)。在农业生态系统中,土壤微生物彼此相互作用形成复杂的互作网络关系(Kaiser-Bunbury et al, 2017; 李海东等, 2021)。土壤微生物多样性和微生物网络复杂性与养分循环、有机质分解、植物生产、抵御病原体等生态系统功能呈显著正相关(Wagg et al, 2014; Delgado-Baquerizo et al, 2020),微生物多样性

较低或者微生物网络简单的土壤生态系统往往具有较低的功能独特性(Wagg et al, 2019)。研究发现,施用尿素降低小麦土壤生态功能性,可能是由于稀有微生物类群更容易驱动土壤生态功能的多样性,而施用尿素会导致一些稀有类群的丢失(Chen et al, 2020)。长期施用尿素会改变土壤微生物多样性,进而影响土壤生态系统功能。土壤生态系统受到影响,作物病虫害增加,营养供应不足,反过来影响作物产量和质量(李奕赞等, 2022)。因此,需要加强尿素施用管理,增加土壤微生物多样性,提高作物产量及质量,保证农业生态系统功能完好,使得农业生产与生态相互促进、实现良性互动、可持续发展。

6 扩增引物差异对土壤细菌和真菌多样性研究的影响

DNA高通量测序技术是一种高效低成本获得微生物群落结构的方法,该技术有力推动了土壤微生物组学的研究。然而实验过程中,选择不同的引物往往会导致研究结果的差异性。如Walters等(2016)指出,相比最初的引物515f Original + 806r Original,各改变1个碱基后的新引物515f Modified + 806r Modified显著提高了对细菌SAR11 clade和古菌Thaumarchaeota的覆盖率,增加了鉴定结果的真实性。扩增子测序使用的PCR扩增引物,往往是针对某一特定区域进行设计,例如用于细菌和古菌鉴定的核糖体DNA小亚基(16S rDNA)和用于真菌鉴定的内转录间隔区(ITS),这些区域通常包含用于区分研究对象组成的高度可变区,两侧是可以作为PCR引物结合位点的高度保守区。PCR扩增引物不同,对DNA序列的亲合力可能不同,这种亲合力偏好性会影响PCR扩增结果。例如,ITS1-F、ITS1和ITS5更适于担子菌ITS片段的扩增,而ITS2、ITS3和ITS4更适于子囊菌扩增(Bellemain et al, 2010)。当然,扩增过程中偏好性来源除了引物因素即可变区的选择、扩增子片段大小之外,还与PCR循环次数等有关。因此,优化引物、优化PCR扩增、减少引物偏好性和错配性有助于更好地评估土壤细菌和真菌多样性。

7 展望

如前所述,土壤细菌与真菌对尿素响应的阈值

与施肥量、施肥年限及作物类型等因素相关。目前大多数研究仅在扩增子层面分析尿素对土壤细菌与真菌多样性、组成的影响,对于微生物功能以及响应机制的研究仍处于起步阶段。关于土壤微生物组的研究建议从以下几方面进一步展开。

7.1 重视从食物网的角度全面研究土壤微生物组

原生动物已被证明是对施加氮肥响应敏感的微生物类群(Song et al, 2023), 尽管在控制细菌和真菌类群方面发挥着关键作用, 但以前对于土壤微生物组的研究往往忽略了原生动物的的重要性。原生动物在土壤食物网中占据关键位置, 它们以细菌、酵母等为食, 将能量流动与营养循环联系起来(Valencia et al, 2018)。施加尿素可以改变食物网的相互作用, 影响土壤微生物组结构和功能的变化(Geisen et al, 2018)。因此, 了解原生动物多样性的变化动态及其食物网相互作用有利于预测土壤微生物组的变化。未来的微生物组和土壤生物多样性研究应包括原生动物群落分析, 否则可能会丢失有关微生物组结构的重要信息。

7.2 设计开发土壤微生物组平行扩增引物

随着高通量测序技术以及生物信息学的发展, 土壤微生物组学的研究达到前所未有的阶段, 打破了传统上99%的土壤微生物组不可培养的局限, 为土壤微生物组的研究提供了有力工具(Lagier et al, 2012)。目前, 大多数研究使用PCR扩增技术, 探讨土壤微生物组多样性以及组成的变化, 然而不同微生物类群之间扩增时所需的引物存在差异。细菌和真菌(丛枝菌根真菌除外)的常用引物分别为核糖体DNA小亚基(16S rDNA)和内转录间隔区(ITS), 而核糖体DNA小亚基(18S rDNA)则是丛枝菌根真菌等以及原生动物的特异性引物。由于引物偏好性和错配性可能会导致混合样本中50%的目标DNA序列丢失, 产生不同的扩增结果(Hong et al, 2009; Bellemain et al, 2010)。所以, 应研究开发多个平行扩增引物以最大限度地呈现土壤微生物组全貌。


7.3 多组学方法联合使用研究土壤微生物组


虽然越来越多的研究发现施用尿素对土壤微生物组结构及其功能产生影响, 但是有关土壤微生物组在环境中的动态变化以及土壤微生物组代谢潜能的研究仍不够深入(朱永官等, 2021)。因此, 应利用多组学技术的优势, 通过多学科交叉挖掘土壤


微生物组对尿素的响应。从基因组学角度揭示土壤微生物组的功能潜势, 从宏转录组学和代谢组学分析其功能基因表达及微生物代谢(朱永官等, 2021)。更加重视土壤微生物组在土壤生态系统中的关键作用, 促进农业可持续发展。

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