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EDITED BY
Rameshwar Kanwar,
Iowa State University, United States

REVIEWED BY
Uday Bhanu Prakash Vaddevolu,
Texas A&M University, United States
Xing Wang,
Northwest A&F University, China

*CORRESPONDENCE
Mingzhi Zhang
✉ mingzhiz@hhstu.edu.cn

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Irrigation frequency and irrigation amount of micro-sprinkler irrigation mulched regulate N_2O emission of tomato (*Solanum lycopersicum*) soil

Haijian Yang[1], Mingzhi Zhang[1]*, Wenqian Wu[1], Na Xiao[1], Mengmeng Sun[1] and Yuan Li[2]

[1]Faculty of Engineering, Huanghe Science and Technology University, Zhengzhou, China, [2]School of Geography and Tourism, Shaanxi Normal University, Xian, China

Introduction: There is a limited amount of research available on how changes in soil hydrothermal cycles impact soil N_2O emissions in greenhouses that use a tomato irrigation system with micro-sprinkler irrigation mulched (MSM).

Methods: This study examined the effects of different irrigation frequency (F, F1 which is every 3 days, F2 which is every 5 days, F3 which is every 7 days) and irrigation amount (I, I1 which is 0.7 Epan, I2 which is 1.0 Epan, I3 which is 1.2 Epan) on soil N_2O emissions in tomato cultivation. The research was carried out using a randomized experimental design over two consecutive growing seasons for greenhouse tomatoes in Northwest China.

Results: The findings revealed that F1 and F3 did not support the accumulation of microbial biomass carbon and nitrogen in the tomato soil under MSM. This limitation hindered the enhancement of soil extracellular enzymes BG and LAP, and decreased the diversity of the bacterial community structure. The functional genes related to bacterial nitrogen metabolism were abundant. The application of I2 treatment can result in a high accumulation of microbial biomass carbon and nitrogen in tomato soil, leading to enhanced soil BG and LAP activities and contributing to the stability of the soil bacterial community structure. As the F decreased, the cumulative emission flux of N_2O in tomato soil initially decreased, then increased. Increasing the I showed a rising trend in the cumulative emission flux of N_2O in tomato soil. The yield of spring and autumn tomatoes in F2 was higher compared to F1 and F3 at approximately 5.27 and 3.24%, and 19.31 and 11.30%, respectively. The yield of spring and autumn tomatoes in I2 was around 24.44 and 26.15% higher than in I1 and 1.64 and 3.06% higher than in I3. The regulation of the irrigation system in MSM resulted in a favorable interaction among tomato soil, microbial biomass carbon and nitrogen, soil extracellular enzymes, and soil bacterial community. When the I increased by 1.00%, the cumulative N_2O emission flux and yield of tomato soil increased by at least 30.68 and 39.24%, respectively. For every 1.00% increase in F, the cumulative N_2O emission flux and yield of tomato soil decreased by at least 7.41% and 11.23%, respectively. A quadratic relationship was observed between soil N_2O emission flux and the abundance and yield of soil bacterial nitrogen metabolism functional genes. The assessment of tomato yield potential in the area could be indirectly done by examining the abundance of soil bacterial nitrogen metabolism functional genes. The study demonstrates the feasibility of regulating soil N_2O emissions under the MSM irrigation system. Moreover, the findings indicate that F2I2 can significantly improve tomato yield without causing a considerable rise in soil N_2O emission flux.

Discussion: This conclusion can provide a scientific basis for the optimization of irrigation system in facility agriculture, so as to ensure the high yield of crops and reduce the negative impact on the environment. It is also of great significance for the green development of agriculture under the background of global climate change.

KEYWORDS

microbial biomass carbon and nitrogen, extracellular enzyme, bacterial community, N_2O emission flux, yield

1 Introduction

Currently, CO_2, CH_4 and N_2O are widely acknowledged as the primary greenhouse gases (Li et al., 2022). N_2O, a significant greenhouse gas in the atmosphere, has a warming potential 298 times greater than that of CO_2 and can engage in various photochemical reactions (Li et al., 2025; Chen et al., 2018). Temperature, moisture, oxygen content and many other factors restrict the emission of N_2O. Agricultural activities contribute around 13.80% to global greenhouse gas emissions, with 66% of N_2O emissions stemming from crop production. It is projected that N_2O emissions will double by 2050 (Bracken et al., 2021; Gu et al., 2023). Irrigation plays a crucial role in maintaining stable farmland yields. However, it impacts soil enzyme activity, respiration, nitrification, denitrification and mineralization, thereby affecting N_2O emissions in farmlands (Fernández-Ortega et al., 2023; Kong et al., 2024; Ortega-Farias et al., 2022). Hence, determining the optimal balance between irrigation and N_2O emissions is vital for the sustainable development of agriculture and the environment.

Facility agriculture is characterized by rapid crop growth and a high demand for soil water and fertilizer. Currently, there is a significant focus on research related to measuring soil water and fertilizer levels. The nutrients crucial for plant development primarily originate from the soil, where soil microorganisms and soil enzyme activities play a crucial role in the breakdown of soil nutrients and their absorption by plant roots (Jafari et al., 2018; Morio et al., 2022). This process results in the greenhouse gas N_2O being produced under both aerobic and anaerobic conditions. Studies have indicated that soil nitrogen-fixing bacteria can transform atmospheric nitrogen into usable sources, enhance plant root growth to meet plant requirements, and minimize plant nutritional stress (Gandhamanagenahalli et al., 2024; Wang J. et al., 2022). The feedback loop between plants and soil can be positive when plant roots respond to soil dryness by developing fine roots that create conducive micro-environments for microbial activity and nutrient release (Veresoglou et al., 2022; Xiao et al., 2023). Furthermore, the substances released by root growth provide energy for soil microorganisms, influencing the soil nitrogen cycle and subsequently impacting N_2O emissions (Helfrich et al., 2024; Zhang et al., 2025). Thus, investigating the interplay among soil bacterial communities, soil microbial biomass, soil extracellular enzyme activity and N_2O emissions in facility agriculture is crucial for controlling greenhouse gas emissions in this type of agricultural system.

The redistribution of water and heat in soil is closely related to field irrigation management measures. These practices directly or indirectly alter soil enzyme activity, soil respiration, nitrification, denitrification, and mineralization. Consequently, they influence the development of soil microbial communities and plant root morphology, which in turn affects the emission of the greenhouse gas N_2O (Feng et al., 2023; Lou et al., 2024; Vera et al., 2023). Irrigation frequency and irrigation amount not only affect the nitrogen cycle in soil, but also play a key role in the production and emission of N_2O. Frequent irrigation may lead to reduced soil aeration, thereby increasing N_2O emissions from denitrification; the unreasonable irrigation amount may affect the soil moisture content, change the living environment of soil microorganisms, and further affect the emission of N_2O. In order to ensure the increase of plant yield and limit the emission of greenhouse gas N_2O, researchers have proposed methods such as microbial inoculation and growth regulator addition. However, the implementation of the above methods has many problems such as high investment cost and environmental pollution (Boddington and Dodd, 1999; Zhao et al., 2017). At the same time, some researchers have found that yield increase and emission limitation can be achieved by adjusting crop irrigation management methods. For example, in the high-temperature forage planting system, water management synergistically increases or decreases forage yield and soil N_2O emissions (Andrews et al., 2022). High and low frequency irrigation helps to increase soil N_2O emissions (Mumford et al., 2019). Insufficient irrigation helps to reduce N_2O emissions from winter wheat soil (Zhong et al., 2021). Therefore, exploring the changing patterns and correlation between soil greenhouse gas N_2O emission and crop yield under changes in irrigation management is of significant guidance for reducing agricultural crop emissions and increasing yield.

Micro-sprinkler mulched (MSM) system, as a new type of water-saving irrigation technology, has been widely used in facility agricultural production in recent years. A large number of studies have shown that the MSM system has significant water-saving and yield-increasing effects. For example, in the greenhouse crop planting in the northwest region, the MSM system evenly penetrates the water droplets into the soil through its fine atomization nozzle, which effectively avoids the problems of soil compaction and water waste caused by traditional irrigation methods. At the same time, combined with plastic film mulching technology, the soil moisture retention ability and fertilizer retention level are further improved, creating a good soil environment for crop growth. At present, the MSM system has achieved good application results in the cultivation of cucumber, celery, watermelon and other greenhouse crops. Previous studies have found that different micro-sprinkler irrigation frequencies have significant effects on the growth characteristics and quality of greenhouse mini-watermelon. The growth and yield of celery under MSM system showed that the irrigation technology could significantly improve the yield and quality of celery (Zeng et al., 2021; Xie, 2019; Yin et al., 2021). However, although there are many studies on the MSM system in terms of water saving and yield increase, there are relatively few studies on how it regulates N_2O emissions from greenhouse tomato soil. Previous studies have focused on the effects of traditional irrigation methods on soil N_2O emissions. For example, some studies have shown that irrigation methods such as drip irrigation can affect soil microbial

activity by changing soil moisture and ventilation conditions, thereby affecting soil N_2O production and emissions. However, these studies are different from the unique mechanisms of MSM systems in soil improvement, water and nutrient cycling, and greenhouse gas emission reduction. In addition, the combined effects of different irrigation frequency and irrigation amount on soil microbial community, soil microbial biomass carbon and nitrogen, soil exoenzyme activity and soil bacterial community structure in MSM system, and the quantitative relationship between these factors and soil N_2O emission and tomato yield are still unclear. Therefore, under the background of MSM system, this study systematically explored the effects of different irrigation frequency and irrigation amount on greenhouse tomato soil N_2O emission and tomato yield, and deeply analyzed its relationship with soil microbial related factors.

The purpose of this study was to comprehensively and systematically study the comprehensive effects of different irrigation frequency and irrigation amount on greenhouse tomato soil N_2O emission, soil microbial biomass carbon and nitrogen, soil exonuclease activity, soil bacterial community structure and tomato yield, and to construct a multi-factor MSM combination. The comprehensive analysis system of these factors provides a more comprehensive perspective for understanding the role of irrigation system in the soil ecosystem of facility agriculture. Advanced experimental techniques and analytical methods were used, such as chloroform fumigation-K_2SO_2 extraction method for the determination of soil microbial biomass carbon and nitrogen content, and Illumina MiSeq sequencing technology for the analysis of soil bacterial community structure. At the same time, combined with a variety of models and analytical methods, such as Cobb–Douglas model, Pearson correlation and regression analysis, the experimental data were deeply excavated and comprehensively analyzed, and the complex relationship between irrigation frequency and irrigation amount and soil N_2O emission and tomato yield was quantitatively described (Zhang et al., 2022). The influence mechanism of MSM irrigation system on soil N_2O emission and tomato yield was discussed, which provided a new perspective for understanding the relationship between soil ecological process and greenhouse gas emission in facility agriculture, and also provided a scientific basis for realizing the green and sustainable development of facility agriculture.

2 Materials and methods

2.1 Experimental site and management

A controlled cultivation experiment was conducted from March 27, 2019, to January 30, 2020, at the Xi'an Modern Agricultural Science and Technology Extension Center (34.03°N, 108.52°E) in Shaanxi Province, China. The experimental setup utilized greenhouse facilities with detailed soil characteristics and irrigation water quality parameters documented in Table 1. The 'Jingfan 401' tomato cultivar was systematically planted using a spatial arrangement of 50 cm row spacing and 40 cm plant spacing within rows, with experimental plots measuring 3.4 m in length. Figure 1 illustrates the phenological development stages of the tomato plants. Throughout the growth cycle, all plots received standardized management practices including scheduled fertilization, regulated irrigation, and coordinated pest control measures to maintain experimental consistency.

TABLE 1 Soil and water quality related parameters.

Soil parameters		Water quality parameters	
Index		Index	
Bulk density	1.48 g/cm^3	pH	6.8
Water holding capacity of field weight	27.40%	Chemical oxygen demand	53.2 mg/L
Organic matter	15.53 g/kg	Anionic surfactant	3.2 mg/L
Total phosphorus	10.12 g/kg	Chloride	0.48 mg/L
Total potassium	2.01 g/kg		
Total nitrogen	1.36 g/kg		
Available nitrogen	70.45 mg/kg		
Available phosphorus	112 mg/kg		
Available potassium	85.23 mg/kg		

2.2 Experimental design

In this study, two factors were identified as irrigation frequency (F) and irrigation amount (I) as depicted in Table 2. Irrigation frequency and irrigation amount are set at 3 levels, in which the interval of irrigation frequency was 3 days, 5 days and 7 days respectively; the irrigation amount was controlled by the basis of the cumulative evaporation (Epan, a 20-cm diameter standard pan), which was realised by a control coefficient (kcp), The kcp (the crop pan coefficient) was 0.7, 1.0, and 1.2. A completely randomized trial design was used, the treatments are shown in Table 3. Each of treatments were repeated 3 times, a total of 27 experimental plots.

Pan evaporation amount was monitored at 8.00 am on the same day of each irrigation frequency. Equation 1 is used to calculate irrigation amount (Table 2) (Zhang et al., 2021).

$$W = A \times E_{pan} \times k_{cp} \tag{1}$$

In the formula, E_{pan} represents the evaporation within the interval of two irrigation, based on the cumulative evaporation from a 20 cm diameter pan (mm); A represents the capillary control area (mm) and k_{cp} represents the crop-pan coefficient.

2.3 Measurements and computational methods

2.3.1 Soil greenhouse gas N_2O emission flux

Samples of N_2O gas in the soil were obtained using the static dark box method, with the sampling device consisting of a box and a base. The box, measuring 25 cm in length, width, and height, was constructed from 6 mm thick polyvinyl chloride (PVC) material. To ensure accuracy in sampling, the outer surface of the box was covered with sponge and tin foil paper, and a small fan was installed at the top for proper air circulation. The base of the static box (25 × 25 cm^2) was

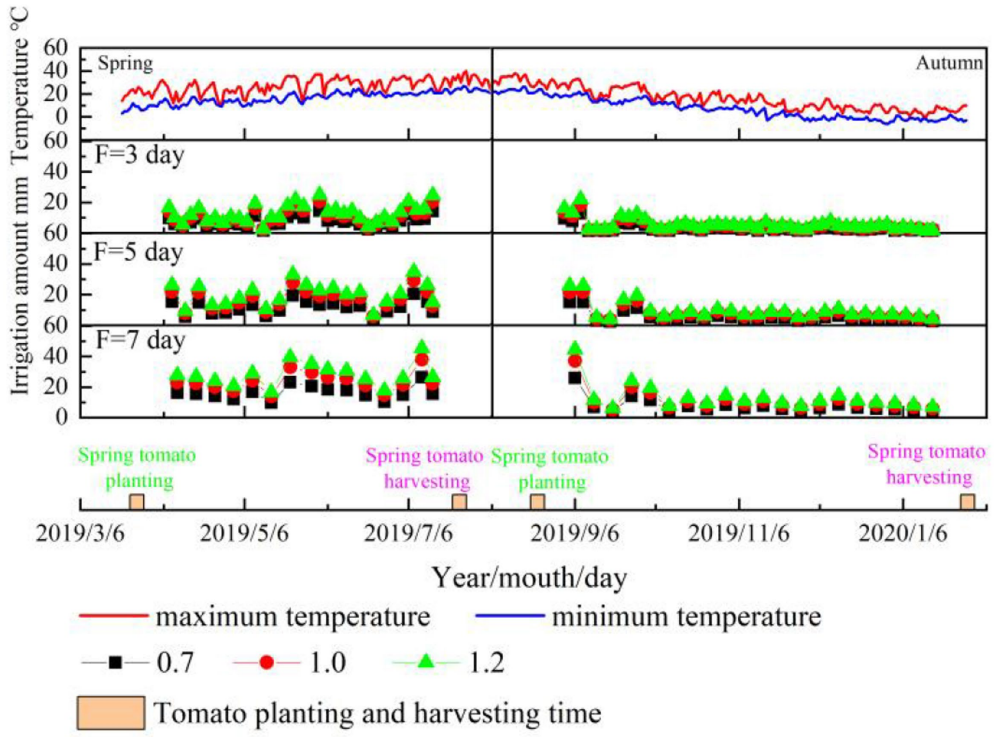

FIGURE 1
Greenhouse tomato growth period temperature, spring and autumn tomato growth period and irrigation amount under different treatments. Spring represents the spring tomato; Autumn represents the autumn tomato.

TABLE 2 Experimental factor and design.

Treatment	K_{cp}	Irrigation amount (I)				Irrigation frequency (F) days
		Spring of tomato (1 year)		Autumn of tomato (1 year)		
		I mm	Irrigation times	I mm	Irrigation times	
F1I1	0.7	247.12	33	152.73	47	3
F1I2	1.0	353.03	33	218.19	47	3
F1I3	1.2	423.64	33	261.83	47	3
F2I1	0.7	247.12	21	152.73	28	5
F2I2	1.0	353.03	21	218.19	28	5
F2I3	1.2	423.64	21	261.83	28	5
F3I1	0.7	247.12	15	152.73	20	7
F3I2	1.0	353.03	15	218.19	20	7
F3I3	1.2	423.64	15	261.83	20	7

Spring represents the spring tomato; Autumn represents the autumn tomato. F represents the irrigation frequency, I represents the irrigation amount.

buried between two tomato seedlings in the center of each ridge on the day of transplanting. It was inserted 5 cm deep into the soil as a sampling point until the tomatoes were harvested. Regular weeding was conducted during the tomato growth phase. A shallow groove at the top of the base was used to hold the static box securely, and a water injection seal was applied to isolate the box from the external environment during sampling. Gas samples were collected at 18, 36, 51, 72, 91, and 110 days after planting the tomatoes. Four gas sampling sessions took place at 10:00, 10:20, 10:40, and 10:60 using a 50 mL syringe with a three-way valve, drawing 30 mL of gas each time for concentration analysis on the same day. Outliers were eliminated to obtain a linear regression coefficient of $R^2 \geq 0.90$ for the concentration measurements of the four samples over time (Table 4).

The concentration of N_2O in the soil was determined using an Agilent Technologies 7890 A GC System (USA), and the flux of N_2O emission from the soil was calculated as described in Li et al. (2022). While collecting gas samples, the temperature inside the container was monitored using a mercury thermometer placed at the top. The air temperature during sampling was recorded with a mercury thermometer located about 1.5 m above the ground. Furthermore, the

TABLE 3 Abbreviations.

No	Abbreviations	Full name
1	Spring	spring tomato
2	Autumn	autumn tomato
3	F	irrigation frequency
4	I	irrigation amount
5	BG	soil β-Glucosidase active enzyme
6	LAP	soil Leucine aminopeptidase activity
7	ACE	ACE index of soil bacterial
8	SHN	SHN index of soil bacterial
9	ANFG	abundance of soil bacterial nitrogen-fixing functional genes
10	ANIG	abundance of soil bacterial nitrification functional genes
11	ANDG	abundance of soil bacterial denitrification functional genes
12	ANG	abundance of soil bacterial nitrogen metabolism functional genes
13	NCE	soil N_2O emission flux
14	MBC	soil microbial biomass carbon
15	MBN	soil microbial biomass nitrogen
16	X1	soil microbial biomass carbon
17	Y1	soil microbial biomass nitrogen
18	X2	soil β-Glucosidase active enzyme
19	Y2	soil Leucine aminopeptidase activity
20	X3	abundance of soil bacterial nitrogen metabolism functional genes
21	Y3	ACE index of soil bacterial
22	Y	yield
23	NCL	N_2O cumulative emissions

soil temperature of the soil layer that was 5 cm deep was measured using a soil thermometer.

2.3.2 Soil microbial biomass, soil extracellular enzyme activity, soil bacterial community

(1) Seventy-two days after planting in both spring and autumn, soil samples were taken from the rhizosphere of tomato plants. The soil was collected using the shaking soil method, which involved excavating a 5–25 cm portion of the tomato root system and shaking off loose soil. The soil adhering closely to the greenhouse tomato root system was gently brushed off with a soft brush to obtain the greenhouse tomato rhizosphere soil. Three random soil samples were selected, brought to the laboratory and plant residues were removed. According to the specific requirements of different analysis, the soil samples were divided into two parts. One part was used for the timely determination of soil microbial biomass carbon and nitrogen and soil extracellular enzyme activity, and the other part was stored in a refrigerator at −20°C and immediately contacted Shanghai Meiji Biomedical Technology Co., Ltd. (China) for the determination of soil bacterial community. Analysis of soil-related indicators was completed within 10 days.

(2) The microbial biomass carbon and nitrogen content in the tomato rhizosphere soil were determined using the chloroform fumigation-K_2SO_4 extraction method. The levels of microbial biomass carbon and nitrogen in the extracted filtrate were measured utilizing a Multi N/C 3100 total organic carbon/nitrogen analyzer.

(3) The activity of soil extracellular enzymes β-glucosidase (BG) and leucine aminopeptidase (LAP), was determined by extracting them using an enzyme-linked immunosorbent assay and analyzing them with a microplate reader (RT-6100, Shanghai Precision Instrument Co., Ltd., China) (Puissant et al., 2019).

(4) The analysis of the soil bacterial community involved three key steps: DNA extraction and PCR amplification, Illumina MiSeq sequencing and processing of sequencing data. Specific analyses were conducted using the Shanghai Meiji Biological Cloud Platform (Shanghai Meiji Biomedical Technology Co., Ltd., China), with references to the Kyoto Encyclopedia of Genes and Genomes and relevant literature (Wang et al., 2020). Functional genes related to nitrogen fixation, nitrification, denitrification, and phosphorus metabolism were identified in the soil bacteria. The nitrogen metabolism of soil bacteria was evaluated based on the collective abundance of functional genes associated with nitrogen fixation, nitrification, and denitrification.

2.3.3 Yield

Yield quantification was conducted through random sampling of four representative tomato plants at harvest maturity. For each sampled plant, four fruits reaching commercial ripeness were selected, and their fresh mass was determined using an analytical balance (±0.01 g). Measurements were standardized to per-hectare productivity using established agricultural conversion metrics, accounting for planting density (row spacing: 50 cm; plant spacing: 40 cm) and plot dimensions (3.4 m length). Total yield was extrapolated to estimate metric tons per hectare (kg/ha) based on the sampled fresh weight data and spatial planting parameters.

2.4 Data analysis

The Cobb-Douglas model was utilized to both qualitatively and quantitatively depict the impact of F and I on tomato ANG, NCL, and

TABLE 4 Effects of different treatments on soil extracellular enzyme activities of greenhouse tomato.

Tomato planting period	Treatment	BG			LAP		
		36	72	110	36	72	110
Spring	F1I1	2.73 ± 0.32c	3.31 ± 0.27c	3.28 ± 0.15c	13.53 ± 1.07e	15.27 ± 1.82c	13.46 ± 1.41c
	F1I2	3 ± 0.13bc	3.96 ± 0.5b	3.94 ± 0.25b	16.09 ± 1.78b	18.55 ± 1.57b	17.05 ± 0.94b
	F1I3	3.03 ± 0.23b	3.9 ± 0.36b	3.86 ± 0.38b	16.9 ± 1.61bc	18.94 ± 0.83b	16.99 ± 1.28b
	F2I1	2.94 ± 0.5bc	3.94 ± 0.35b	3.82 ± 0.24b	15.04 ± 1.15 cd	19.08 ± 1.52b	17.69 ± 0.8b
	F2I2	3.3 ± 0.17a	4.42 ± 0.24a	4.24 ± 0.18a	18.85 ± 1.02a	21.94 ± 1.28a	20.63 ± 0.82a
	F2I3	3.38 ± 0.23a	4.34 ± 0.27a	4.26 ± 0.26a	19.23 ± 1.06a	22.6 ± 1.34a	21.14 ± 1.45a
	F3I1	2.37 ± 0.25d	3.02 ± 0.52c	2.97 ± 0.27d	10.33 ± 1.71f	13.79 ± 1.03c	12.21 ± 1.09d
	F3I2	2.75 ± 0.25bc	3.31 ± 0.49c	3.16 ± 0.27 cd	13.75 ± 1.52de	15.33 ± 1.9c	13.62 ± 1.64c
	F3I3	2.77 ± 0.19bc	3.31 ± 0.44c	3.35 ± 0.36c	13.46 ± 1.18e	15.42 ± 2.63c	13.2 ± 1.16 cd
	F-value						
	F	30.860**	44.928**	82.992**	97.074**	103.767**	216.881**
	I	15.817**	12.038**	23.923**	55.810**	26.091**	43.404**
	F*I	0.209 ns	0.563 ns	1.695 ns	0.823 ns	1.245 ns	3.663*
Autumn	F1I1	2.45 ± 0.2bc	3.23 ± 0.29c	2.98 ± 0.51b	14.42 ± 0.43c	16.79 ± 1.7c	14.05 ± 1.35d
	F1I2	2.75 ± 0.42ab	3.68 ± 0.36b	3.32 ± 0.56ab	17.78 ± 2.03b	18.83 ± 2.27b	16.25 ± 1.39bc
	F1I3	2.72 ± 0.34ab	3.67 ± 0.34b	3.31 ± 0.52ab	17.68 ± 1.15b	18.77 ± 1.63b	16.19 ± 1.19bc
	F2I1	2.53 ± 0.41bc	3.66 ± 0.37b	3.03 ± 0.39b	17.48 ± 1.32b	19.16 ± 1.23b	15.09 ± 0.63 cd
	F2I2	2.99 ± 0.21a	4.16 ± 0.27a	3.54 ± 0.36a	20.83 ± 1.32a	21.77 ± 1.65a	17.71 ± 1a
	F2I3	2.95 ± 0.36a	4.01 ± 0.36a	3.42 ± 0.53a	20.47 ± 2.05a	21.66 ± 1.69a	17.02 ± 1.66ab
	F3I1	2.1 ± 0.34d	2.81 ± 0.21d	2.41 ± 0.26c	12.59 ± 0.97d	14.54 ± 1.07d	11.47 ± 0.89e
	F3I2	2.33 ± 0.22 cd	3.25 ± 0.4c	3.04 ± 0.33b	14.18 ± 0.49c	16.66 ± 2.33c	14.1 ± 1.11d
	F3I3	2.37 ± 0.39 cd	3.27 ± 0.4c	3.01 ± 0.41b	14.38 ± 2.11c	16.99 ± 2.1c	14.01 ± 1.37d
	F-value						
	F	19.508**	40.679**	9.858**	110.726**	48.937**	55.837**
	I	8.802**	15.056**	10.332**	31.761**	14.658**	34.155**
	F*I	0.326 ns	0.157 ns	0.349 ns	1.237 ns	0.111 ns	0.295 ns

Spring represents the spring tomato; Autumn represents the autumn tomato. F represents irrigation frequency; I represents irrigation amount; BG represents β-Glucosidase active enzyme; LAP represents Leucine aminopeptidase activity. The data are shown as the average ± standard deviation in the table. Different lowercase letters indicate that there are significant differences between different treatments at the 0.05 level. * represents the $p \leq 0.05$, ** represents the $p \leq 0.01$, ns represents the $p > 0.05$, the same below.

yield. The relationship between soil bacterial community, soil microbial biomass, soil extracellular enzyme activity, N_2O emission flux and yield was quantitatively explained through Pearson correlation and regression analyses. Significance testing was conducted using the F test in SPSS 22.0 (IBM Crop., Armonk, New York, NY, USA) with a significance level set at $p < 0.05$. Pearson's two-tailed test was performed using SPSS 22.0 (IBM Crop., Armonk, New York, NY, USA). Graphs were generated using OriginPro 2019 (Origin Lab Corporation, Northampton, MA, USA), while Excel 2016 (Microsoft Excel, Microsoft, Washington, USA) was employed for regression analysis.

2.5 Abbreviations

The abbreviations of this article are explained in Table 3.

3 Results

3.1 Effects of different treatments on soil microbial biomass carbon and nitrogen in greenhouse tomato

From Figure 2, it is evident that as the tomato growth period progresses, the soil MBC and MBN of both spring and autumn tomatoes treated with MSM show an upward trend. F and I significantly affect the soil MBC and MBN of spring and autumn tomatoes. As F decreases, soil MBC and MBN first increase and then decrease. Specifically, under F2 treatment, the soil MBC of spring and autumn tomatoes is approximately 7.40 and 8.94% higher than under F1 treatment, and about 8.96 and 8.78% higher than under F3 treatment. The soil MBN under F2 treatment is around 5.51 and 6.93% higher than under F1 treatment, and approximately 14.32 and 11.29% higher than under F3 treatment. Similarly, as I increases, soil MBC and MBN first rise and

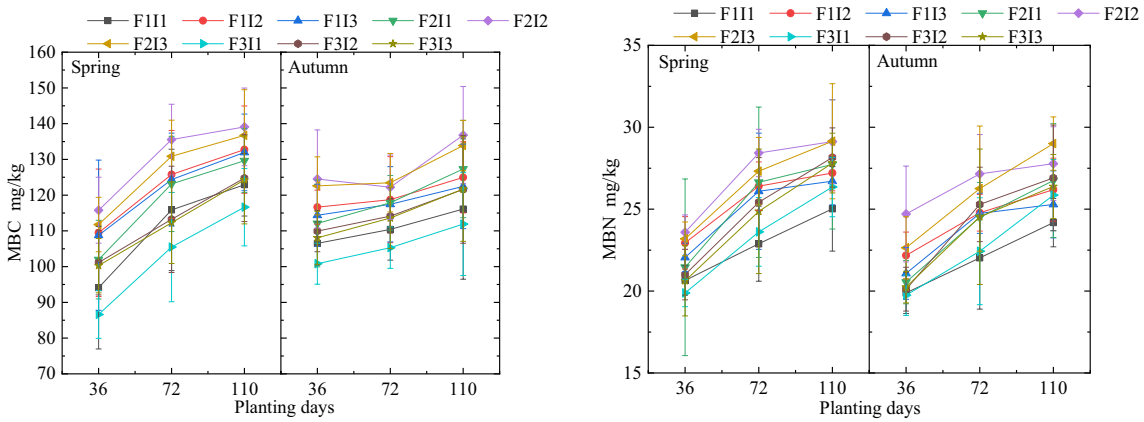

FIGURE 2
Effect of irrigation scheme regulation on soil microbial biomass carbon and nitrogen content. Spring represents the spring tomato; Autumn represents the autumn tomato. F represents irrigation frequency; I represents irrigation amount. The MBC represents the soil microbial biomass carbon, the MBN represents the soil microbial biomass nitrogen. The data are shown as the average ± standard deviation in the figure.

then fall. Under I2 treatment, the soil MBC of spring and autumn tomatoes is 9.34 and 11.18% higher than under I1 treatment, and about 2.13 and 2.83% higher than under I3 treatment. The soil MBN under I2 treatment is 10.62 and 7.90% higher than under I1 treatment, and approximately 1.90 and 1.30% higher than under I3 treatment. This trend can be attributed to the balance between soil aeration and moisture retention under different irrigation regimes. F1 leads to excessive soil moisture, reducing soil aeration and inhibiting microbial activity. In contrast, F3 results in soil drying and re-wetting cycles, which also stress microbial communities. The F2 provides optimal conditions for microbial growth. Similarly, increasing I initially enhances soil MBC and MBN by improving moisture availability, but I3 causes water-logging, reducing microbial biomass due to hypoxic conditions.

3.2 Effects of different treatments on soil extracellular enzyme activity of greenhouse tomato

It can be seen from Table 5 that the F and I significantly impacted soil BG and LAD activities at 36, 72, and 110 days after spring and autumn tomato planting. For BG activity, a decrease in F initially increased and then decreased activity. During the growth period, F2 treatment resulted in BG activity that was approximately 11.56 and 7.61% higher than F1, and 27.93 and 23.10% higher than F3. An increase in I showed a similar pattern, with I2 treatment leading to BG activity that was about 14.02 and 1.35% higher than I1, and 14.02 and 1.81% higher than I3. For LAD activity, the same trend was observed: F2 treatment increased LAD activity by approximately 19.99 and 13.36% compared to F1, and by 45.55 and 32.85% compared to F3. I2 treatment increased LAD activity by about 20.38 and 2.33% compared to I1, and by 16.85 and 1.30% compared to I3. This can be explained by the fact that F1 reduced soil oxygen levels, suppressing aerobic microbial activity and enzyme production. F3 caused soil desiccation, limiting enzyme activity by reducing substrate availability. In contrast, the F2 maintained adequate soil moisture and aeration, promoting enzyme synthesis and activity. Similarly, I2 supported a balanced bacterial community structure.

3.3 Effects of different treatments on bacterial community structure diversity and nitrogen functional gene abundance in greenhouse tomato soil

3.3.1 Diversity of soil bacterial community structure

It can be seen from Figure 3 that F and I had significant effects on soil bacteria ACE and SHN in spring tomato and autumn tomato ($p \leq 0.05$). With the decrease of F, the soil bacteria ACE and SHN increased first and then decreased. Among them, the soil bacteria ACE and SHN in F2 were higher than those in F1 by about 13.43 and 6.09%, 8.47% and −0.64%, respectively ($p \leq 0.05$). The ACE and SHN of soil bacteria in I2 was also higher than F3 by about 7.68% and 18.03%, 2.32% and 1.12% ($p \leq 0.05$). With the increase of I, the ACE and SHN of soil bacteria showed a trend of increasing first and then decreased ($p \leq 0.05$). Among them, the ACE and SHN of soil bacteria in I2 were about 23.56% and 12.79%, 5.97% and 4.12% higher than that of I1 ($p \leq 0.05$). The ACE and SHNN of soil bacteria in I2 was also higher than I3 by about 2.78% and 2.76%, 0.63% and 1.72% ($p \leq 0.05$).

3.3.2 Abundance of functional genes related to soil bacterial nitrogen metabolism

In Figure 4, The ANFG, ANIG and ANG in spring tomato and autumn tomato soil treated with F2I2 was not significantly lower than that of F2I3, but higher than that of F1I1, F1I2, F1I3, F2I1, F3I1, F3I2 and F3I3, indicating that F2I2 treatment could improve the abundance of nitrogen metabolism functional genes and promote soil nitrogen cycle. With the decrease of F, the ANFG, ANIG and ANG in tomato soil increased first and then decreased. Among them, the ANFG, ANIG and ANG in spring tomato and autumn soil of F2 was higher than that of F1 by about 77.66% and 5.69%, 37.53% and

TABLE 5 Effects of soil bacterial community-soil microbial biomass-soil extracellular enzyme activity on soil N_2O emission flux.

Tomato planting period	Dependent variable	Regression equation	R^2	Combination of treatment for max N			
				x/d	y	N_{max}	
Spring	Microbial biomass	NCE = −6,698.26 + 1.58 X_1^2 + 11.40 Y_1^2 − 67.10 X_1 + 842.41 Y_1 − 12.00 X_1 Y_1	0.7385	119.18	25.81	172.37	(2)
	Extracellular enzyme	NCE = −642.33 + 280.95 X_2^2 + 13.31 Y_2^2 + 427.74 X_2 − 1.18 Y_2 − 133.556 X_2 Y_2	0.6867	3.90	19.61	180.05	(3)
	Bacterial community	NCE = 3,009.75 + 0.01 X_3^2 − 32.16 Y_3^2 + 0.09 X_3 − 10,045 $Y3_2$ + 0.51 X_3 Y_3	0.9082	2,681.38	5.85	194.74	(4)
Autumn	Microbial biomass	NCE = −3,515.26 − 1.05 X_1^2 − 11.21 Y_1^2 + 93.71 X_1 − 138.14 Y_1 + 5.98 X_1 Y_1	0.6381	113.44	24.10	135.81	(5)
	Extracellular enzyme	NCE = 168.42 + 2,682.67 X_2^2 + 89.28 Y_2^2 − 684.90 X_2 + 126.42 Y_2 − 979.47 X_2 Y_2	0.8707	1.12	5.45	128.49	(6)
	Bacterial community	NCE = 17,187.51 + 0.01 X_3^2 + 283.75 Y_3^2 − 0.95 X_3 − 5,054.16 Y_3 − 0.47 X_3 Y_3	0.7067	3,375.45	6.12	123.79	(7)

Spring represents the spring tomato; Autumn represents the autumn tomato. NCE represents soil N_2O emission flux. X1represents soil microbial biomass carbon, Y1 represents soil microbial biomass nitrogen, X2 represents soil β-Glucosidase active enzyme, Y2 represents soil Leucine aminopeptidase activity, X3 represents abundance of soil bacterial nitrogen metabolism functional genes, Y3 represents ACE index of soil bacterial.

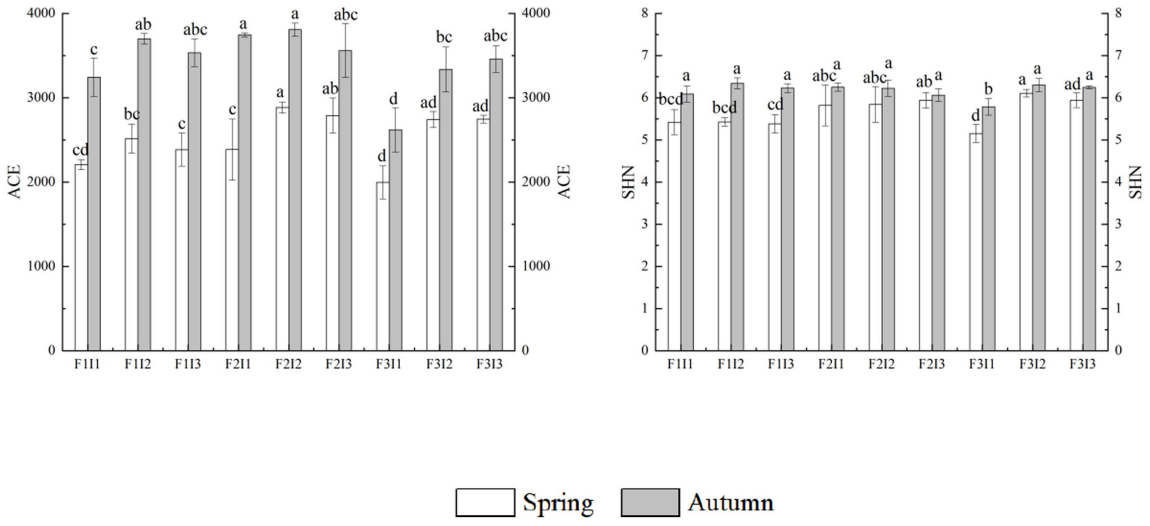

FIGURE 3
Effects of different treatments on bacterial community structure diversity in greenhouse tomato soil. The white histogram represents spring tomatoes, and the gray histogram represents autumn tomatoes. Spring represents the spring tomato; Autumn represents the autumn tomato. F represents irrigation frequency; I represents irrigation amount. The ACE represents ACE index of soil bacterial, SHN represents SHN index of soil bacterial. The data are all average ± standard deviation in the figure. Different lowercase letters indicate that there are significant differences between different treatments at the 0.05 level, the same as blow.

10.76%, 40.01% and 1.10%, respectively ($p \leq 0.05$). The F2 was about 35.69% and 1.85%, 19.37% and 2.62%, 21.61% and 0.99% higher than that of F3 ($p \leq 0.05$). With the increase of I, the ANFG, ANIG and ANG in tomato soil increased first and then decreased ($p \leq 0.05$). The ANG in spring tomato and autumn tomato with I2 was higher than that of I1 by about 12.36% and 8.33% ($p \leq 0.05$). The I2 was also higher than that of I3 treatment by about 15.33% and 7.90% ($p \leq 0.05$).

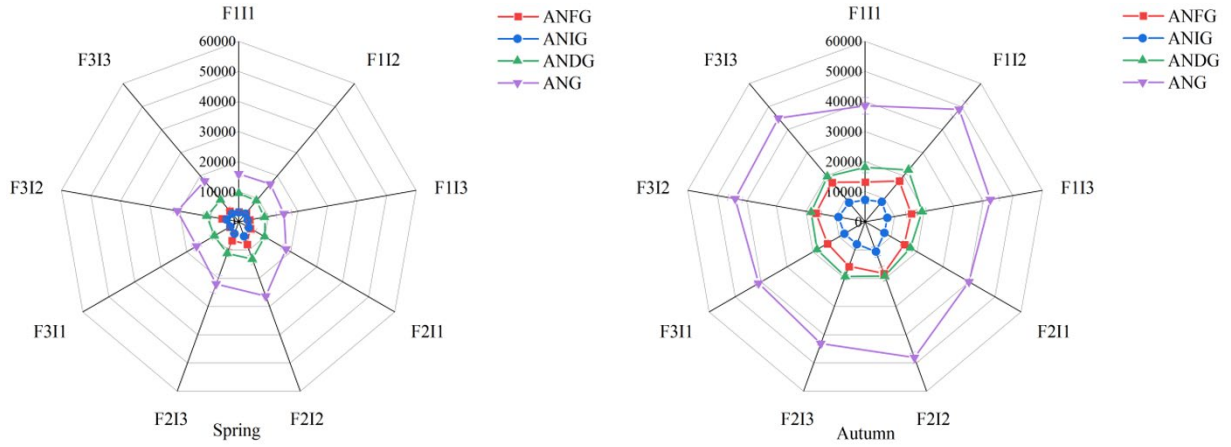

FIGURE 4
Irrigation schedule regulates the abundance of functional genes related to soil bacterial nitrogen metabolism. Spring represents the spring tomato; Autumn represents the autumn tomato. F represents irrigation frequency; I represents irrigation amount. The data are all average ± standard deviation in the figure. ANFG represents abundance of soil bacterial nitrogen-fixing functional genes, ANIG represents abundance of soil bacterial nitrification functional genes, ANDG represents abundance of soil bacterial denitrification functional genes, ANG represents abundance of soil bacterial nitrogen metabolism functional genes.

3.4 Effects of different treatments on greenhouse tomato soil N_2O emissions

3.4.1 N_2O emission flux of tomato soil

From Figure 5, it can be seen that with the advance of tomato growth period, the N_2O emission flux of spring tomato soil increased first and then decreased, and the N_2O emission flux of autumn tomato soil decreased, indicating that the effect of temperature on soil N_2O emission flux was significantly higher than the regulation of irrigation system in this study. During the growth period of tomato, F and I had significant effects on N_2O emission flux of tomato soil ($p \leq 0.05$). With the decrease of F, the N_2O emission flux of tomato soil decreased first and then increased. Under F2 (mean of tomato growth period, the same below) treatment, the N_2O emission flux of spring tomato and autumn tomato soil was about 28.38% and 15.26% lower than that of F1 treatment and also lower than that of F3 treatment by about 15.59% and 10.15%. With the increase of I, the N_2O emission flux of tomato soil showed an increasing trend.

3.4.2 Cumulative N_2O emission flux of tomato soil

It can be seen from Figure 6 that F and I had a significant effect on the cumulative N_2O emission flux of tomato soil ($p \leq 0.05$). With the decrease of F, the cumulative N_2O emission flux of tomato soil decreased first and then increased. Among them, the cumulative N_2O emission flux of spring tomato and autumn tomato soil under F2 treatment was lower than that of F1 by about 28.26% and 15.46%. The F2 was also lower than F3 about 15.72% and 10.37%. When the I increased from I1 to I3, the cumulative N_2O emission flux of tomato soil increased by about 20.50% and 15.19%.

3.5 Effect of different treatments on yield of greenhouse tomato

The data presented in Figure 7 that the yield of F2I2 of spring tomato and autumn tomato was significantly higher than that of F1I1, F2I1, F3I1, F3I2 and F3I3 by about 33.44% and 31.00%, 31.88% and 28.03%, 44.08% and 43.38%, 27.49% and 16.73%, 21.04% and 32.03%. The yield of F2I2 spring tomato and autumn tomato was higher than F1, F3 was about 5.27% and 3.24%, 19.31% and 11.30%. The yield of F2I2 spring tomato and autumn tomato in I2 was about 24.44% and 26.15% higher than that in I1, and 1.64% and 3.06% higher than that in I3.

3.6 Effects of soil bacteria-microbial biomass-extracellular enzymes on N_2O emission and yield of greenhouse tomato

As shown in Figure 8, through the Pearson double tail test, it was found that there was a pairwise correlation among soil microbial biomass carbon and nitrogen, soil extracellular enzyme, soil bacterial community, soil N_2O emission flux and yield. Indicating that there was a positive interaction between soil microbial biomass carbon and nitrogen, soil extracellular enzyme and soil bacterial community. Rich soil microbial biomass carbon and nitrogen, high soil extracellular enzyme activity and stable bacterial community positively promoted the increase of tomato yield. However, the positive promotion of soil N_2O emission flux was small. In order to further quantitatively describe how soil microbial biomass carbon and nitrogen, soil extracellular enzymes, and soil bacterial communities affect tomato soil N_2O emission flux. Therefore, this study used multiple regression analysis to qualitatively and quantitatively describe the correlation between soil microbial biomass carbon and nitrogen, soil extracellular enzymes, soil bacterial community and soil N_2O emission flux (Table 5). The higher abundance of nitrogen metabolism functional genes increased the soil N cycle. Although the risk of soil N_2O emission flux was slightly increased, the increase of tomato yield was significant. In order to further express the balance relationship between the three, regression analysis was used to quantitatively describe the relationship between the abundance of nitrogen metabolism functional genes and soil N_2O emission flux, soil N_2O emission flux

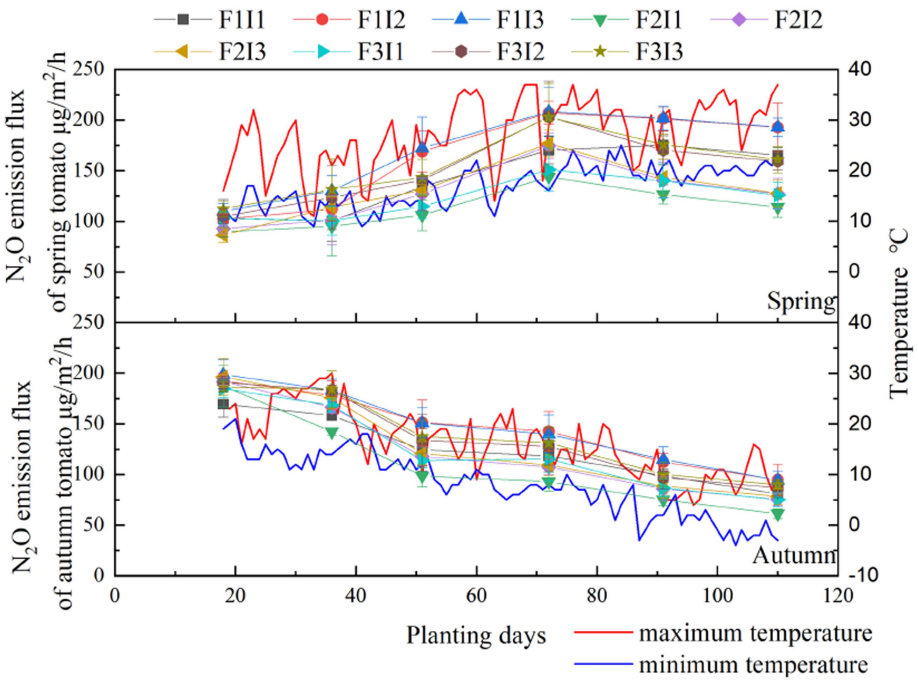

FIGURE 5
Effects of different treatments on greenhouse tomato soil N_2O emission flux. Spring represents the spring tomato; Autumn represents the autumn tomato. F represents irrigation frequency; I represents irrigation amount. The data are shown as the average ± standard deviation in the figure.

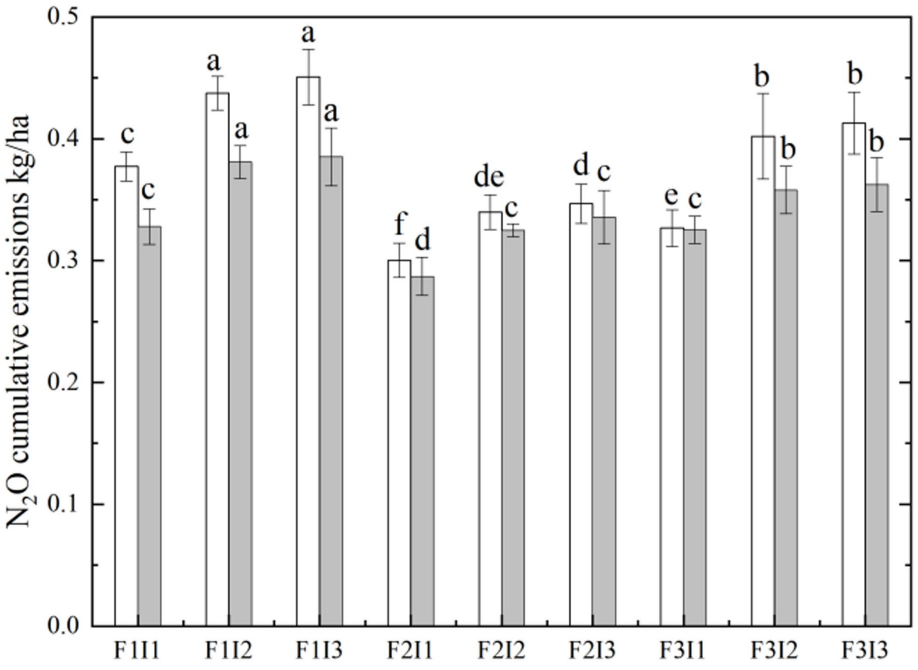

FIGURE 6
Effects of different treatments on cumulative N_2O emission flux of tomato soil. The white histogram represents spring tomatoes, and the gray histogram represents autumn tomatoes. Spring represents the spring tomato; Autumn represents the autumn tomato. F represents irrigation frequency; I represents irrigation amount. The data are all average ± standard deviation in the figure. Different lowercase letters indicate that there are significant differences between different treatments at the 0.05 level, the same below.

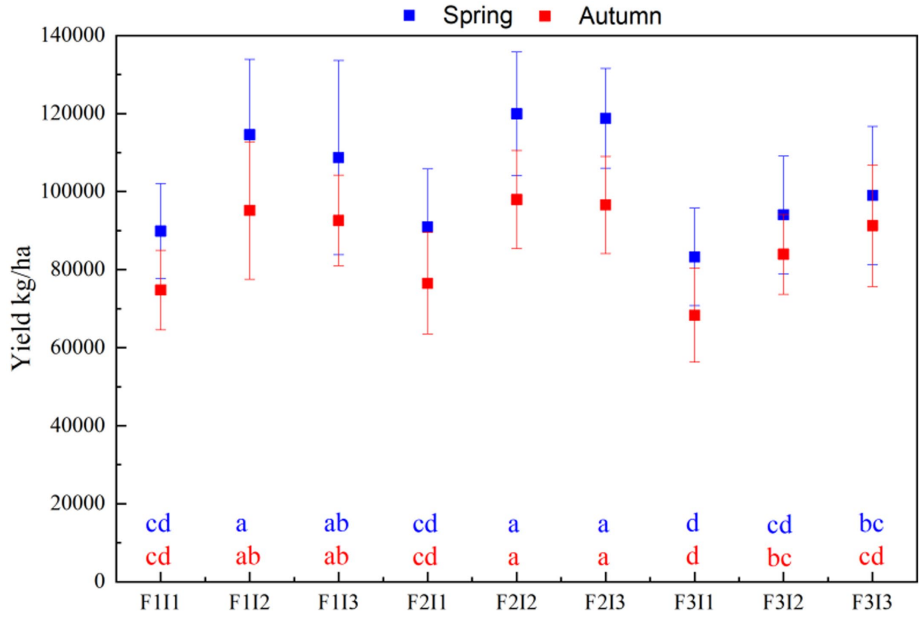

FIGURE 7
Effect of different treatments on yield of greenhouse tomato. Spring represents the spring tomato; Autumn represents the autumn tomato. F represents irrigation frequency; I represents irrigation amount. The data are all average ± standard deviation in the figure. Different lowercase letters indicate in the same column that there are significant differences between different treatments at the 0.05 level, the same below.

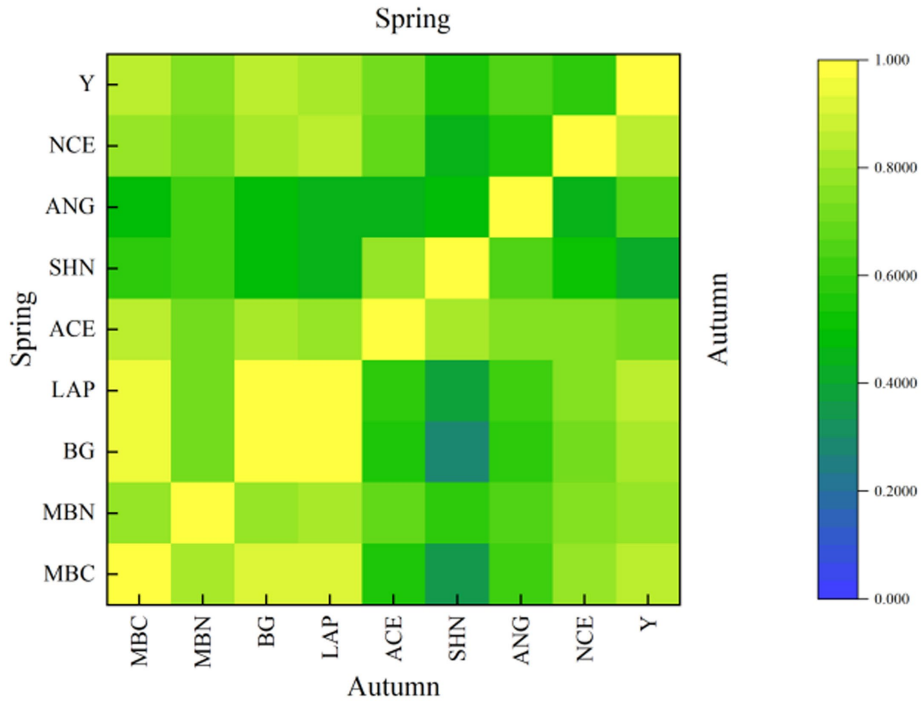

FIGURE 8
Correlation between soil bacterial community, soil microbial biomass, soil extracellular enzyme activity, N_2O emission flux and yield. Spring represents the spring tomato; Autumn represents the autumn tomato. The MBC represents the soil microbial biomass carbon, the MBN represents the soil microbial biomass nitrogen, the BG represents the soil β-glucosidase, the LAP represents the soil leucine aminopeptidase, the ACE represents ACE index of soil bacterial, SHN represents SHN index of soil bacterial, the ANG represents the abundance of soil bacterial nitrogen metabolism functional genes, the NCE represents the soil N_2O emission flux, the Y represents the yield.

and tomato yield, in order to obtain the balance relationship between the micro-sprinkler irrigation system under the membrane to regulate the tomato soil N cycle, N_2O emission flux and yield (Figure 9).

It can be seen from Figure 9 that the abundance of soil bacterial nitrogen metabolism functional genes and soil N_2O emission flux showed a quadratic parabolic curve relationship, in which the determination coefficient $R^2 \geq 0.6277$, indicating that the change of soil bacterial nitrogen metabolism functional gene abundance in the regression model can explain 62.77% of the change of N_2O emission flux of tomato soil. The relationship between tomato soil N_2O emission flux and yield showed a quadratic parabolic curve, and the determination coefficient $R^2 \geq 0.6607$, The results showed that the N_2O emission flux of tomato soil in the regression model could explain 66.07% of the change of tomato yield. The tomato soil N_2O emission flux can be used to estimate the yield, and the tomato production potential in the region can also be indirectly evaluated by the abundance of soil bacterial nitrogen metabolism functional genes. In this study, the changes of gene activity were indirectly inferred by analyzing the structure of soil bacterial community and the abundance of functional genes, combined with the changes of soil enzyme activity and microbial biomass. For example, under F2I2 treatment, soil microbial biomass carbon and nitrogen increased significantly, and soil enzyme activities (BCG and LAP) also increased significantly, indicating that the activity of functional genes related to nitrogen metabolism may be enhanced.

The data from Equations (8)–(13) in Table 6 reveal that controlling I and F of MSM has a greater impact on the abundance of bacterial nitrogen metabolism functional genes in tomato soil, the total emission of soil N_2O, and the yield elasticity of tomatoes. Specifically, a 1.00% increase in I led to at least a 32.47% increase in the abundance of bacterial nitrogen metabolism genes, a 30.68% increase in N_2O emissions, and a statistically significant 39.24% increase in yield. On the other hand, a 1.00% increase in F resulted in at least a statistically significant 11.11% decrease in the abundance of nitrogen metabolism genes, a statistically significant 7.41% decrease in N_2O emissions, and a statistically significant 11.23% decrease in tomato yield. The Cobb–Douglas model fitting indicated that the impacts of F and I on the total N_2O emissions of tomato soil aligned with the F test. The regulation of the irrigation system in MSM through optimizing irrigation frequency and amount resulted in a favorable interaction among tomato soil, microbial biomass carbon and nitrogen, soil extracellular enzymes, and soil bacterial community. This interaction notably boosted tomato yield and without a statistically significant increased soil N_2O emissions.

4 Discussion

4.1 Effects of different treatments on soil micro-environment of tomato

Previous studies have found that differences in irrigation management measures can significantly affect soil microbial biomass carbon and nitrogen (Han et al., 2010). This study shows that as F decreases, the content of microbial biomass carbon and nitrogen initially increases and then decreases, which may be due to the positive effect of microbial biomass carbon and nitrogen, and soil water distribution. When high-frequency irrigation is executed, the water potential in the environment increases sharply. High osmotic pressure can kill microorganisms that cannot withstand the pressure, thereby reducing soil microbial biomass carbon and nitrogen content (Kumar et al., 2017; Sang et al., 2024). At the same time, when shallow soil moisture is maintained at a high level for a long period, the evaporation of ineffective water increases, and soil denitrification and N_2O and CH_4 emissions also increase (Tan et al., 2025; Vogeler et al., 2019). There are larger dry and humid areas and longer dry and humid duration in low frequency irrigation soil. Crop roots are vulnerable to soil drought and low oxygen stress, which reduces root morphological development and activity, slows root metabolism, and is not conducive to the accumulation of crop root metabolism (secretion), litter and microbial residues (Jiang et al., 2023; Leng et al., 2022). Previous studies have shown that soil microorganisms and plant residues are the main components of soil microbial biomass carbon and nitrogen (Buckeridge et al., 2020; Zhang et al., 2009). This conclusion is consistent with Xue's study, which found that an appropriate increase in F helps improve the soil microbial biomass carbon of winter wheat (Xue et al., 2018). The study also found that, under MSM conditions, an irrigation

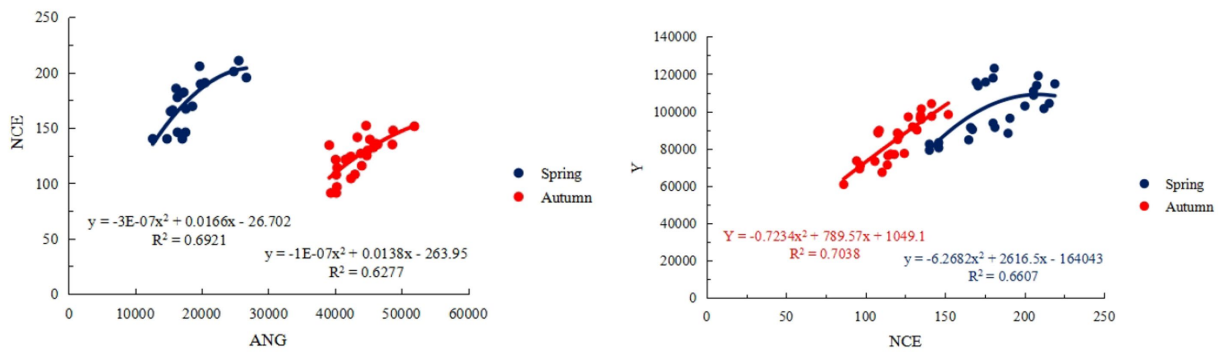

FIGURE 9
Regression analysis of soil N_2O emission and soil bacterial nitrogen metabolism functional gene abundance and yield. Spring represents the spring tomato; Autumn represents the autumn tomato. NCE represents the soil N_2O emission flux; ANG represents the abundance of soil bacterial nitrogen metabolism functional genes; Y represents the yield.

TABLE 6 Cobb–Douglas model.

Dependent variable	Tomato planting period	Equation	R^2	
ANG	Spring	$ANG = e^{5.3884}F^{-0.1111}I^{0.3907}$	0.7957	(8)
	Autumn	$ANG = e^{5.0607}F^{-0.1720}I^{0.3247}$	0.6667	(9)
NCL	Spring	$NCL = e^{-6.941}F^{-0.1703}I^{0.3400}$	0.7448	(10)
	Autumn	$NCL = e^{-0.9261}F^{-0.0741}I^{0.3068}$	0.8238	(11)
Y	Spring	$Y = e^{11.7346}F^{-0.1171}I^{0.4058}$	0.8357	(12)
	Autumn	$Y = e^{11.5591}F^{-0.1123}I^{0.3924}$	0.8087	(13)

Spring represents the spring tomato; Autumn represents the autumn tomato. F represents the irrigation frequency, and I represents the irrigation amount. ANG represents the abundance of soil bacterial nitrogen metabolism functional genes, NCL represents the N_2O cumulative emissions; Y represents the yield.

efficiency of 5 days could significantly increase the activity of extracellular enzymes related to the soil N cycle. This may be because the irrigation efficiency of 3 days in sandy loam is too high, reducing soil aeration which the irrigation efficiency of 7 days would led to the soil being over-dried or over-wet for a long time. Soil microorganisms cannot adapt to environmental changes due to soil moisture and hypoxia stress, which reduces the source of soil enzymes. This is inconsistent with Li's research, which found that the number of soil microorganisms is large and the soil enzyme activity is high after 8 days of irrigation. This conclusion may be due to differences in irrigation methods, regional climate and soil texture. Further research and demonstration are needed (Li et al., 2014). Changing F can alter the frequency of soil dry-wet alternation, thereby affecting the diversity and abundance of soil microbial communities. According to previous studies, dry-wet alternation can lead to about 58.00% of microbial death, but the active organic matter released by soil dry-wet changes is conducive to the growth of surviving microorganisms (Qin et al., 2025; Van Gestel et al., 1993). In this study, we found that the abundance of soil nitrogen metabolism functional genes was higher under F2, which may be due to the small wetting body and long wetting time of the soil with F1. Soil with long-term wetting state has a large amount of evaporation and poor soil aeration. Smaller wetting body and higher frequency irrigation can easily increase surface soil water filling porosity, promote the decrease of soil aeration, lead to competition among aerobic bacteria for survival in soil nitrogen fixation, nitrification and denitrification, and limit the increase of soil bacterial population abundance (Adu and Oades, 1978; Wang, 2017). However, when F was too low (F3), the average soil volumetric water content of spring and autumn tomato in the cultivated layer was lower than that of F2 by about 2.16% and 6.02%, respectively. The soil moisture in the cultivated layer became the main factor limiting the bacteria in the rhizosphere soil of greenhouse tomato under MSM (Xu et al., 2024; Wang, 2017). In addition, the spatial and temporal distribution of soil volumetric water content is uneven when the F is F3, and the soil at the root of the crop will be dry or wet for a long time. The abundance of soil microorganisms decreases8 due to the environmental filtration mechanism (Gregorutti and Caviglia, 2019; Wang et al., 2020). Water and low oxygen stress led to a decrease in the number of roots in the cultivated layer, and the amount of root exudates also decreased, which reduced the source of bacterial survival substrates. Moreover, the growth and reproduction of functional bacteria related to nitrogen metabolism were squeezed by the niche of other functional bacteria in the soil, resulting in a decrease in their abundance (Maheshwari, 2011; Wang et al., 2019). The abundance of soil phosphorus metabolism functional genes was higher than that of F1 or F3 when the F of MSM was F2, which further indicated that the irrigation frequency of F2 was beneficial to improve the soil P cycle metabolism (Balemi and Negisho, 2012; Monokrousos et al., 2020).

This study also showed that as I increased, the total organic carbon in soil initially increased and then decreased, which may be due to the uniform distribution of soil moisture in I2. There was no hypoxia and water stress caused by too high or too low soil volumetric water content in soil wetted body, which promoted the development of crop root morphology. The better root morphology development was beneficial to improve the abundance of root microbial population. The residues of plants and microorganisms provided sufficient carbon for crop rhizosphere soil (Buckeridge et al., 2020; Yao et al., 2019). With the increase of I, the activities of soil enzymes (β-glucosidase and leucine aminopeptidase) under micro-sprinkler irrigation under greenhouse tomato film increased first and then decreased. It may be that soil moisture is one of the main factors limiting soil enzyme activity under small I. When the I was too high, the soil aeration was poor (the soil water filling porosity of 1.20 Epan was higher than that of I2 by about 3.55 and 2.25%). The low oxygen soil micro-environment would inhibit the increase of aerobic microorganisms, resulting in the decrease of soil microbial community structure diversity and population abundance, the decrease of root absorption and utilization of soil nutrients, and the restriction of crop root metabolic cycle. The lower root cycle metabolites, root exudates and soil microbial biomass directly limit the improvement of soil enzyme activity (Wang et al., 2025; Zhang et al., 2019; Wang, 2017). With the increase of I, the soil volumetric water content increased. Weakening of soil permeability. This study also showed that the abundance of bacterial nitrogen metabolism functional genes in the rhizosphere soil of spring tomato with I2 was better. It may be due to the I1, the soil is easy to produce water stress limitation, and the soil volumetric heat capacity decreases with the decrease of soil water content, which is not conducive to the daily variation of soil temperature in a small range, and the fluctuation of soil internal fine structure also increases. The unstable soil structure limits the rapid increase of soil dominant flora abundance (Meisner et al., 2021; Han et al., 2020). At the same time, the lower irrigation amount is not conducive to the development of crop root morphology, resulting in a decrease in the input of organic matter such as root exudates and litter, which limits the increase in the abundance of soil bacterial nitrogen metabolism functional genes (Lin et al., 2024; Xiao C. et al., 2024; Xiao H. et al., 2024; Zhu et al., 2022). I3 makes the water fill the soil pores, and the external air is difficult to enter, which is easy to cause the decrease of soil oxygen content. The hypoxia stress of crop roots is easy to reduce the soil pH, and the reproduction of aerobic bacteria (nitrogen-fixing bacteria and rhizobia) in soil bacteria will be limited (González et al., 2015; Jiang et al., 2006). At the same time, there is a phenomenon of oxygen competition between crop roots and soil aerobic bacteria, which will greatly reduce the diversity and abundance of soil bacterial community structure (Zhou et al., 2024; Jiang et al., 2006; Yuan et al., 2020).

4.2 Effects of different treatments on N_2O emission of tomato soil

Soil moisture is a limiting factor for the growth of plant roots and soil microorganisms (Xia et al., 2025). Different irrigation regimes can significantly affect a variety of soil abiotic factors, such as water availability, gas, heat distribution and porosity. At the same time, changes in soil environmental factors will affect the growth of microorganisms and plant roots. The growth of plant roots affects soil nutrient nitrification and denitrification, which in turn changes soil N_2O gas emissions (He et al., 2024; Storch et al., 2023). This study found that too high (F1) or too low (F3) irrigation frequency could increase soil N_2O emissions. Soil wetting and drying increased the substrate availability generated by soil microbial senescence and degradation of soil aggregates that protect organic matter, accelerated soil C and N mineralization rates, promoted aerobic respiration and reduced soil O_2 levels. Subsequently, the anoxic zone formed on the soil promoted the rapid growth and activity of denitrifying bacteria, resulting in a significant increase in N_2O emissions. Wu et al. (2022) found that the increase of rainfall frequency will increase the N_2O emission flux of grassland soil. The conclusion is inconsistent, which may be due to the difference in the cycle of water entering the soil or the type of crop. The highest irrigation frequency of Wu grassland is 1 week, and the lowest irrigation frequency of vegetables in this study is 1 week. It is inconsistent with the results of Mumford et al. (2019) that high frequency and low frequency irrigation can increase soil N_2O emission. It may be because Owens et al. (2016) believed that increasing F will reduce N_2O emission by increasing surface soil moisture and reducing soil O_2 concentration, which is consistent with the conclusion that N_2O emission is lower than F1 under F2 in this study.

Soil water content often leads to changes in soil physical and chemical properties, thereby regulating soil denitrification (Li et al., 2024; Wu et al., 2022). Researchers generally believe that soil denitrification increases with the increasing water content, but some studies have found that soil N_2O flux is the largest under critical saturated water content (Thiloka Edirisooriya et al., 2024). This study found that with the increase of I, tomato soil N_2O emissions showed an increasing trend, may be due to the increase of soil water content will reduce the gas diffusion rate, and by limiting the main electron acceptor (such as oxygen) and substrate supply to directly affect the activity of microorganisms in the soil and its dominant nitrification and denitrification, improve soil microorganisms and plant root anaerobic respiration, increase tomato soil N_2O emissions. It is consistent with the conclusion of Shang et al. (2020) and Gultekin et al. (2023) that drip irrigation can increase the N_2O emission of greenhouse tomato soil, which further indicates that the effect of MSM on N_2O emission of greenhouse tomato soil is similar to that of drip irrigation.

4.3 The correlation among soil micro-environment, N_2O emission and yield of tomato under MSM

Previous research has shown that differences in soil water distribution resulting from irrigation can have a significant impact on the structure of soil bacterial communities, soil enzyme activity, microbial biomass carbon and nitrogen, as well as influencing soil N_2O emissions and crop yield (Wang Z. et al., 2022; Wang et al., 2021). The current study revealed a strong positive correlation between soil microbial biomass carbon and nitrogen, extracellular enzymes and the soil bacterial community in the rhizosphere soil of tomatoes. This correlation is likely influenced by the diverse and abundant structure of the soil bacterial community, which facilitates the decomposition of soil organic matter, accelerating the carbon and nitrogen cycling in the soil. Increased levels of soil microbial biomass carbon and nitrogen, extracellular enzymes and soil bacterial communities can enhance plant roots' ability to access soil moisture and nutrients, leading to higher tomato yields. Interestingly, the study discovered that the impact of I on tomato soil N_2O emissions and yield was more pronounced compared to that of F, possibly due to the increased irrigation. The increased irrigation led to a notable rise in soil moisture content compared to the control group, reducing the frequency of soil dry and wet cycles. With higher moisture, oxygen levels in the soil diminish, promoting the production of N_2O by microorganisms in low oxygen conditions. Previous research has shown a consistent linear relationship between irrigation amounts and soil N_2O emissions. Altering the micro-sprinkler irrigation schedule under plastic film influenced the soil bacterial community composition, enzyme activities, and the interplay between soil microbial carbon and nitrogen, subsequently affecting N_2O emissions (Xiao et al., 2024; Xiao et al., 2024). Depletion of soil nitrogen would likely hinder the growth of tomato plants. Remarkably, the F2I2 treatment resulted in increased soil microbial carbon and nitrogen biomass, enhanced enzyme activities, a stable bacterial community, and reduced N_2O emissions, facilitating nitrogen uptake by tomato plants and ensuring a consistent tomato yield (Liu et al., 2024; Yang et al., 2023). The success of the F2I2 treatment may stem from increased nitrogen absorption by tomatoes, encouraging root colonization by microorganisms, strengthening root-microorganism interactions, limiting available nitrogen sources for soil microbes and ultimately reducing N_2O emissions under this treatment.

4.4 Insights for facility agriculture from MSM irrigation system regulation

The present study provides valuable insights into optimizing the MSM irrigation system for enhanced tomato yield and controlled soil N_2O emissions in facility agriculture. By systematically investigating the effects of different irrigation frequencies and amounts, we have demonstrated that a balanced irrigation strategy (F2I2 treatment) can significantly improve crop yield while maintaining N_2O emissions at a relatively low level. These findings imply that precise irrigation management is crucial for achieving sustainable agricultural production in greenhouse settings. The interaction between soil microbial biomass, extracellular enzyme activity, and bacterial community diversity under varying irrigation regimes offers a deeper understanding of soil ecological processes. This knowledge can guide farmers and agricultural practitioners in making informed decisions regarding irrigation practices, thereby promoting efficient resource utilization and mitigating environmental impacts. Furthermore, the observed correlation between soil bacterial nitrogen metabolism

functional gene abundance and tomato yield provides a potential biological indicator for assessing soil fertility and crop production potential in facility agriculture. Overall, these insights highlight the importance of tailoring irrigation strategies to specific crop requirements and soil conditions to optimize productivity and sustainability.

5 Conclusion

By exploring the response mechanism of tomato soil N_2O emission under the regulation of MSM, the results showed that high frequency irrigation (F1) and low frequency irrigation (F3) were not conducive to the accumulation of microbial biomass carbon and nitrogen in tomato soil under MSM, limiting the increase of soil extracellular enzymes BCG and LAP, reducing the diversity of bacterial community structure and the abundance of functional genes related to bacterial nitrogen metabolism. The I2 can ensure the accumulation of microbial biomass carbon and nitrogen in tomato soil, promote the increase of soil BCG and LAP activities, and facilitate the stability of soil bacterial community. With the decrease of F, the cumulative N_2O emission flux of tomato soil decreased first and then increased. With the increase of I, the cumulative emission flux of soil N_2O also increased first and then decreased. The yield of spring tomato and autumn tomato under F2 was higher than that of F1 and F3 about 5.27% and 3.24%, 19.31% and 11.30%. The yield of spring tomato and autumn tomato under I2 was higher than that of I1 about 24.44% and 26.15%, also higher than that of I3 about 1.64% and 3.06%. Pearson two-tailed test and regression analysis showed that there was a positive interaction among soil microbial biomass carbon and nitrogen, soil extracellular enzymes and soil bacterial community structure, which was beneficial to the increase of tomato yield. There was a quadratic curve relationship among soil N_2O emission flux, the abundance of soil bacterial nitrogen metabolism functional genes and yield. The tomato production potential and greenhouse gas emissions in this region could be indirectly evaluated by the abundance of soil bacterial nitrogen metabolism functional genes. In this study, it is feasible to regulate soil N_2O emissions under the MSM irrigation system. The specific performance is that F2I2 treatment can increase tomato yield on the basis of limiting N_2O emission flux of tomato soil. This study provides data support for yield increase and emission limitation and soil production potential prediction in facility agriculture.

Data availability statement

The original contributions presented in the study are included in the article/supplementary material, further inquiries can be directed to the corresponding author/s.

Author contributions

HY: Data curation, Writing – original draft. MZ: Writing – original draft, Writing – review & editing. WW: Formal analysis, Writing – original draft. NX: Supervision, Writing – original draft. MS: Resources, Writing – original draft. YL: Writing – review & editing.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Generative AI statement

The authors declare that no Gen AI was used in the creation of this manuscript.

Publisher's note

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