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综合肥料管理对水稻根际微生物群落功能的影响

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摘要 为考察综合肥料管理(integrated fertilization management, IFM)策略和农民常规处理(farmer's practice, FP)对微生物群落和土壤功能的影响差异, 本研究利用2013—2014年设立的双季稻田间试验包括综合肥料管理(IFM)和农民实践(FP)2种处理, 通过在晚稻生长季节的3个时间点采集根际和非根际土壤, 调查土壤化学性质和酶活性, 使用磷脂脂肪酸(phospholipid fatty acids, PLFA)鉴定微生物生物量和群落组成。结果显示: 与FP处理相比, IFM处理降低了根际土壤的革兰氏阳性(Gram-positive bacteria, GP)和阴性细菌(Gram-negative bacteria, GN)的比值(GP/GN)和微生物胁迫指数。IFM处理促进了幼穗分化期和齐穗期根际土壤中蔗糖酶、酸性磷酸酶、芳基硫酸酯酶活性, 抑制了成熟期脲酶活性。冗余分析表明, 有效氮和总氮可分别解释微生物群落和酶活性变异的15.9%和12.5%, 这表明氮的有效性和氮水平分别是影响稻田环境微生物群落和酶功能的关键因素。此外, 革兰氏阴性细菌、真菌和丛枝菌根真菌对土壤酶活性改变的解釋率分别达到5.39%、3.88%和3.09%。微生物胁迫指数与磷酸酶和蔗糖酶活性呈负相关, 这表明细菌和真菌都参与土壤酶功能调节。研究表明, IFM主要通过调控稻田氮投入节奏改变微生物群落组成从而提升成熟期前的土壤酶活性, 促进水稻生长过程中的养分循环。

关键词 综合肥料管理; 微生物群落; 微生物胁迫指数; 酶活性; 水稻土

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作物管理与施肥策略在提升作物生产力及优化稻田生态系统功能中起着举足轻重的作用^[1]。这些人为因素会改变土壤性质, 并引发微生物群落结构的变化^[2]。鉴于微生物群落在调控土壤功能中的核心地位, 理解其如何响应环境变化显得尤为重要。研究表明, 微生物在适应环境变迁时展现出多样的策略, 包括高产(Y)、资源获取(A)以及胁迫耐受(S)^[3]。例如当土壤中营养过剩时, 部分微生物通过快速生长来充分利用资源; 而另一部分则通过分泌胞外酶来分解复杂底物, 从而获取必要的养分。微生物胞外酶不仅在微生物资源获取发挥作用还能为植物提供养分。在面临环境压力时, 一些微生物还能够合成特定的脂质, 以增强细胞膜的稳定性与完整性^[4]。然而, 作物管理与施肥策略如何影响与Y-A-S策略相关的微生物群落特征, 目前相关研究较少。

无机肥料管理作为提升水稻产量的主要策略,

在农业生产中得到广泛应用。长期施用化肥会引发细菌群落的显著变化, 进而提升光合作用、氮循环和硫呼吸的功能潜力^[5]。然而, 不恰当的无机肥料使用也可能对土壤健康产生负面影响。长期施用矿物肥料会改变腐殖酸的结构, 削弱其抑制植物病原真菌的能力, 从而给水稻土带来潜在的生态风险^[6]。此外, 过量施氮会降低固氮菌的多样性, 因此, 抑制了土壤本身的固氮作用^[7]。因此, 合理的施肥策略对于维持生态系统平衡和促进水稻土健康发展至关重要。与常规施肥处理(施用273 kg/hm²氮、59 kg/hm²磷和112 kg/hm²钾)相比, 长期(10 a)采用240 kg/hm²氮、52 kg/hm²磷和198 kg/hm²钾的浅间歇灌溉施肥, 能够显著减少氮损失, 提高土壤氮素利用率和水稻产量, 促进放线菌、蓝细菌、疣微菌、毛霉的增殖^[8]。事实上, 长期且平衡的施肥方案可以在不显著改变微生物多样性的前提下, 有效改善红壤性水

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稻土的养分状况,进而提升水稻产量^[9]。在稻田生态系统中,根际对土壤微生物的选择性过程降低了生物多样性^[10]。全球范围内的植物根际细菌群落分析显示,富营养菌的富集显著增强了有机化合物转化、固氮和反硝化等功能,但削弱了硝化作用,而裸土中的微生物群落则呈现出更高的寡营养型特征,这些微生物能够消耗顽固碳源并产生更多的孢子^[11]。这些结果表明,富营养生物的增加可能有助于活化与植物生长关系密切的养分循环过程。

近年来,为提高江汉平原的生产力,农民开始将新技术与以往的常规处理(farmer's practice, FP)相结合,形成了一种新的管理模式:综合肥料管理(integrated fertilization management, IFM)或称最佳管理实践。目前尚不清楚IFM是否能够更有效地维护微生物多样性和生态系统功能。IFM与FP的主要差异在于前者施用了更高水平的氮、磷和钾肥,且其施用节奏更贴合水稻的生长需求;此外,IFM还采用了更大的种植密度。IFM通过增加穗数、提高辐射利用效率和总氮吸收量,增强了养分的可利用性并刺激了水稻生产^[12]。因此,本研究假设IFM可能通过改变根际微生物群落特征来激活某些土壤功能,如增强土壤酶活性以提高养分可用性,改变微生物群落组成(由磷脂脂肪酸分析指示)或资源获取能力的提升(土壤酶活性可能反映微生物对资源获取的需求)。为验证这一假设,本研究对FP和IFM处理下的微生物群落结构、胁迫指数以及4种关键的土壤酶活性进行比较分析,旨在全面评估IFM对微生物生态的潜在影响。

1 材料与方法

1.1 场地描述与土壤取样

本田间试验选址于湖北省武穴县大山镇,气候类型属亚热带季风气候。2013年至2014年间,此地实施了双季稻种植制度。试验设计采用随机区组布局,包括综合肥料管理(IFM)和传统农民习惯(FP)2种处理,其中,FP处理作为本研究的对照组。每个处理均设有3个重复,确保结果的可靠性。每个重复的地块大小为13 m×9.5 m,总面积为123.5 m²。

在FP处理中,整个水稻生长周期(一年两季)内,总施肥量为氮195.0 kg/hm²、磷40.0 kg/hm²和钾75 kg/hm²。其中,磷肥、钾肥、锌肥(ZnSO₄·7H₂O)以及65%的氮肥作为基肥一次性施入,剩余的35%氮肥则在分蘖期分阶段施入田间。FP处理的种植密度为基本苗29.4 cm/株。对于IFM处理,早稻阶段,

每个重复地块施用的氮肥总量为245 kg/hm²、磷肥为75 kg/hm²、钾肥为180 kg/hm²。晚稻阶段则调整为氮肥260.0 kg/hm²、磷肥50.0 kg/hm²、钾肥205.0 kg/hm²。磷肥和钾肥作为基肥施入,与免耕处理保持一致。晚稻的氮肥施用策略为:50%作为基肥,30%在分蘖中期施入,剩余的20%则在幼穗分化期施入。钾肥的施用节奏与氮肥保持一致。IFM处理的种植密度为基本苗24.1 cm/株。

在2014年晚稻生长期,于穗分化、齐穗期和成熟期,采集0~20 cm的土壤样品。在每个处理的地块中,围绕作物均匀收集5个土壤芯样,并将这些芯样混合成1个复合样本,以代表该地块的土壤^[4]。将每个土壤样品分成3份,第1份样本经过冷冻干燥处理后,储存在-80℃的低温环境中,用于进行磷脂脂肪酸(phospholipid fatty acids, PLFA)分析。第2份样本则储存在4℃,并立即进行酶活性分析。最后一份样本风干后,通过2 mm的筛,用于测试土壤性质。所有数据采集均在2014-2015年完成。

1.2 土壤化学性质和酶活性的测量

土壤湿度(moisture, MOI)通过传统的干燥法进行测量,其pH值在土/水比为1:5(m/V)时测定。其他土壤特性,诸如土壤总碳(total C, TC)、土壤总氮(total N, TN)、有效氮(available N, AN)、铵态氮(NH₄⁺-N)、硝态氮(NO₃⁻-N)、总磷(total P, TP)、有效磷(available P, AP)、总钾(total K, TK)和有效钾(available K, AK)的测定方法,均参照文献[13]进行。

蔗糖酶、脲酶、酸性磷酸酶和芳基硫酸酯酶的活性均采用分光光度法(北京东讯天地仪器有限公司)进行测定。蔗糖酶在8%的蔗糖磷酸缓冲液体系中37℃反应24 h于508 nm波长测定;脲酶在10%的尿素磷酸-柠檬酸缓冲液(pH 6.7)体系中38℃反应3 h于578 nm波长下测定;酸性磷酸酶在5 mL 0.5%苯基磷酸二钠硼酸缓冲液(pH 5.0)中37℃反应12 h于570 nm波长测定;芳基硫酸酯酶在含0.005 mol/L硝基苯酚硫酸钾的0.5 mol/L乙酸缓冲液中37℃反应1 h,并于400 nm波长测定^[14]。

1.3 PLFA分析

采用单相氯仿-甲醇-水(体积比为1:2:0.8)体系提取冻干土壤样品中的磷脂。随后,磷脂经水解和甲醇化处理,利用安捷伦6850系列毛细管气相色谱仪(Agilent Technologies, Wilmington, DE)对所得脂肪酸甲酯进行鉴定和定量。采用MIDI软件,以19:0作为内标进行PLFA的鉴定和定量。PLFA分

组后被用作特定微生物群体的生物标志物^[15],包括真菌(Fun,以18:2 ω 6c和18:3 ω 6c为代表)、丛枝菌根真菌(AMF,以16:1 ω 5c为特征)、厌氧细菌(Ana,包括15:0-3OH,16:0-OH和18:0-OH)、放线菌(Act,以10-甲基脂肪酸为标记)^[16]、真核生物(Euk,以20:4 ω 6c和20:4 ω 9c为指示)、革兰氏阳性细菌(GP,特征为异和反饱和支链脂肪酸)以及革兰氏阴性细菌(GN,包括cy17:0、cy19:0和单不饱和脂肪酸)^[16]。细菌应激指数通过cy17:0/16:1 ω 7c、cy19:0/18:1 ω 7c和环丙基脂肪酸/单烯酸前体(cy17:0+cy19:0/16:1 ω 7c+18:1 ω 7c)的比率评估^[17]。

1.4 统计分析

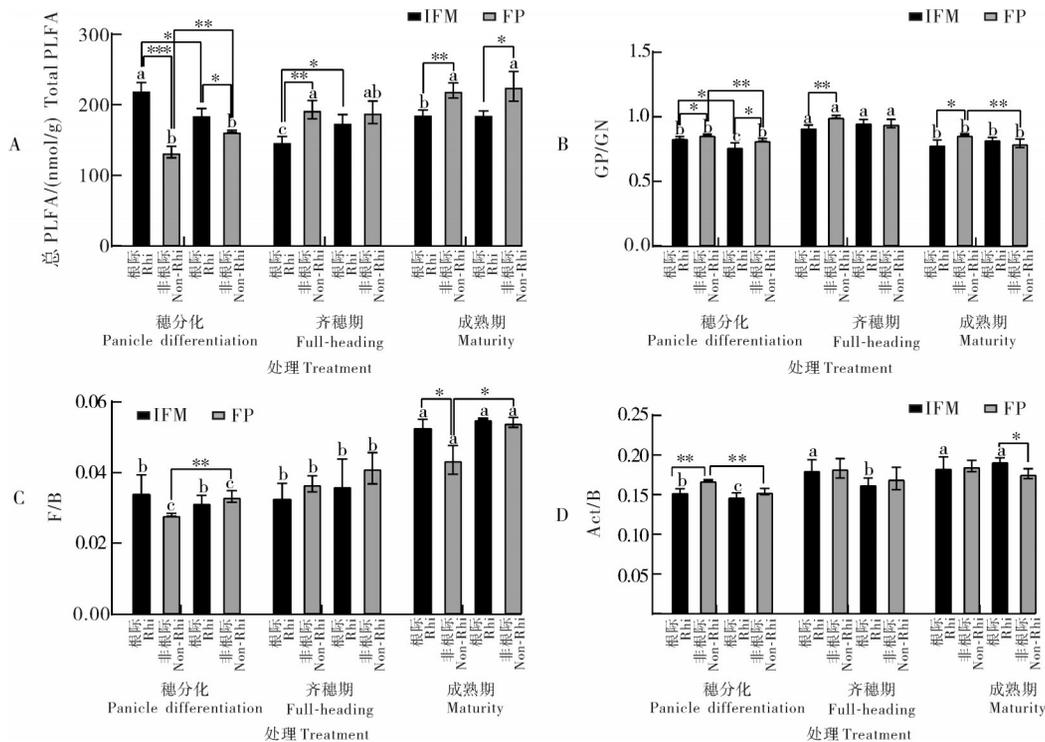
研究数据分析使用R语言版本4.0.2。柱状图通过GraphPad Prism 9.0.0软件绘制。检验处理、生长阶段和土壤类型之间的差异性,采用三因素方差分析。此外,图中的HSD(honest significant difference)方法被用作事后检验。为探究土壤微生物结构、酶

活性和微生物胁迫指数之间的潜在关系,采用Spearman相关检验。为深入探索2种处理之间磷脂脂肪酸的差异,运用R语言进行STAMP(statistical analysis of metagenomic profiles)分析和冗余分析^[18],以探究群落结构、环境因素和酶活性之间的潜在联系。在冗余分析中,解释变量的选择首先基于方差膨胀系数,随后通过Akaike信息标准模型进行优化。最后,为确保冗余分析结果的可靠性,采用重复1999次的置换检验进行验证。在数据处理过程中,必要时采用归一化处理后的数据进行统计分析。

2 结果与分析

2.1 对土壤特性的影响

对根际、非根际土壤理化性质的测定结果显示,相较于FP处理,IFM处理显著影响总磷($F=17.315, P<0.001$)、有效钾($F=32.918, P<0.001$)、总碳($F=8.393, P<0.01$)和pH($F=3.248, P<0.001$)。



误差棒表示值的平均标准偏差($n=3$);不同字母表示在不同生长阶段存在显著差异;*表示在特征之间存在显著差异(不同处理)($*, P<0.05; **, P<0.01; ***, P<0.001$),下同。Error bars represent the standard variance of the value mean ($n=3$). Different letters indicate a significant difference in different growth stages. Asterisks denote significant differences in traits between different variation ($*, P<0.05; **, P<0.01; ***, P<0.001$). The same as below.

图1 不同水稻生长阶段、施肥处理和土壤类型的总PLFA(A)、革兰氏阳性细菌与阴性细菌比例(B)、真菌与细菌比例(C)和放线菌与细菌比例(D)

Fig.1 Total PLFA(A), Gram-positive to Gram-negative bacteria ratio(B), fungi to bacteria ratio(C), and actinomycete to bacteria ratio(D) under different paddy growth stage, fertilization treatment and soil type

除C/N外,其他土壤性质均受生育期与施肥措施交互作用影响。此外,非根际土壤的有效钾明显高于根际土壤(表1)。

2.2 对微生物群落结构和胁迫指数影响

在幼穗分化期,IFM处理显著提升了微生物生物量。但在齐穗期和成熟期,IFM处理则导致总磷脂脂肪酸(tPLFA)下降(图1A)。革兰氏阳性菌与革兰氏阴性菌之比(GP/GN)在齐穗期呈现上升趋势,而在成熟期则有所下降(图1B)。IFM处理导致根际土壤的GP/GN比例降低,幼穗分化期真菌与细菌比率(F/B)增加、放线菌与细菌比率(Act/B)下降,成熟期F/B增加(图1C,图1D)。STAMP分析结果显示,IFM处理组的土壤革兰氏阴性菌指标(17:1 ω 8c)和厌氧菌指标(2OH 16:0)的水平较高。相反,FP处理组中可作为放线菌指标的10Me 18:0和真菌指标的18:3 ω 6c更为丰富(图2)。此外,根际土壤中的细菌应激指数在FP处理下高于IFM处理。冗余分析显示(图3),环境变量解释了62.53%的微生物

组成。其中,AN和MOI对微生物群落变异的贡献最大,分别为15.91%和10.57%;pH、总钾和有效磷也对微生物群落结构产生显著的影响(图4)。

2.3 酶活性及其驱动因素

蔗糖酶、脲酶、酸性磷酸酶和芳基硫酸酯酶的活性被用于评估与大量养分循环相关的土壤微生物功能。结果显示,随着生长阶段改变,这4种酶的活性出现显著变化(图5)。例如,在幼穗分化期,IFM处理提高了蔗糖酶的活性,还使得根际酸性磷酸酶活性略有上升(图5A)。蔗糖酶活性在齐穗期下降,在成熟期上升(图5B)。幼穗分化期在非根际土壤中的脲酶,其活性明显高于根际土壤中的。齐穗期在非根际土壤中的脲酶活性在IFM处理下降低(图5C)。而在幼穗分化期,芳基硫酸酯酶的活性较低(图5D)。

冗余分析显示,前2个轴共同解释了由土壤性质引起的土壤酶活性变化的86.65%(图4B)。土壤理化性质中的TN、AN、AK、pH和TP显著解释了土壤

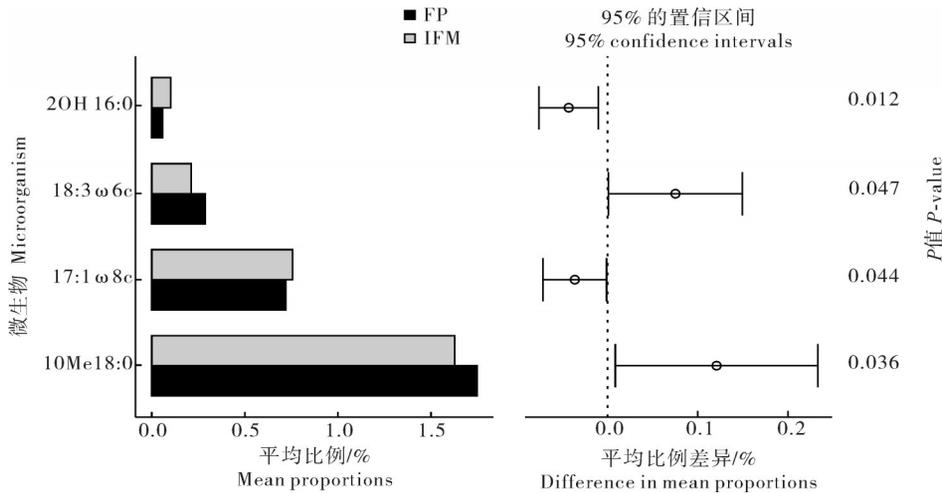
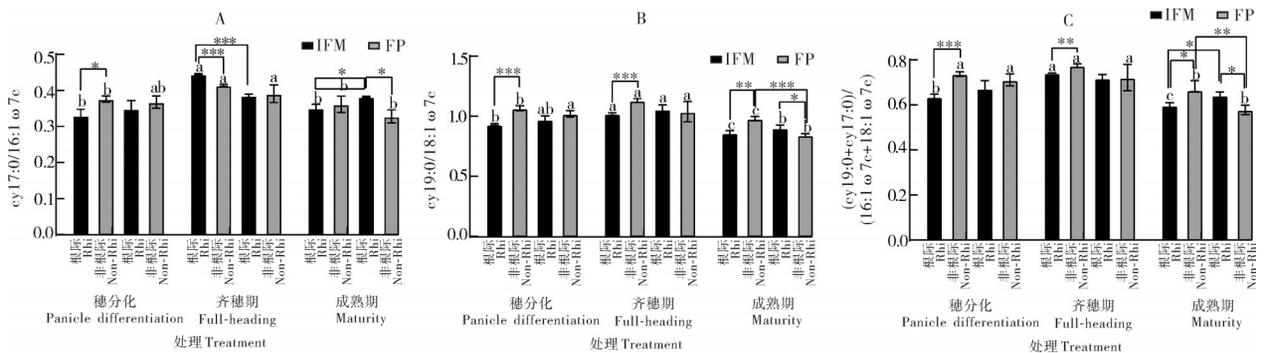


图2 基于STAMP分析的差异PLFAs

Fig.2 Differential PLFAs based on STAMP analysis



A: cy17:0/16:1 ω 7c; B: cy19:0/18:1 ω 7c; C: (cy19:0+cy17:0)/(16:1 ω 7c+18:1 ω 7c).

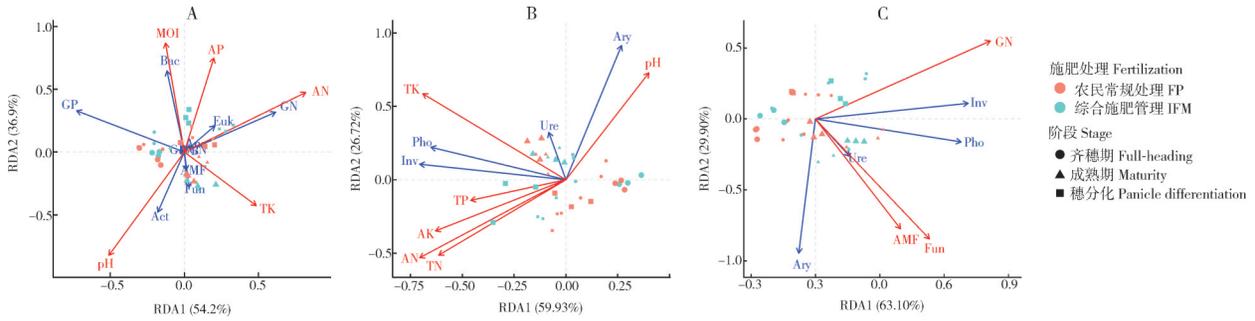
图3 不同生长阶段、土壤类型和施肥处理下的微生物胁迫指标

Fig.3 Microbial stress indicators under different growth stage, soil type and fertilization treatment

表 1 土壤理化性质
Table 1 Soil properties

时期 Stage	类型 Type	处理 Treatment	TP/ (mg/kg)	TK/ (mg/kg)	AP/ (mg/kg)	AK/ (mg/kg)	AN/ (mg/kg)	MOI/%	TN/%	TC/%	C/N	pH
幼穗分化期 Panicle differentiation	根际 Rhizosphere	IFM	901.1a	2 366.1bcd	24.3a	82.0ab	137.1ab	38.20a	0.21a	2.14a	9.98ab	5.08i
		FP	694.0d	2 460.9abcd	14.9bcde	82.4ab	121.0bcde	32.02bcd	0.18cde	1.81d	9.95ab	5.16g
	非根际 Non-rhizosphere	IFM	844.5ab	2 156.2cd	21.8a	84.3a	147.4a	33.75bc	0.19b	1.91b	9.82 ab	4.92j
		FP	728.2cd	2 146.6cd	14.9bcde	86.0a	125.8bc	33.02 bc	0.19bc	1.85c	9.57b	5.12h
齐穗期 Full-heading	根际 Rhizosphere	IFM	740.8cd	1 535.9 e	10.7e	43.0ef	101.2f	31.34cde	0.16f	1.66h	10.14ab	5.54c
		FP	723.8cd	1 524.0 e	16.0bcd	31.1f	105.2ef	32.18bcd	0.17ef	1.73f	10.14ab	5.60b
	非根际 Non-rhizosphere	IFM	765.0bcd	2 682.0abc	16.2bc	80.3abc	102.6ef	34.66b	0.18de	1.84c	10.23ab	5.33f
		FP	764.6bcd	1 892.5de	16.1bc	53.9de	102.8ef	33.93bc	0.18de	1.78e	10.05ab	5.51d
成熟期 Maturity	根际 Rhizosphere	IFM	715.3cd	2 779.8ab	11.7de	64.1cd	117.9cdef	29.77de	0.16f	1.69g	10.45a	5.64a
		FP	754.4cd	3 024.5a	12.3cde	52.6de	113.8cdef	31.49cde	0.18bcd	1.85c	10.10ab	5.64a
	非根际 Non-rhizosphere	IFM	719.5cd	3 000.4a	11.9cde	82.3ab	106.7def	28.81e	0.16f	1.64h	10.00ab	5.54c
		FP	788.0bc	2 881.3ab	17.2b	66.1bcd	124.7bcd	33.24bc	0.18bcd	1.90b	10.32a	5.36e
时期 Stage(S)		10.649***	77.730***	47.160***	96.675***	64.880***	42.392***	131.154***	2 279.434***	9.854***	9.189×10 ²⁶ ***	
采样部位 Site(T)		2.059	7.039*	7.525*	76.846**	1.157	1.625	4.148	5.187*	3.024	2.176×10 ²⁶ ***	
施肥处理 Fertilization(F)		17.315***	2.153	2.984	32.918***	2.345	0.143	2.203	8.393**	1.211	3.248×10 ²⁷ ***	
S×T		1.910	20.320***	6.838**	17.792***	1.505	16.159***	10.980***	642.079***	0.998	6.857×10 ²⁶ ***	
S×F		46.997***	5.083*	53.378***	10.603***	13.617***	37.786***	67.343**	2 552.921***	0.251	5.474×10 ²⁷ ***	
T×F		5.960*	9.578**	0.430	2.541	0.975	12.968**	5.463*	250.411***	0.376	1.012×10 ²⁶ ***	

注 Note: TP:总磷 Total phosphorus; TK:总钾 Total potassium; AP:有效磷 Available phosphorus; AK:有效钾 Available potassium; AN:有效氮 Available nitrogen; MOI:水分 Moisture; TN:总养分 Total nitrogen; TC:总碳 Total carbon; C/N:碳氮比 Carbon to nitrogen ratio. 不同符号的HSD检验差异有统计学意义 ($P < 0.05$). 星号表示这些因素显著地解释了样本间的差异 (*, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$). Different letters with Tukey HSD tests indicated significant differences ($P < 0.05$). Asterisks indicated that the factors significantly explained the variation among the samples (*, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$).



A: 环境变量 vs. PLFA 组成 Significant environmental variables effect on PLFA composition; B: 酶活性的影响 Enzyme activity; C: 微生物群落对酶活性影响 Microbial community effect on enzyme activity. 较大的符号代表根际土壤, 较小的符号代表非根际土壤 Bigger symbols represented rhizosphere soil while smaller symbols represented non-rhizosphere soil.

图4 冗余分析结果

Fig.4 Redundancy analysis results

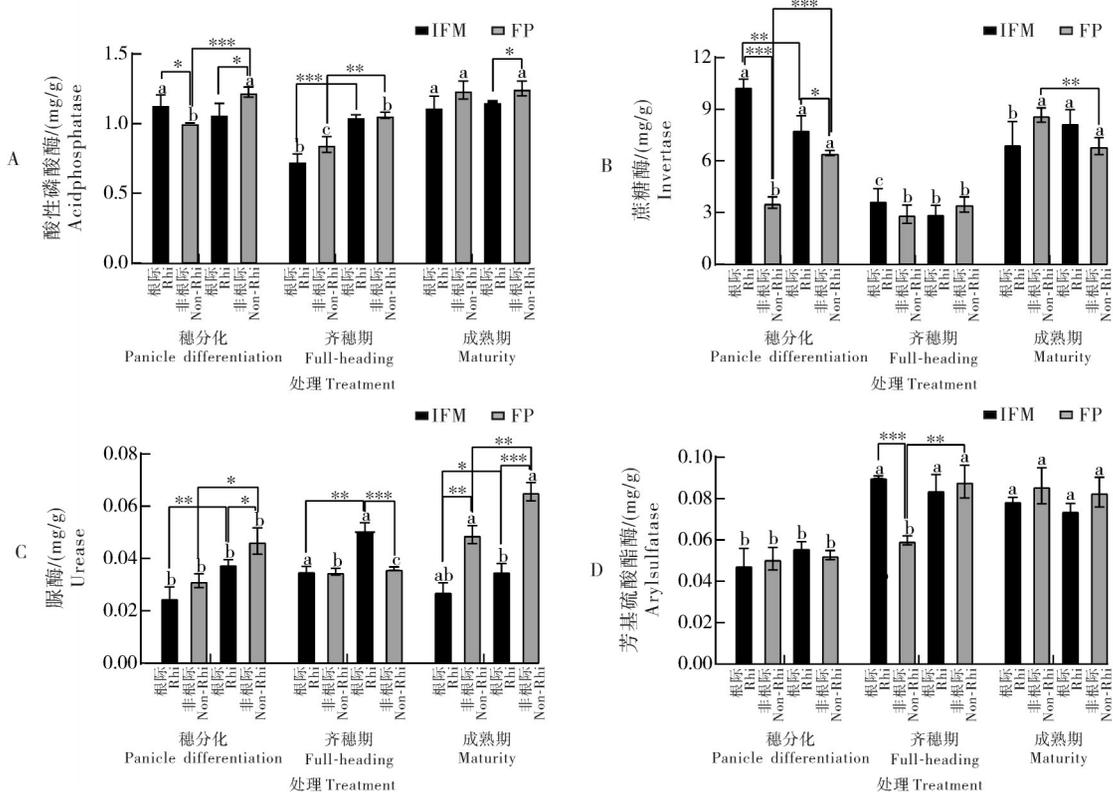


图5 不同生长阶段、施肥处理和土壤类型对酶活性的影响

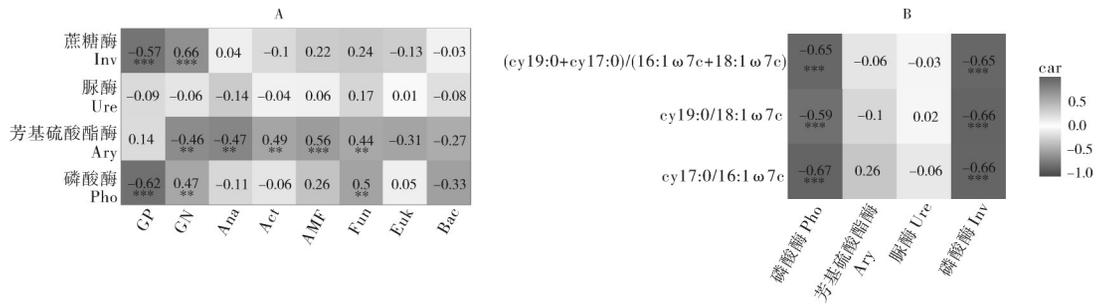
Fig.5 Enzyme activities under different growth stage, fertilization treatment and soil type

酶活性的变化, 解释率分别为 12.15%、5.95%、5.17%、5.00% 和 4.14%。此外革兰氏阴性细菌、真菌和丛枝菌根真菌对土壤酶活性改变的贡献率分别为 5.39%、3.88% 和 3.09%。这表明革兰氏阴性细菌和真菌在调节土壤酶功能方面起重要作用。相关分析进一步支持了微生物群落与土壤酶活性之间的关系。Pho 与革兰氏阴性细菌 ($P < 0.01$) 和真菌 ($P < 0.01$) 呈正相关, 而与革兰氏阳性细菌呈负相关 ($P < 0.001$)。蔗糖酶呈现出类似的趋势。此外, 芳基硫酸

酯酶与放线菌、丛枝菌根真菌和真菌呈正相关, 而与革兰氏阴性细菌和厌氧细菌呈负相关。胁迫指数与磷酸酶和蔗糖酶活性呈负相关(图6)。

3 讨论

化肥的施用为土壤微生物提供了直接养分来源。除养分供应, 不同的管理过程也许也对养分化学计量和土壤微生物群落的时间变化产生影响^[19]。在穗分化期, IFM 处理的根际土壤中, 总 PLFA 含量高于 FP 处理。这表明 IFM 在水稻生育期早期采用



星号表示相关性的重要性 Asterisks indicate the significance of the correlations.

图6 土壤酶活与微生物组成(A)、微生物胁迫指数(B)的相关性热图

Fig.6 Heatmap of soil enzyme activities responses to microbial component(A) and microbial stress index(B)

的高剂量施肥促进了微生物生长,然而这一趋势在齐穗期和成熟期出现了逆转(图1A),这暗示IFM处理可能促进植物生长^[12]而强化了植物对养分的吸收从而抑制了微生物生物量的增加。

根据先前的研究,革兰氏阴性细菌对有效碳的响应更为敏锐,而真菌、放线菌以及革兰氏阳性细菌可分解一些难降解的底物^[20]。值得注意的是,GP/GN的上升与生态系统生产力的降低有着密切的关联^[21]。研究发现,IFM处理降低了根际土壤中GP/GN值(图1B)。此外,高施肥量和多次施肥可能促进根际沉积,从而吸引更多的富营养生物。研究表明,真菌与细菌的比率(F/B)与土壤的碳储存潜力紧密相关^[22],并且真菌群落对化肥的响应尤为敏感^[23]。本研究中,F/B在成熟期达到峰值,且IFM处理进一步提高了这一比率(图1C)。这一发现暗示,在IFM处理下,水稻成熟时,植物地下部生物量或残体的积累可能会有利于真菌的繁殖。冗余分析结果表明,有效氮、含水率、pH、总钾、有效磷是影响微生物群落的主要因素,其中有效氮对群落变异的解释度最高。氮在调节水稻养分、根系生长和微生物群落中的作用至关重要^[24]。此外,有效磷也是被认为影响稻田微生物群落的关键因素之一^[25-26]。

一般认为,有环脂肪酸与不饱和脂肪酸的比率可用于评估微生物群落的生理营养压力^[27]。对于细菌来说,cy19:0/18:1ω7的比率可以指示来自高温或低氧和酸性的环境压力^[28]。此外,(cy19:0+cy17:0)/(16:1ω7c+18:1ω7c)是细菌群落营养胁迫的指标^[17],但微生物群落组成变化也可能引起压力指数的变化^[27]。研究发现,在根际土壤中,与FP处理相比,IFM处理降低了cy19:0/18:1ω7c和(cy19:0+cy17:0)/(16:1ω7c+18:1ω7c)(图3),意味着IFM处理可能会减少对微生物的外部压力,或

影响产生相应脂肪酸的微生物数量。

IFM引起的土壤性质TN、AN、AK、pH和TP的变化显著地解释了土壤酶活性的变化。除了化学性质之外,革兰氏阴性细菌、真菌和丛枝菌根真菌解释了蔗糖酶、脲酶、酸性磷酸酶和芳基硫酸酯酶的大部分变化(图4C),表明革兰氏阴性细菌和真菌在调节土壤酶活性方面发挥了很大作用。在未施氮的稻田中发现影响相同酶类的关键因素是放线菌和革兰氏阳性细菌^[29]。一般认为,在水稻土中,细菌群落比真菌在调节土壤酶功能方面更为重要^[14]。长期施肥条件下,稻田生态酶化学计量与微生物群落结构高度相关^[30]。本研究中,革兰氏阳性细菌的比例与蔗糖酶和酸性磷酸酶的活性呈负相关,相反,革兰氏阴性细菌与这些酶呈正相关,这些结果表明在本研究中革兰氏阴性细菌可能表达更多的蔗糖酶、酸性磷酸酶。芳基硫酸酯酶活性与放线菌和真菌PLFA显著相关。这一结果不同于在油菜-水稻轮作系统中所报道的磷酸酶和硫酸酯酶与土壤粒径组分中革兰氏阳性细菌的相关性更强^[31]。

考虑到PLFA谱可以指示外部压力或产生特定脂肪酸的微生物,而生产酶和表达基因以承受环境压力都需要能量成本^[4],因此微生物胁迫指数和群落水平功能之间可能存在相关性。较高的胁迫水平可能会削弱生态系统功能,例如微生物产酶的能力^[32]。研究发现,微生物胁迫指数与酸性磷酸酶和蔗糖酶呈负相关。这暗示,酸性磷酸酶和蔗糖酶可能比脲酶和芳基硫酸酯酶更容易受到环境胁迫的负面影响。还有一种合理的推测是,产生相关脂肪酸的微生物可能存在产生或不产生相关酶的偏好。

IFM和FP处理之间的主要区别在于种植密度、总磷投入、氮水平和施肥节奏。适当的氮素输入可以缓解土壤的氮素限制,降低氮素降解酶的活性^[33]。这一假设与IFM处理中脲酶活性下降具有一致性。

均衡施肥可以提高水稻土的微生物功能^[34]。本研究发现不同(IFM与FP)处理下,微生物群落与养分循环相关的酶功能表达存在差异,这是因为IFM处理下,在穗分化期和抽穗期可能招募了特定的微生物从而在根际产生更多的酶(脲酶除外)。然而,IFM对水稻土微生物群落和功能的长期影响仍有待探索。

综上所述,IFM可以在穗分化阶段增加微生物PLFA,但在分化后期降低微生物数量,这可能有利于植株生长初期的生长,减少生长过程中微生物与植株之间的营养竞争;通过降低根际土壤的GP/GN比率影响微生物群落;降低微生物胁迫指数,调节植物不同发育阶段蔗糖酶、酸性磷酸酶和芳基硫酸酯酶的活性,从而将微生物群落总体特征从胁迫耐受型转为资源获取型,进而产生有利于养分循环、促进植物生长的微生物区系。然而,IFM需要更多的成本和劳动力投入。未来的施肥研究还应考虑纳入节省劳动力成本、更加精准高效地实现养分管理。

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Effect of comprehensive fertilizer management on function of rice rhizosphere microbial community

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Abstract Integrated fertilizer management (IFM) with a higher N dose and more fertilizer splits has been designed to increase rice yield for the full double rice system instead of for farmers in the subtropical regions of China. Higher levels of chemical fertilizers negatively affect the environment and microbial ecology, but more splits to meet plant demand might reduce adverse effects and promote soil function. A field experiment for double rice cropping conducted in 2013–2014 was used to study whether integrated fertilizer management has beneficial effects on the microbial community and microbial function compared with conventional practices of farmers (FP). A randomized block including integrated fertilizer management (IFM) and conventional practices of farmers (FPs) was designed. Rhizosphere and non-rhizosphere soils were collected at three time points during the season of growing late rice to investigate the chemical properties and enzyme activity in soil. The phospholipid fatty acids (PLFA) were used to identify microbial biomass and community composition. The results showed that IFM treatment reduced the ratio of Gram-positive bacteria (GP) to Gram-negative bacteria (GN) and the index of microbial stress in rhizosphere soil compared with the FP treatment. IFM promoted the activity of sucrase, acid phosphatase, and arylsulfatase in the rhizosphere soil at the stage of panicle differentiation and full-heading, while inhibiting the activity of urease at the stage of maturity. The results of analyzing redundancy showed that available nitrogen and total nitrogen explained 15.9% and 12.5% of the variability in the microbial community and enzyme activities, indicating that N availability and its level play key roles in regulating the microbial community and enzyme functions in paddy soil. The enzyme activity was significantly explained by Gram-negative bacteria (GN, 5.39%), fungi (3.88%) and AM fungi (3.09%). The index of microbial stress was negatively correlated with the activity of phosphatase and sucrase, indicating that both bacteria and fungi are involved in the regulation of enzyme activity in soil. It is indicated that IFM mainly regulates the rhythm of nitrogen incorporation in paddy soil to change the composition of microbial communities, thereby enhancing enzyme activity in soil before maturity and promoting nutrient cycling during the growth of rice.

Keywords integrated fertilizer management; microbial community; index of microbial stress; enzyme activity; paddy soil

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