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Magnesium-induced changes in soil chemical and microbial properties facilitate improvements in sugarcane yield and fertilizer use efficiency

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KEYWORDS

Sugarcane yield, fertilizer use efficiency, bacterial and fungal communities, magnesium application, acidic red soil

HIGHLIGHTS

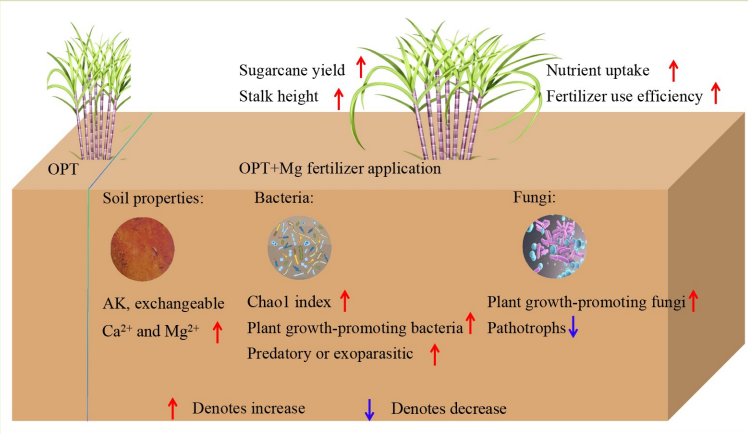
- All three Mg fertilizer application treatments increased the 2-year average sugarcane yield, primarily attributed to the increase in stalk height.
- The bacterial Chao1 index was increased while fungal diversity indices were not influenced by Mg application.
- Various plant growth-promoting microorganisms were enriched while certain pathogenic microorganisms were suppressed by Mg application.
- Variations in soil bacterial and fungal community structure were significantly correlated with available potassium and available silicon, respectively.

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GRAPHICAL ABSTRACT



ABSTRACT

Soil magnesium (Mg) deficiency limits sugarcane yield and quality, underscoring the need for optimized Mg fertilization. A field experiment was conducted to compare the effects of three types of Mg fertilizer (magnesium sulfate, silicon-magnesium, and boron-magnesium-zinc) on sugarcane yield, nutrient utilization, and the microbial community. Compared with the optimized fertilization treatment (OPT), all three Mg application treatments increased the 2-year average sugarcane yield, with the greatest increase observed in the OPT plus boron-magnesium-zinc fertilizer treatment (OPT+BMgZn). The use efficiencies of phosphorus, potassium, and Mg fertilizer were significantly greater in the OPT+BMgZn treatment than in OPT. Compared with the OPT, the bacterial Chao1 index increased in the Mg application treatments, whereas the fungal Chao1 and Shannon indices were unaffected ($P < 0.05$). Moreover, compared with OPT, the relative abundances of the plant growth-promoting microorganisms *Bradyrhizobium*, *Acidothermus*, and *Conexibacter* increased in the OPT+BMgZn treatment, whereas those of the pathogenic microorganisms *Fusarium* and *Vanrija* decreased in all Mg

application treatments. Functional prediction revealed enrichment of predatory or exoparasitic functions in the bacterial community and reduced fungal pathotrophs in all Mg application treatments compared with OPT. Correlation analysis revealed that sugarcane yield and nutrient uptake were positively correlated with exchangeable Mg^{2+}; bacterial community composition and function were primarily affected by available phosphorus and pH, whereas fungal composition and function were mainly influenced by available potassium and exchangeable Mg^{2+}. Overall, integrating sugarcane yield, nutrient use efficiency, and microbial community structure and function identified OPT+BMgZn as the optimal Mg fertilization strategy for acidic red soils in South China.

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1 Introduction

Magnesium (Mg) is an essential macronutrient for crop growth and plays irreplaceable physiological roles in plants[1]. It constitutes the core component of chlorophyll and functions critically in protein biosynthesis, photosynthetic electron transport, and enzyme activity regulation. However, in modern agricultural production, the long-term overapplication of nitrogen (N), phosphorus (P), and potassium (K) fertilizers coupled with inadequate secondary and micronutrient supplementation has resulted in a severe soil Mg imbalance in Chinese farmlands[2]. Surveys reveal that approximately 63% of the nation's cultivated land suffers from Mg deficiency, with the most severe conditions occurring in the acidic soil regions of South China[3]. In these areas, high temperatures and abundant rainfall facilitate Mg leaching. Moreover, soil acidification reduces the bioavailability of secondary and micronutrients, such as Mg, silicon (Si), and boron (B). Therefore, the scientific supplementation of Mg fertilizer has become an important strategy for enhancing agricultural quality and efficiency.

Sugarcane in China is distributed mainly in Guangxi, Guangdong, Yunnan and Hainan Provinces, where soil Mg is present primarily in easily weathered minerals[2]. The soil Mg pool is continuously depleted under intense weathering and leaching. Furthermore, with the increasing intensification of sugarcane production and the adoption of high-yielding varieties, the amount of Mg removed by sugarcane has increased annually[4]. Moreover, insufficient Mg fertilizer input under traditional practices and a declining organic fertilizer application rate have resulted in a severe imbalance in soil Mg budgets. Thus, Mg deficiency has become a key limiting factor restricting the improvement in sugarcane yield and quality[5]. Currently, a wide variety of Mg fertilizers are available on the market, including fast-acting magnesium fertilizers (e.g., magnesium sulfate and magnesium nitrate), slow-release magnesium fertilizers (e.g., magnesium oxide and silicon-calcium-magnesium fertilizer), and multifunctional compound magnesium fertilizers (e.g., potassium-magnesium sulfate and boron-magnesium-zinc compound fertilizer). The properties and agronomic efficiencies of these fertilizers differ substantially[6]. In addition to the specificity of soil conditions and crop Mg requirements across different ecological regions, the development of region- and crop-specific Mg fertilizer application practices is urgent.

Soil microorganisms, primarily bacteria and fungi, can influence soil quality through multiple processes, including the decomposition of organic matter, nutrient cycling, and the modification of soil aggregate structure. Several studies have confirmed that Mg fertilization can alter soil physicochemical properties, thereby regulating microbial networks. In tea plantation soils, the application of Mg increases soil pH, carbon, available N, and exchangeable calcium and Mg contents. Changes in these nutrients shape the structure and function of microbial communities[7]. Mg-containing phosphate fertilizer (struvite) increases Olsen P in maize rhizosphere soil by 30%–40%, which may be due to the enrichment of *nitrosphaeraceae* associated with P cycling[8]. Short-term Mg addition increases microbial biomass carbon in both high-organic-matter and low-organic-matter soils; however, its effects on bacterial community composition differ markedly between the two soils[9]. Nevertheless, research on

the effects of various types of Mg fertilizer on the composition and function of bacterial and fungal communities in sugarcane soils remains limited. Conducting research in this area would facilitate the selection of suitable Mg fertilizer types for sugarcane production.

As a dominant sugarcane production belt in China, western Guangdong Province has experienced a continuous decline in sugarcane yield since 2019. Previous investigations have revealed that excessive amounts of N, P, and K fertilizers are applied and that the supplementation of Mg is severely inadequate. This leads to low use efficiency of fertilizer and severe Mg deficiency in sugarcane[5]. Furthermore, continuous years of sugarcane monocropping have caused ecological problems, including soil acidification, compaction, and microbial flora imbalance, which threaten the sustainable development of the sugarcane industry[10]. In this study, a field experiment was performed to compare the different effects of three types of Mg fertilizers (magnesium sulfate, boron-magnesium-zinc, and silicon-magnesium) on sugarcane performance and soil health under chemical fertilizer reduction. The specific aims were (1) to investigate the effects of different types of Mg fertilizers on sugarcane yield, fertilizer use efficiency and soil properties; (2) to evaluate changes in bacterial and fungal communities and the relationships between core microbial genera and sugarcane yield and related agronomic traits; and (3) to elucidate the differences in soil bacterial and fungal functions and their driving factors.

2 Materials and methods

2.1 Experimental site

A field experiment was conducted in Suixi County, Zhanjiang City, Guangdong Province, China (110°28′ E, 21°36′ N). The region has a subtropical monsoon climate, with an average annual temperature of 23.2 °C and an average annual precipitation of 1540 mm. The soil is classified as Eutric Cambisol. The properties of the basic soil (0–20 cm) were as follows: a pH of 4.73 (soil:water ratio of 1:2.5), soil organic matter (SOM) content of 49.77 g·kg^{-1}, total nitrogen (TN) content of 1.74 g·kg^{-1}, total phosphorus (TP) content of 1.93 g·kg^{-1}, total potassium (TK) content of 1.84 g·kg^{-1}, available nitrogen (AN) content of 124.10 mg·kg^{-1}, available phosphorus (AP, Bray P) content of 215.25 mg·kg^{-1}, available potassium (AK) content of 163.94 mg·kg^{-1}, available silicon (ASi) content of 61.5 mg·kg^{-1}, available boron (AB) content of 0.22 mg·kg^{-1}, available zinc (AZn) content of 0.55 mg·kg^{-1}, exchangeable calcium (exchangeable Ca^{2+}) content of 218.47 mg·kg^{-1}, and exchangeable magnesium (exchangeable Mg^{2+}) content of 33.74 mg·kg^{-1}.

2.2 Experimental design

An experiment was performed to investigate the effects of different types of Mg fertilizers. Five treatments were designed: (1) no fertilizer control (CK); (2) optimized fertilization treatment (OPT, compound fertilizer, in which the local conventional application rates of N, P_2O_5, and K_2O were reduced by 7%, 34% and 20%, respectively); (3) OPT plus magnesium sulfate (OPT+Mg, containing 27% MgO); (4) OPT plus silicon-magnesium fertilizer (OPT+SiMg, containing 15% MgO and 9% SiO_2); and (5) OPT plus boron-magnesium-zinc fertilizer (OPT+BMgZn, containing 25% MgO, 0.6% B_2O_3, and 0.6% Zn). The compound fertilizer (25% N, 10% P_2O_5, 16% K_2O, w/w) was applied at a rate of 1800 kg·ha^{-1} in all fertilized treatments. The detailed fertilizer application rates are presented in Table 1.

Compound fertilizer was applied in two split applications: 17% as basal fertilizer before planting and 83% as tillering fertilizer. The magnesium sulfate, silicon-magnesium, and boron-magnesium-zinc fertilizers were also split-applied, with 50% as basal fertilizer and 50% as tillering fertilizer. For pest and weed control, carbofuran (3%) and acetochlor were applied. All the treatments were managed under conventional practices.

2.3 Sample collection and analysis

2.3.1 Sample collection

At the sugarcane maturity stage, three representative plants per plot were sampled. The roots were removed, and the aboveground parts were separated into stalks and leaves. The stalk and leaf samples, each composed of a mixture of three sugarcane plants, were oven-dried at 105 °C for 30 min for enzyme deactivation, followed by drying at 70 °C to a constant weight. The dried samples were then ground using a grinder and passed through a 0.5 mm sieve for further analysis. The nutrient contents (N, P, K, and Mg) of the stalks and leaves were determined separately. The fresh and dry weights were recorded, and the water contents of the stalks and leaves were calculated. The sugarcane yield was measured as the actual harvest weight per plot.

Table 1 Annual rates of chemical fertilizer under different treatments

Treatment	Annual rates of fertilizer (kg·ha^{-1})			
	N	P_2O_5	K_2O	MgO
CK	0	0	0	0
OPT	450	180	288	0
OPT+Mg	450	180	288	60
OPT+SiMg	450	180	288	60
OPT+BMgZn	450	180	288	60

Note: CK, no fertilizer; OPT, optimized fertilization treatment; OPT+Mg, OPT plus magnesium sulfate; OPT+SiMg, plus silicon-magnesium fertilizer; OPT+BMgZn, plus boron-magnesium-zinc fertilizer. Fertilizer types and their nutrient contents are detailed in the text.

During the 2023–2024 sugarcane maturity stage, soil samples were collected from the 0–20 cm plough layer using a soil auger (5 cm inner diameter). Three soil cores per plot were mixed to form one composite sample. A portion of the fresh soil sample was passed through a 2-mm sieve and stored at −40 °C for microbial analysis. The remaining soil sample was air-dried and sieved for physicochemical property analysis.

2.3.2 Soil and plant chemical analysis

The plant (stalks and leaves) samples were digested with H_2SO_4-H_2O_2, and the N, P, K, and Mg concentrations were determined using a continuous flow analyser. The soil pH was measured using a pH meter (soil:water ratio of 1:2.5). SOM was determined using the $K_2Cr_2O_7$ external heating method, TN by the Kjeldahl method, TP following H_2SO_4–$HClO_4$ digestion using the molybdenum blue method, and TK by the NaOH fusion method. AN was determined using the alkaline diffusion method, AP by the Bray I method, and AK by extraction with 1 mol·L^{-1} NH_4OAc followed by flame photometry. ASi, AZn, and AB were extracted using 0.025 mol·L^{-1} citric acid, DTPA solution (pH 5.3), and hot 0.01 mol·L^{-1} $CaCl_2$ solution, respectively, and the extracts were analysed by inductively coupled plasma–mass spectrometry (ICP–MS; Shimadzu, Japan).

2.3.3 Soil microbial community analysis

Fresh soil samples (0.5 g) were used for DNA extraction. DNA was extracted using the MoBio PowerSoil DNA Isolation Kit (MoBio Laboratories, USA), with three biological replicates per treatment. The quality and concentration of the extracted DNA were assessed using a Qubit™ 3.0 fluorometer. The DNA samples were stored at −40 °C.

The hypervariable V4 region of the bacterial 16S rRNA gene was amplified using the primers 515F (5'-GTGCCAGCMG CCGCGG-3') and 907R (5'-CCGTCAATTCMTTTRAGTTT-3')[9]. For fungal community analysis, the ITS1 region of the internal transcribed spacer was amplified using the primers ITS1F (5'-GGAAGTAAAAGTCGTAACAAGG-3') and ITS1R (5'-GCTGCGTTCTTCATCGATGC-3')[11]. PCR products were checked for quality using 1% agarose gel electrophoresis, purified using an OMEGA gel extraction kit, and quantified using a Qubit 2.0 fluorometer. Equal amounts of purified PCR products from different samples were mixed, and the quality of the pooled products was verified. Sequencing was performed on the Illumina HiSeq 2500 platform. The sequences were clustered into operational taxonomic units (OTUs) using VSEARCH (v2.13.4) at 97% similarity. Alpha diversity indices were calculated using Mothur software.

2.4 Data analysis

The fertilizer uses efficiency (FUE) was calculated using the balance method as follows:

$$FUE = U_n/F_n \times 100\% \quad (1)$$

where U_n (kg·ha^{-1}) is the total nutrient taken up by the sugarcane crops (stalks and leaves) in the treatments in which fertilizer was applied. F_n (kg·ha^{-1}) is the amount of fertilizer applied.

All the data were compiled using Microsoft Excel. One-way analysis of variance (ANOVA) was performed using SAS software (version 9.2), and the significance of differences among treatment means (three replicates) was tested using Duncan's multiple range test at the $P < 0.05$ level. Functional predictions were conducted using the PICRUSt database for bacterial communities (based on 16S rRNA gene sequences)

and the FUNGuild database for fungal communities (based on ITS sequences). Correlations among sugarcane agronomic traits, soil properties, and soil microbial communities were assessed using Spearman's correlation coefficients, and the results were visualized as heatmaps.

3 Results

3.1 Sugarcane yield and related agronomic traits

Sugarcane yields were lower, whereas sucrose content and sugar yields were higher in 2023–2024 than in 2022–2023 (Fig. 1). Mg fertilizer application significantly increased the sugarcane yield, sugar yield, and stalk height. Compared with OPT, the 2-year average sugarcane yields in OPT+Mg, OPT+SiMg, and OPT+BMgZn increased by 6.8%, 7.6%, and 11.6%, respectively; the sugar yield increased by 14.5%, 16.5%. and 17.8%, respectively; and the stalk height increased by 5.6%, 7.3%. and 7.3%, respectively ($P < 0.05$). In contrast, compared with OPT, the application of Mg fertilizer did not significantly affect the sucrose content, stalk diameter, or number of mill able stalks.

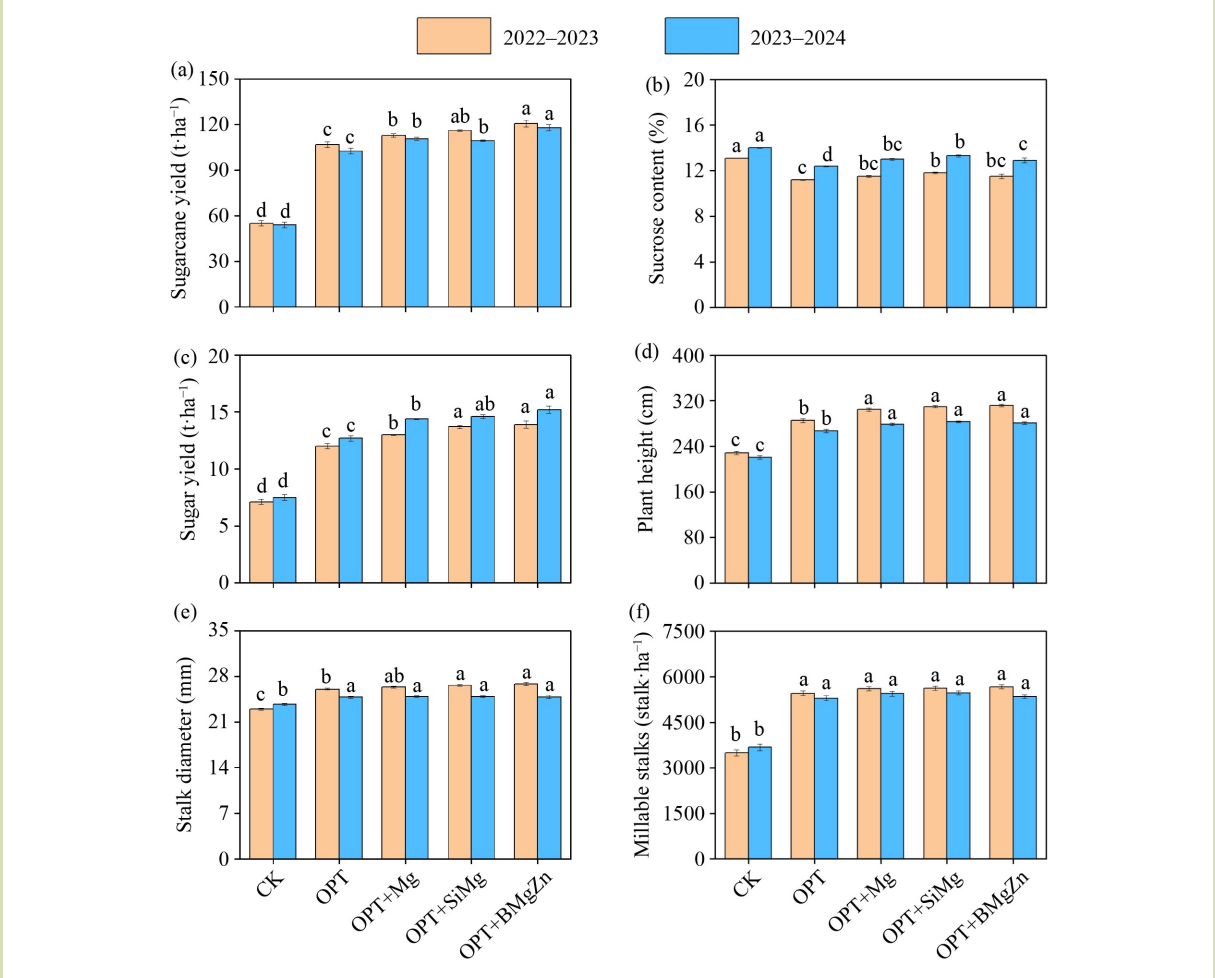


Fig. 1 Sugarcane yield and related agronomic traits under different fertilization treatments for 2022–2023 and 2023–2024 (mean ± standard error, $n = 3$). Lowercase letters among treatments denote significant differences ($P < 0.05$). CK, no fertilizer; OPT, optimized fertilization treatment; OPT+Mg, OPT plus magnesium sulfate; OPT+SiMg, plus silicon-magnesium fertilizer; OPT+BMgZn, plus boron-magnesium-zinc fertilizer.

3.2 Nutrient uptake and fertilizer use efficiency

The nutrient uptake and fertilizer use efficiency of sugarcane were lower in 2023–2024 than in 2022–2023 (Table 2). The application of Mg fertilizer increased the nutrient uptake of sugarcane. Compared with OPT, the 2-year mean uptake of K increased in OPT+Mg, the uptake of P increased in OPT+SiMg, and the uptakes of P and K increased in OPT+BMgZn ($P < 0.05$). The 2-year average nitrogen use efficiency (NUE), phosphorus use efficiency (PUE), and potassium use efficiency (KUE) among the four fertilization treatments were 38.1%–47.2%, 20.9%–29.1%, and 97.7%–126.7%, respectively. Compared with OPT, the average KUE increased in OPT+Mg, the PUE increased in OPT+SiMg, and both the PUE and the KUE increased in OPT+BMgZn ($P < 0.05$). The uptake of Mg under all three Mg application treatments was significantly higher than that under OPT, and the average Mg use efficiency of OPT+BMgZn was significantly higher than that of OPT+Mg.

3.3 Soil properties

The application of Mg fertilizer significantly changed many important soil properties, such as AP, AK, exchangeable Mg^{2+}, and exchangeable Ca^{2+} (Table 3). Compared with OPT, the AK, exchangeable Ca^{2+}, and exchangeable Mg^{2+} contents in OPT+Mg, OPT+SiMg, and OPT+BMgZn increased, whereas the SOM and AP contents decreased ($P < 0.05$). Compared with OPT, the pH in the three Mg fertilizer application treatments increased slightly, but the differences were not significant. There were no significant differences in the TN, TP, or TK contents among the five treatments.

3.4 Soil microbial community structure and function

3.4.1 Microbial community structure

With respect to bacteria, Acidobacteria, Proteobacteria, Actinobacteria, Firmicutes, and Gemmatimonadota were the dominant phyla across all the treatments, with the total relative abundance of these five bacterial phyla ranging from 85.9% to 87.1% (Fig. 2(a)). The application of Mg fertilizer significantly changed the relative abundance of the soil bacterial community structure. Compared with OPT, the relative abundance of Firmicutes decreased while that of Myxococcota increased in OPT+SiMg, and the relative abundances of Acidobacteriota and Firmicutes decreased while that of Actinobacteria increased in OPT+BMgZn ($P < 0.05$). At the genus level, the top five bacterial genera across all treatments were *Bryobacter*, *Candidatus_Solibacter*, *Acidothermus*, *Conexibacter*, and *Sphingomonas* (Fig. 2(b)). Compared with CK, the relative abundance of *Acidibacter* in OPT, OPT+SiMg, and OPT+BMgZn increased, whereas those of *Burkholderia_Caballeronia_Paraburkholderia* and *Pseudonocardia* decreased ($P < 0.05$). Compared with OPT, the relative abundance of

Table 2 Sugarcane nutrient uptake and fertilizer use efficiency under different fertilization treatments

Year	Treatment	Nutrient uptake (kg·ha^{-1})				Fertilizer use efficiency (%)			
		N	P	K	Mg	N	P	K	Mg
2022–2023	CK	84.4 (7.2) c	21.5 (1.8) d	207.9 (24.3) d	5.5 (0.7) d				
	OPT	175.1 (11.1) b	38.3 (2.0) c	285.9 (18.9) c	8.5 (0.2) c	38.9 (2.5) b	21.3 (1.1) c	99.3 (6.6) c	
	OPT+Mg	189.3 (8.2) b	45.2 (6.1) b	332.0 (9.6) b	14.5 (0.8) b	42.1 (1.8) b	25.1 (1.3) b	115.3 (3.3) b	24.2 (1.3) b
	OPT+SiMg	190.2 (11.8) b	49.4 (3.3) ab	316.7 (12.7) b	15.2 (1.6) b	42.3 (2.6) b	27.5 (1.4) ab	110.0 (4.4) b	25.3 (2.6) b
	OPT+BMgZn	212.8 (13.9) a	56.1 (4.2) a	389.4 (17.6) a	17.0 (1.2) a	47.3 (3.1) a	31.1 (1.3) a	135.2 (6.1) a	28.4 (3.3) a
2023–2024	CK	62.4 (2.0) b	14.2 (1.5) d	136.2 (9.5) d	4.4 (0.6) d				
	OPT	167.8 (9.8) a	36.9 (2.0) c	276.7 (18.3) c	8.9 (0.3) c	37.3 (4.4) a	20.5 (1.1) c	96.1 (6.3) c	
	OPT+Mg	176.7 (7.6) a	40.1 (0.6) bc	296.5 (8.8) b	13.7 (0.7) b	39.3 (1.7) a	22.3 (0.6) bc	103.1 (3.1) b	22.9 (1.1) b
	OPT+SiMg	181.9 (11.2) a	45.1 (1.2) ab	290.5 (11.6) c	14.7 (1.5) ab	40.4 (2.5) a	25.0 (0.7) ab	100.9 (4.0) c	24.5 (2.5) ab
	OPT+BMgZn	194.4 (12.6) a	48.8 (1.2) a	340.2 (15.0) a	15.9 (1.7) a	43.2 (2.8) a	27.1 (1.3) a	118.1 (5.2) a	26.5 (2.9) a

Note: Lowercase letters among treatments denote significant difference ($P < 0.05$). CK, no fertilizer; OPT, optimized fertilization treatment; OPT+Mg, OPT plus magnesium sulfate; OPT+SiMg, plus silicon-magnesium fertilizer; OPT+BMgZn, plus boron-magnesium-zinc fertilizer.

Table 3 Changes in soil properties under different fertilization treatments in 2023–2024

Item	CK	OPT	OPT+Mg	OPT+SiMg	OPT +BMgZn
pH (soil:water=1:2.5)	4.81 (0.03) a	4.71 (0.05) a	4.87 (0.05) a	4.77 (0.08) a	4.75 (0.02) a
SOM ($g \cdot kg^{-1}$)	45.97 (0.07) b	49.59 (0.98) a	46.41 (0.33) b	45.38 (0.52) b	45.25 (1.03) b
TN ($g \cdot kg^{-1}$)	1.88 (0.05) a	1.91 (0.07) a	1.87 (0.06) a	1.86 (0.03) a	1.85 (0.09) a
TP ($g \cdot kg^{-1}$)	1.77 (0.05) a	1.75 (0.14) a	1.64 (0.06) a	1.76 (0.05) a	1.65 (0.11) a
TK ($g \cdot kg^{-1}$)	6.49 (0.10) a	6.65 (0.08) a	6.35 (0.05) a	6.66 (0.10) a	6.66 (0.11) a
AN ($mg \cdot kg^{-1}$)	150.70 (3.67) a	143.42 (2.42) ab	140.82 (2.42) ab	141.05 (2.51) ab	136.13 (3.65) b
AP ($mg \cdot kg^{-1}$)	78.59 (2.35) d	207.99 (8.19) a	149.98 (5.58) c	183.71 (8.68) b	186.83 (7.30) b
AK ($mg \cdot kg^{-1}$)	115.57 (6.85) d	163.83 (5.26) c	244.12 (6.86) a	216.51 (4.60) b	220.80 (5.49) b
ASi ($mg \cdot kg^{-1}$)	59.54 (0.57) b	51.06 (0.38) c	50.74 (1.23) c	72.12 (1.11) a	49.33 (0.82) c
AB ($mg \cdot kg^{-1}$)	0.21 (0.01) b	0.19 (0.01) bc	0.18 (0.01) bc	0.17 (0.00) c	0.26 (0.02) a
AZn ($mg \cdot kg^{-1}$)	0.55 (0.03) b	0.46 (0.02) c	0.48 (0.01) c	0.47 (0.01) c	0.66 (0.03) a
Exchangeable Ca^{2+} ($mg \cdot kg^{-1}$)	136.99 (6.99) b	97.37 (1.77) d	119.40 (2.89) c	139.62 (2.93) b	157.20 (6.75) a
Exchangeable Mg^{2+} ($mg \cdot kg^{-1}$)	21.26 (0.89) c	20.28 (1.26) c	34.64 (2.17) b	42.42 (1.35) a	44.91 (1.37) a

Note: The value in parentheses is standard error (n=3). Lowercase letters among treatments denote significant difference ($P < 0.05$). CK, no fertilizer; OPT, optimized fertilization treatment; OPT+Mg, OPT plus magnesium sulfate; OPT+SiMg, plus silicon-magnesium fertilizer; OPT+BMgZn, plus boron-magnesium-zinc fertilizer. SOM, soil organic matter; TN, TP and TK denote total nitrogen, phosphorus and potassium, respectively; AN, AP, AK, ASi, AB and AZn denote available nitrogen, phosphorus, potassium, silicon, boron and zinc, respectively; Exchangeable Ca^{2+} and Exchangeable Mg^{2+} denote exchangeable calcium and exchangeable magnesium.

Bryobacter in OPT+Mg and OPT+SiMg increased, and the relative abundances of *Bradyrhizobium*, *Acidothermus,* and *Conexibacter* increased in OPT+BMgZn ($P < 0.05$).

The bacterial Chao1 index significantly increased, whereas the Shannon–Wiener index was not affected by the application of Mg fertilizer (Fig. 2(c)). Compared with OPT, the Chao1 index in OPT+Mg, OPT+SiMg and OPT+BMgZn increased by 4.8%, 3.3%, and 6.9%, respectively ($P < 0.05$). In addition, redundancy analysis (RDA) revealed that soil pH, SOM, AN, AP, AK, ASi, AB, AZn, exchangeable Ca^{2+}, and exchangeable Mg^{2+} together explained 82.4% of the variation in the bacterial community structure, with the first two axes accounting for 66.9% and 11.7% of the variation, respectively (Fig. 2(d)). The bacterial community structure was primarily influenced by AK, AZn, and pH, and its variation was positively correlated with AK ($P < 0.05$).

With respect to fungi, the dominant phyla across all the treatments were Ascomycota, Mortierellomycota, and Basidiomycota, with the total relative abundance of these three phyla ranging from 86.9% to 92.3% (Fig. 3(a)). There were no significant differences in the abundances of the top ten dominant fungal phyla between the three Mg fertilizer application treatments and OPT. At the genus level, the top five fungal genera across all treatments were *Mortierella*, *Fusarium*, *Arxotrichum*, *Gymnopilus*, and *Trichoderma* (Fig. 3(b)). Compared with OPT, the relative abundance of *Talaromyces* increased, while the relative abundances of *Fusarium* and *Vanrija* decreased in the three Mg fertilizer application treatments ($P < 0.05$).

There were no significant differences in the fungal Chao1 or Shannon–Wiener indices between the three Mg fertilizer application treatments and OPT (Fig. 3(c)). RDA revealed that key soil properties explained 84.5% of the variation in the fungal community structure, with the first two axes explaining 73.2% and 8.7% of the variation, respectively (Fig. 3(d)). The fungal community structure was primarily driven by ASi and AN, and its variation was positively correlated only with ASi ($P < 0.05$).

3.4.2 Microbial community function

According to the FAPROTAX results, bacterial functions were related mainly to C and N cycling in the soil (Fig. 4(a)). Chemoheterotrophy, aerobic_chemoheterotrophy, and cellulolysis functions were the most abundant functions in all

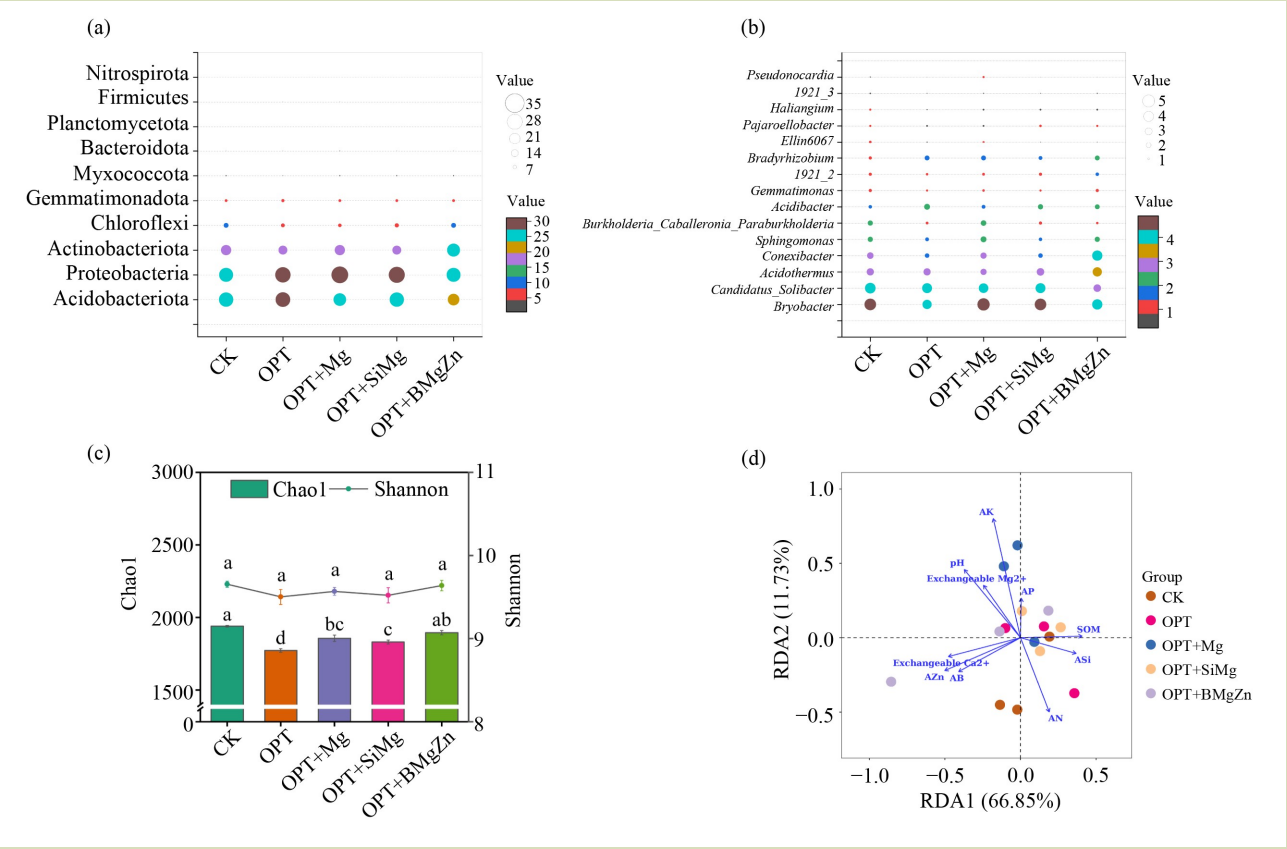


Fig. 2 Relative abundance of dominant bacterial taxa (phylum (a) and genus (b)), diversity indices (c), and redundancy analysis (RDA) of bacterial communities with different soil properties (d). CK, no fertilizer; OPT, optimized fertilization treatment; OPT+Mg, OPT plus magnesium sulfate; OPT+SiMg, plus silicon-magnesium fertilizer; OPT+BMgZn, plus boron-magnesium-zinc fertilizer. SOM, soil organic matter; AN, AP, AK, ASi, AB and AZn denote available nitrogen, phosphorus, potassium, silicon, boron and zinc, respectively; Exchangeable Ca^{2+} and Exchangeable Mg^{2+} denote exchangeable calcium and exchangeable magnesium.

five treatments, with relative abundances of up to 82.1%. Compared with CK, the four fertilization treatments increased the abundance of genes involved in nitrogen_fixation, ureolysis, and iron_respiration functions but decreased the abundance of genes involved in predatory or exoparasitic, phototrophy, photoautotrophy, and oxygenic_photoautotrophy functions ($P < 0.05$). Compared with OPT, the three Mg fertilizer application treatments increased the abundance of genes involved in predatory or exoparasitic functions ($P < 0.05$). According to the FUNGuild results, fungal functions were related mainly to saprotrophs, pathotrophs, and parasites at the guild level (Fig. 4(b)). Saprophytes were the dominant functional group in all the five treatments, with an abundance ranging from 58.2% to 73.6%. The relative abundance of pathotrophs ranged from 9.58% in OPT+BMgZn to 15.9% in CK. The relative abundance of parasites was relatively low in the five treatments, ranging from 4.22% to 16.7%. Compared with OPT, OPT+Mg and OPT+SiMg significantly increased the relative abundance of genes involved in saprotrophs but decreased that of pathotrophs. Compared with OPT, OPT+BMgZn increased the relative abundance of genes involved in parasites but decreased that of pathotrophs.

The correlations between key soil properties, dominant microbial genera, and functional gene abundance were further analysed. With respect to bacteria, the relative abundances of *Sphingomonas* and *Ellin6067* were positively correlated with pH but negatively correlated with AP, whereas *Acidibacter* abundance was the opposite ($P < 0.05$). *Pajaroellobacter*

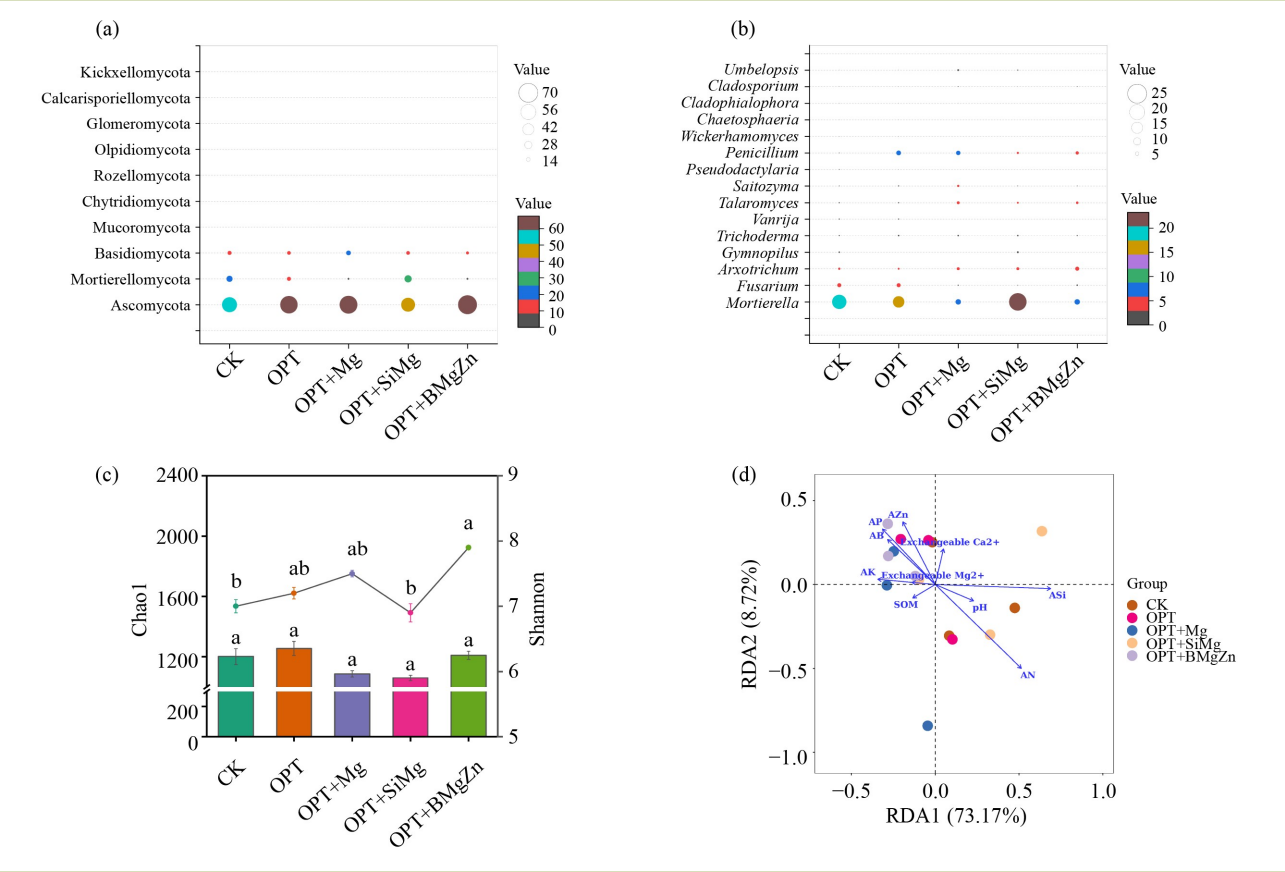


Fig. 3 Relative abundance of dominant fungal taxa (phylum (a) and genus (b)), diversity indices (c), and redundancy analysis (RDA) of fungal communities with soil properties (d). CK, no fertilizer; OPT, optimized fertilization treatment; OPT+Mg, OPT plus magnesium sulfate; OPT+SiMg, plus silicon-magnesium fertilizer; OPT+BMgZn, plus boron-magnesium-zinc fertilizer. SOM, soil organic matter; AN, AP, AK, ASi, AB and AZn denote available nitrogen, phosphorus, potassium, silicon, boron and zinc, respectively; Exchangeable Ca^{2+} and Exchangeable Mg^{2+} denote exchangeable calcium and exchangeable magnesium.

abundance was positively correlated with exchangeable Ca^{2+} but negatively correlated with SOM, and *Haliangium* abundance was negatively correlated with SOM and AP ($P < 0.05$) (Fig. 4(c)). The relative abundance of cellulolysis was positively correlated with AP but negatively correlated with pH, whereas that of predatory_or_exoparasitic was negatively correlated with AP and SOM, and that of hydrocarbon_degradation was negatively correlated with ASi ($P < 0.05$). With respect to fungi, the relative abundance of *Umbelopsis* was negatively correlated with AB and AZn, *Talaromyces* abundance was positively correlated with exchangeable Mg^{2+} and AK, and *Vanrija* abundance was positively correlated with SOM but negatively correlated with exchangeable Mg^{2+} and exchangeable Ca^{2+}; *Mortierella* abundance was positively correlated with AN and ASi but negatively correlated with AK ($P < 0.05$) (Fig. 4(d)). The relative abundance of litter saprotrophs was negatively correlated with pH, and the relative abundance of lichen parasites was negatively correlated with exchangeable Mg^{2+} ($P < 0.05$).

3.5 Correlations between soil properties, the microbial community, and sugarcane agronomic traits

The correlations among the key soil properties, dominant microbial genera, and sugarcane agronomic traits were analysed. Sugarcane yield, stalk height, and nutrient (P, K, and Mg) uptake were positively correlated with exchangeable Mg^{2+}

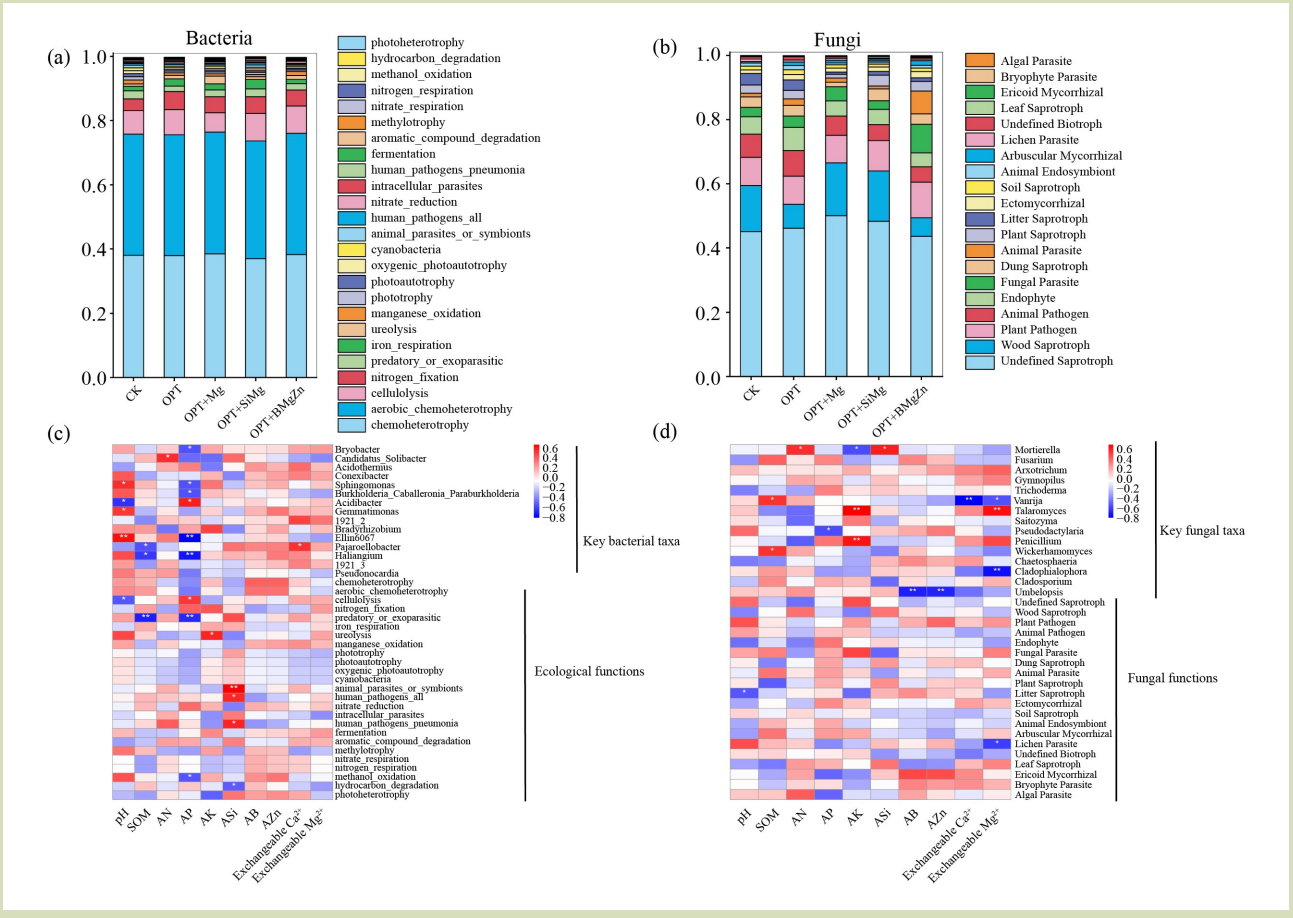


Fig. 4 Soil bacterial (a) and fungal (b) ecological functions and correlations between soil-dominant microbial genera and ecological functions (bacteria (c) and fungi (d)) and key soil properties. CK, no fertilizer; OPT, optimized fertilization treatment; OPT+Mg, OPT plus magnesium sulfate; OPT+SiMg, plus silicon-magnesium fertilizer; OPT+BMgZn, plus boron-magnesium-zinc fertilizer. SOM, soil organic matter; AN, AP, AK, ASi, AB and AZn denote available nitrogen, phosphorus, potassium, silicon, boron and zinc, respectively; Exchangeable Ca^{2+} and Exchangeable Mg^{2+} denote exchangeable calcium and exchangeable magnesium.

and AK ($P < 0.05$) (Fig. 5(a)). Millable stalks, P uptake, and Mg uptake were negatively correlated with AN. With respect to bacterial genera, sugarcane yield was positively correlated with the relative abundance of *Acidibacter* but negatively correlated with that of *Burkholderia_Caballeronia_Paraburkholderia* ($P < 0.05$) (Fig. 5(b)). Stalk diameter was significantly positively correlated with the relative abundance of *Acidibacter* and negatively correlated with that of *Ellin6067*. Stalk height was negatively correlated with the relative abundances of both *Pseudonocardia* and *Ellin6067* ($P < 0.05$). With respect to fungal genera, the sugarcane yield was positively correlated with the relative abundances of *Talaromyces* and *Penicillium* but negatively correlated with those of *Cladophialophora* and *Pseudodactylaria* ($P < 0.05$) (Fig. 5(c)). Stalk height was positively correlated with the relative abundances of *Talaromyces* and *Penicillium* but negatively correlated with those of *Cladophialophora*, *Pseudodactylaria*, and *Wickerhamomyces*.

4 Discussion

4.1 Effects of Mg application on sugarcane yield, agronomic traits, and fertilizer use efficiency

In this study, sugarcane yields and stalk height significantly

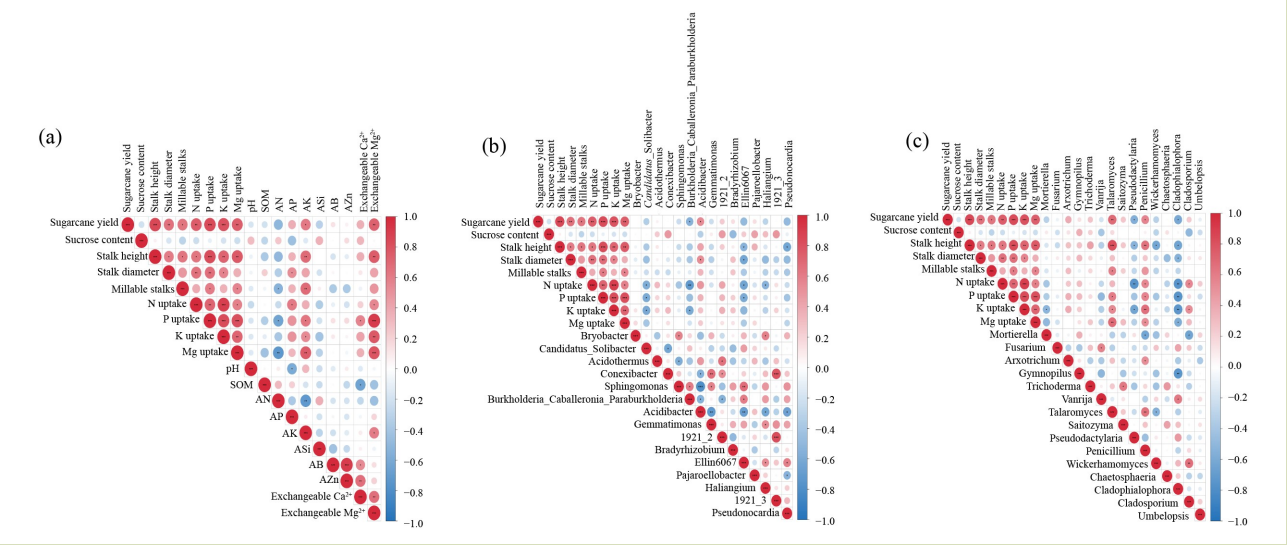


Fig. 5 Relationships between key soil properties (a), dominant bacterial (b), and fungal (c) genera and sugarcane agronomic traits. SOM, soil organic matter; AN, AP, AK, ASi, AB and AZn denote available nitrogen, phosphorus, potassium, silicon, boron and zinc, respectively; Exchangeable Ca^{2+} and Exchangeable Mg^{2+} denote exchangeable calcium and exchangeable magnesium.

increased, whereas the stalk diameter and number of millable stalks were not affected by the application of Mg fertilizer during the 2-year experimental period (Fig. 1). These results indicate that the yield increase induced by Mg fertilization may be primarily attributable to the increase in stalk height. Consistent with our findings, only Mg fertilization or the combined application of Mg and Zn can significantly increase the yields of many crops, such as fresh maize, rapeseed, and sugarcane[5,12,13]. In addition, among all three Mg fertilizer application treatment, the sugarcane yield was highest in OPT+BMgZn. The superior performance of the boron-magnesium-zinc compound fertilizer in improving crop yield may be attributed to the combination of these micronutrients promoting plant growth and enhancing stress tolerance[14].

Compared with OPT, OPT+Mg increased the KUE, OPT+SiMg increased the PUE, and OPT+BMgZn increased both the PUE and the KUE ($P < 0.05$). Similarly, the application of Mg fertilizer can increase the KUE in cabbage, which may be due to the activation of ATPase activity and the facilitation of photosynthate transport[15]. Synergistic application of Si and Mg can increase crop P uptake and the PUE by increasing soil P availability and promoting root development[16]. Previous studies have also shown that a significant yield increase in rice was obtained through the combined application of Si, Mg, Zn, and B, which was accompanied by increased uptake and utilization of macronutrients[17].

4.2 Effects of Mg application on soil properties and microbial community structure and function

The decreased SOM contents in the Mg fertilizer application treatment groups may be related to the alteration of microbial activity, which promoted the decomposition of organic matter. The increase in soil exchangeable Ca^{2+} and AK content after Mg application may be due to the displacement of Ca^{2+} and K^{+}, respectively, from soil colloids by Mg^{2+} via cation exchange[18].

With respect to bacteria, Mg fertilizer application significantly increased the Chao1 index, which may be associated with variations in soil properties. In the present study, the Chao1 index was correlated only with the soil AP content ($r = -0.81$, $P < 0.01$). Similarly, a significant correlation between the Chao1 index and AP content has been found in red soil[10]. At the phylum level, compared with that in the OPT treatment, the relative abundance of Myxococcota was greater in OPT+SiMg, and Actinobacteria was greater in OPT+BMgZn, whereas Firmicutes decreased in both the treatments ($P < 0.05$) (Fig. 2). These changes may be associated with the decrease in

SOM and increase in available nutrients after Mg fertilizer application. Actinobacteria and Myxococcota play important roles in the decomposition of organic matter, and alterations in the SOM content may affect the relative abundance of these bacterial phyla[19,20]. A decrease in Firmicutes abundance often reflects improvement in the soil environment[21]. At the genus level, the relative abundances of *Bradyrhizobium*, *Acidothermus*, and *Conexibacter* were significantly greater in OPT+BMgZn than in OPT. *Bradyrhizobium* enhances soil N fixation and promotes plant growth[22]. *Acidothermus* can decompose organic compounds and participate in the N cycle, thereby providing a favourable environment for plant roots[23]. *Conexibacter* can decompose organic carbon and establish symbiotic relationships with plants[24,25].

With respect to fungi, Mg fertilizer application had no significant effect on the Chao1 index or Shannon index, which may be related to the relatively stable physiological structure and diverse survival strategies of fungi[26]. At the genus level, compared with OPT, the relative abundance of *Talaromyces* increased, whereas the relative abundances of *Fusarium* and *Vanrija* decreased in OPT+BMgZn ($P < 0.05$, Fig. 3). Similarly, the relative abundance of *Fusarium* significantly decreased after the application of Mg fertilizer in ginseng[27]. *Talaromyces* primarily exhibits efficient phosphate-solubilizing activity and promotes plant growth[28]. *Fusarium* is among the most important soilborne plant pathogenic fungi, causing wilt diseases and root rot[29]. *Vanrija* may exhibit strong heavy metal tolerance[30].

With respect to microbial ecological functions, the relative abundances of genes involved in predatory or exoparasitic, saprotrophs or parasites increased, whereas that of genes involved in pathotrophs decreased after Mg fertilizer application. Saprotrophs primarily decompose complex organic matter and thereby promote mineral nutrient cycling[31]. Parasites contribute to nutrient cycling, plant growth promotion and pathogen inhibition[32]. Pathotrophs are detrimental organisms that induce plant wilting, chlorosis, and even mortality[33]. An increase in the relative abundance of saprotrophs or parasites indicates soil health, as it drives nutrient cycling and strengthens plant defence[34].

4.3 Relationships between sugarcane yield, microbial communities, and soil properties

In this study, as the soil was magnesium-deficient for sugarcane, the application of magnesium fertilizer resulted in a marked improvement in sugarcane yield. Sugarcane yield and stalk height were significantly positively correlated with the relative abundances of *Acidibacter*, *Talaromyces* and *Penicillium* but negatively correlated with those of *Cladophialophora* and *Pseudodactylaria*. *Acidibacter* is involved in soil carbon and N cycling and inhibits pathogens, thereby creating a favourable environment for plant growth[35]. *Talaromyces* and *Penicillium* are important plant growth-promoting fungi that can inhibit pathogens and promote plant growth and nutrient uptake[36]. Members of *Cladophialophora* exhibit high lifestyle diversity, and some may act as phytopathogens[37].

Changes in soil physicochemical properties significantly influence microbial community structure and function. In this study, variations in bacterial and fungal community structures were significantly correlated with soil AK and ASi, respectively. The AK contents significantly increased after Mg fertilizer application, which likely drove the observed shifts in the soil bacterial community structure. The available Si content is significantly positively correlated with shifts in fungal community structure in rice[38]. Furthermore, correlation analysis revealed that the composition and functions of many bacteria were influenced primarily by AP, pH, and SOM; several fungal genera and functions were influenced by SOM, exchangeable Mg^{2+}, and AK. Consistently, significant correlations between soil pH, exchangeable Mg^{2+}, AK, and fungal taxa have been reported in tea plantation soils[7]. Furthermore, a review revealed that the primary soil properties that shape soil microbial structure include pH, organic carbon, and nutrient availability[39].

5 Conclusions

In this study, the 2-year average sugarcane yield increased in response to the application of all three types of magnesium fertilizer, which was primarily attributed to the increase in stalk height. The phosphorus use efficiency and potassium use efficiency in OPT+BMgZn were significantly greater than those in OPT. The bacterial Chao1 index was increased, while the fungal Chao1 and Shannon indices were not influenced by the three magnesium fertilizer application treatments compared to the OPT. Moreover, compared with OPT, the relative abundances of *Bradyrhizobium*, *Acidothermus*, and *Conexibacter* increased in OPT+BMgZn, and the relative abundance of *Talaromyces* increased in three magnesium

fertilizer application treatments, most of which can improve nutrient cycling and promote plant growth. In addition, compared with OPT, magnesium fertilizer application treatments increased the relative abundance of genes associated with predatory or exoparasitic functions and decreased those of genes involved in pathotroph, which may have inhibited pathogens and promote the sugarcane development. Overall, our results prove that for magnesium-deficient sugarcane soils, all three magnesium fertilizer application treatments increased sugarcane yield, sugar yield, and nutrient uptake and improved soil microbial community structure and function. The OPT+BMgZn treatment resulted in the best performance and can be recommended as the preferred magnesium supplementation practice for this region.

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Compliance with ethics guidelines

Qihua Wu, Wenling Zhou, Benjie Li, Churong Liu, and Junhua Ao declare that they have no conflicts of interest or financial conflicts to disclose. This article does not contain any studies with human or animal subjects performed by any of the authors.

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