

Article

Effect of Subsurface Drip Irrigation on Soil Desalination and Soil Fungal Communities in Saline–Alkaline Sunflower Fields

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Abstract: A field experiment was conducted on sunflowers in a mild-to-moderate saline–alkaline area in the Tumochuan Plain irrigation region in China. The experimental design included using surface drip irrigation as a control (CK) and four subsurface drip irrigation treatments at burial depths of 10 cm (D10), 15 cm (D15), 20 cm (D20), and 25 cm (D25) to analyze the effect of the drip irrigation belt burial depth on soil physicochemical properties and soil desalination in the main root zone of saline–alkaline sunflower farmland. Based on macro-genome sequencing technology, the diversity, composition, and structure of soil fungal communities in the main root zone were revealed in response to the depth of drip irrigation. The results show that subsurface drip irrigation treatments improved soil desalination with rates ranging from 15.33% to 26.96%. The D25 treatment achieved an 82.01% higher desalination rate than CK and outperformed D10, D15, and D20 by 43.35%, 13.43%, and 24.89%, respectively, demonstrating the most effective desalination with a 25 cm burial depth under the same water and fertilizer management conditions. Additionally, subsurface drip irrigation enhanced the diversity and abundance of soil fungal communities; the Shannon indices for D15 and D20 were 8.1% and 12.3% higher than that of CK, respectively, whereas the Chao1 indices increased by 21.2% and 17.4%, respectively. During the budding stage, the fungal community in the main root zone (20–40 cm) was dominated by Ascomycetes and Tephritobacterium, with Alternaria being the predominant genus. Notably, the relative abundance of Ascomycetes was 118.8% higher in D25 than in CK. Structural equation modeling quantified the relationships between soil physicochemical properties, with an SMC of 0.94, indicating a model fit within an acceptable range. An SEM analysis revealed that the soil water content (SWC), soil EC, and soil NO₃[−]-N exerted the most significant combined effect on soil fungal composition and diversity. This study examined the effects of the drip irrigation tape burial depth on soil physicochemical characteristics, the fungal community structure, and diversity in the main root zone (20–40 cm) of saline–alkaline sunflower fields under subsurface drip irrigation. This study aims to provide theoretical support for water-saving agricultural practices in saline–alkaline soils. We developed a subsurface drip irrigation method for sunflowers in the lightly to moderately saline–alkaline land in the irrigation area of China’s Tumochuan Plain, and the suitable depth of burial of the drip irrigation belt was 25 cm.



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Keywords: saline–alkaline; subsurface drip irrigation; soil fungal; salt leaching; macrogenome sequencing

1. Introduction

Soil salinization is a prominent ecological and environmental problem in arid regions and poses a substantial threat to the sustainable development of irrigated agriculture.

When salinization occurs in the soil, the structure deteriorates, reducing the number of water-stable aggregates in the soil, and the voids become smaller, resulting in poorer bonding and affecting the soil's ability to retain moisture; this results in a constant increase in the colloidal Na^+ within the soil, affecting water availability and triggering cold soil in the spring and autumn due to a lack of low temperatures, which is not conducive to crop seeding and seedling growth [1]. Plant growth can be promoted through improved irrigation techniques [2], deep soil turning [3], and the application of functional fertilizers.

Subsurface drip irrigation is an innovative irrigation technique that has evolved from surface drip irrigation [4,5]. Studies have demonstrated that in comparison to other irrigation methods, subsurface drip irrigation can effectively distribute nutrient-containing wetting bodies in the primary root zone of crops, reduce water and nutrient losses, and enable crops to more fully utilize water and fertilizer [6,7]. Under specific soil matrix conditions, the soil moisture transport and distribution characteristics of subsurface drip irrigation significantly differ from those of surface drip irrigation. Subsurface drip irrigation exhibits strong water retention and excellent water conductivity in terms of the physical and hydromechanical properties of soil [8]. Furthermore, subsurface drip irrigation technology is able to maintain high water conductivity and an effective soil water content over a long period of time due to its high irrigation frequency [9], and it can create a microenvironment in the root zone that is conducive to optimal crop growth [10].

Recent research on saline–alkaline soils has expanded from a sole focus on agricultural resources to encompass a broader perspective, integrating environmental ecology with agricultural resource studies [11]. In saline–alkaline sunflower fields, soil microorganisms are essential for enhancing the inter-root microenvironment [12]. Fungi are critical decomposers in soil ecosystems [13,14] as components of the soil microbial community. Furthermore, soil fungi are frequently used as indicators of soil quality changes because of their responsiveness to environmental alterations [15,16]. Fungi can also establish symbiotic relationships with plants, facilitating their metabolism and uptake of nutrients such as nitrogen and phosphorus [17,18]. Conversely, certain pathogenic fungi can impede plant growth and potentially cause plant mortality [19]. Additionally, some studies have shown that, compared to surface drip irrigation, the increased relative abundance of soil phytopathogenic fungi in the root zone of tomatoes under subsurface drip irrigation contributes to the inhibition of growth and reproduction of disease-causing bacteria and the maintenance of soil environmental health in the root zone, and it supports crop growth [20]. Therefore, soil fungi perform diverse and vital functions, underscoring their importance in soil ecosystems.

The root system, which is in close contact with the soil, continuously absorbs water and nutrients to support crop growth. To accurately assess the impact of subsurface drip irrigation on the physicochemical properties of soil in the sunflower root zone of saline–alkaline fields, this study focused on the primary root distribution zone (20–40 cm) [21]. Limited research exists on the effects of subsurface drip irrigation on the structure and diversity of soil fungal communities in the saline–alkaline root zone. Therefore, this study took the main root zone soil of sunflowers in the irrigation area of the Tumochuan Plain in China with light to moderate saline–alkaline soils as the research object to investigate the effects of subsurface drip irrigation on soil water, soil nitrogen, and desalination in the main root zone and to reveal the changing law of the structure and diversity of the saline–alkaline soil fungal community under subsurface drip irrigation.

2. Materials and Methods

2.1. Description of the Experimental Site

The field experiment was conducted in 2023 in the Tumochuan Plain Irrigation District (S 111°2'30", N 40°41'30"), which is characterized by a typical temperate continental monsoon climate. Key climatic conditions at the site include an average annual temperature of 7.5 °C, with a mean temperature of 21.2 °C during the reproductive period of the sunflower (June–September). The area experiences a frost-free period of 135 days, receives

an average of 2876.6 h of sunlight annually, and has an average of 380 mm of annual precipitation. Figure 1 illustrates the relationship between precipitation and potential evapotranspiration (ET_0) during the sunflower fertility period in 2023.

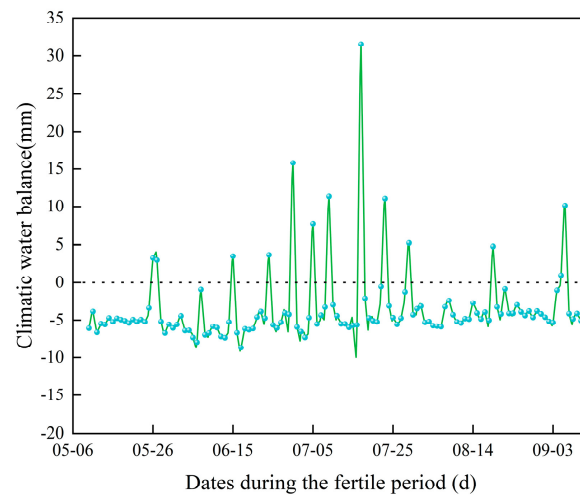


Figure 1. Climatic water balance graph of fertility period of sunflower from May to September of 2023.

The soil at the experimental site, within the 20–40 cm root zone, is classified as sandy loam, with an average bulk density (BD) of $1.73 \text{ g}\cdot\text{cm}^{-3}$, a mean total salt content of $1.61 \text{ g}\cdot\text{kg}^{-1}$, and a pH of 8.61, indicating moderate to mild saline conditions. Soil baseline nutrient levels measured prior to sunflower sowing in 2023 included organic matter (OM) at a content of $13.55 \text{ g}\cdot\text{kg}^{-1}$, available phosphorus (AP) at $35.13 \text{ mg}\cdot\text{kg}^{-1}$, available potassium (AK) at $135.67 \text{ mg}\cdot\text{kg}^{-1}$, and total nitrogen (TN) at $84 \text{ mg}\cdot\text{kg}^{-1}$. During the reproductive period, the water table depth fluctuated between 3 m and 5 m.

2.2. Experimental Treatments and Design

The crop selected for the experiment was the new HZ2399, an edible sunflower variety selected and bred by the Sunflower Research Laboratory of the Economic Crops Research Institute of the Xinjiang Academy of Agricultural Sciences of China over a period of five years, which belongs to a medium-late maturing variety with gray-white stripes between black and gray kernels, large kernels, and a high commerciality rate. The experiment was conducted in the study area from May to September 2023 using a one-way completely randomized design. Surface drip irrigation was designated as the control treatment (CK), whereas subsurface drip irrigation treatments were established with drip tape burial depths of 10, 15, 20, and 25 cm (denoted as D10, D15, D20, and D25, respectively), resulting in five treatments. Each treatment was replicated thrice, yielding a total of 15 plots. Each plot measured $10 \text{ m} \times 16 \text{ m}$, and masonry cement baffles were installed around the perimeter of each plot to prevent the effects of moisture, nitrogen, and salinity. Sunflowers were sown on 1 June 2023. Following the regular local cropping system, each plot contained six in-set drip irrigation lines with a row spacing of 1.0 m and a plant spacing of 0.5 m, achieving a planting density of $21,000 \text{ plants}\cdot\text{hm}^{-2}$. This density was consistently applied across all plots. The drip irrigation system consisted of a network of pressure tanks, stacked filters, Venturi fertilizer injectors, pressure gauges, valves, and distribution lines. The main water supply pipe was a 50 mm diameter PE pipe, while the drip irrigation tape had an inner diameter of 25 mm, a dripper hole diameter of 0.4 mm, a spacing of 30 cm between the drip head, and a dripper flow rate of $2 \text{ L}\cdot\text{h}^{-1}$. Groundwater with a mineralization level of $0.836 \text{ g}\cdot\text{L}^{-1}$ was used for irrigation. The arrangement of the test plots is illustrated in Figure 2.

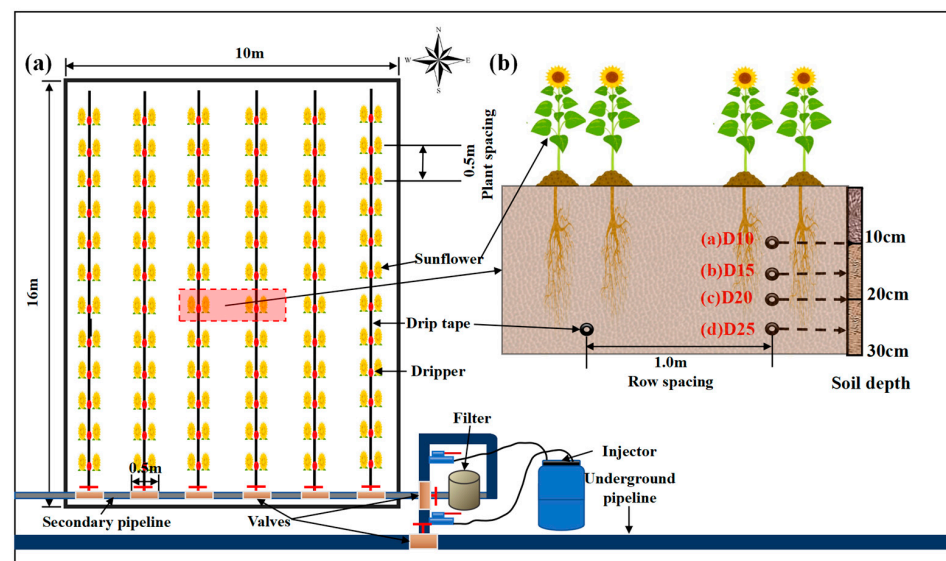


Figure 2. Layout of the test plot ((a) is the layout of the experimental plot, and (b) is a schematic diagram of the burial depth of drip irrigation tape).

For nutrient management, $300 \text{ kg} \cdot \text{hm}^{-2}$ (18% N) of diamine phosphate was applied as the base fertilizer at the time of sowing. Additional application of urea ($300 \text{ kg} \cdot \text{hm}^{-2}$, 46% N) at the budding stage resulted in a total application of $192 \text{ kg} \cdot \text{hm}^{-2}$ of pure N. Other field management practices were consistent with local cultivation protocols. The experimental design is presented in Table 1.

Table 1. Experimental design.

Treatment	Drip Irrigation Placement Depth /(cm)	Irrigation Quota /(m ³ ·hm ⁻²)							Irrigation Norm /(m ³ ·hm ⁻²)
		Pressure Brine	Budding Stage		Flowering Stage		Pustulation Period		
CK	0	900	150	150	112.5	112.5	112.5	112.5	1650
D10	10	900	150	150	112.5	112.5	112.5	112.5	1650
D15	15	900	150	150	112.5	112.5	112.5	112.5	1650
D20	20	900	150	150	112.5	112.5	112.5	112.5	1650
D25	25	900	150	150	112.5	112.5	112.5	112.5	1650

2.3. Measurement Items and Methods

2.3.1. Sample Collection

Soil samples were collected from the main rooting zone (20–40 cm depth) of sunflower plants during the following key reproductive stages: budding (55 d after sowing), flowering (65 d after sowing), pustulation (80 d after sowing), and maturity (105 d after sowing). Samples were collected from each plot in triplicate using a soil auger. Samples from the same plot were thoroughly mixed and divided into two portions. One portion was used to determine the soil water content (SWC) in the main rooting zone using the drying method. The second portion was air-dried indoors, passed through a 2 mm sieve, and used for the analysis of soil physicochemical properties.

Soil microbial assay: Soil microbial samples were collected at the sunflower bud break stage using a five-point sampling method with a soil auger. Samples from the main root zone (20–40 cm depth) of each plot were thoroughly mixed, packed into collection tubes, and immediately stored in a foam box on dry ice. The samples were then transported to the laboratory and stored at -80°C for DNA extraction and subsequent fungal macrogenome sequencing. Soil fungal abundance and diversity were assessed by macrogenome sequencing and analyzed by sequencing on the Illumina MiSeq platform at Parsonage Shanghai (Shanghai, China).

2.3.2. Determination of Basic Physical and Chemical Properties of Soil

The electrical conductivity (EC) and pH of the soil leachate were measured using a soil/water mass ratio of 1:5. EC was determined using a conductivity meter (DDS-307A, Shanghai, China), while pH was measured using a pH meter (Mettler Toledo Instruments, Shanghai, China). Soil ammonium nitrogen was quantified using the indophenol blue colorimetric method following extraction with 2 mol·L⁻¹ KCl. For soil nitrate-nitrogen analysis, 50 mL of (1 mg·L⁻¹) KCl solution was added at a water/soil ratio of 10:1 and measured using a UV spectrophotometer.

2.3.3. Macrogenomic Sequencing Analysis

A quantity of 500 mg of glass beads and 0.2–0.5 g of soil sample were weighed into a 2 mL centrifuge tube, and 0.8 mL of BufferSLXMLu was added. The mixture was vortexed for 1–5 min. Then, 80 µL of Buffer DS was added, and the sample was shaken to mix thoroughly. The tube was incubated at 70 °C for 10 min and centrifuged at 13,000× g for 5 min at room temperature, and 200 µL of BufferSP2 was subsequently added. After a brief shaking step, 100 µL of HTR Reagent was added, and the sample was placed in an ice bath for 5 min before centrifugation. Finally, 40 µL of magnetic beads was added and mixed thoroughly, and 450 µL of Binding Buffer was added. Total microbial genomic DNA was extracted using an OMEGA Mag-Bind Soil Extraction DNA Kit (M5635-02) (Shanghai, China). Following DNA extraction, a QubitTM 4 fluorometer (QubitTM Assay Tube: Q32856; QubitTM 1X dsDNA HS Assay Kit: Q33231) (Invitrogen, Waltham, MA, USA) was used for quantification, with additional verification carried out using agarose gel electrophoresis. The extracted microbial DNA was subsequently prepared using an Illumina TruSeq Nano DNA LT Library Preparation Kit for sequencing.

Raw sequencing reads were processed to obtain high-quality filtered reads for further analyses. Initially, sequencing adapters were removed using Cutadapt (v1.2.1), and low-quality reads were trimmed in fastp using a sliding window algorithm. High-quality reads were analyzed using the RefSeq-derived database Kraken2. Megahit (v11.2) was used to assemble each sample using the mega preset parameters. Overlapping clusters (over 300 bp) were then set to a sequence identity threshold of 0.95 using mmseqs2 and “easy-lincust” mode, with the coverage residuals for shorter overlap clusters set to 90%. The CDS sequences of all samples were clustered using mmseqs2, setting the protein sequence identity threshold to 0.90, and covering the residual amount of shorter overlapping clusters to 90%. Abundance values were normalized to copies per thousand bases per million mapped reads (CPM). Functions of non-redundant genes were obtained by annotation using mmseqs2 in search mode against the protein databases KEGG, EggNOG, and CAZy.

2.4. Structural Equation Modeling

Structural Equation Modeling (SEM) is a comprehensive statistical analysis method that utilizes a covariance matrix of variables to analyze relationships within multivariate data. In this study, SEM was employed to quantitatively examine the interactions between latent variables, as well as between latent variables and explicit variables, with the maximum likelihood estimation method applied to enhance accuracy. Explicit variables refer to observed variables, whereas latent variables represent a linear combination of explicit variables constructed to capture the underlying causal relationships. To mitigate systematic errors and ensure sample comparability, the input data were tested for normality, and sample data with abnormal variable indicators were excluded. Subsequently, the path coefficients of all the paths were calculated to determine the relevant parameters of the structural equation model.

2.5. Data Analysis

Data processing was conducted using the RStudio 2024, following a series of steps to ensure data quality and reliability. First, quality control measures were applied to identify and remove outliers and abnormal data. Interpolation was performed for abnormal and

missing data. Subsequently, the interpolated data were subjected to further processing and quality control, and the persistent outliers were excluded. These outliers were subsequently recorded as null values, and only valid data were retained for the analysis. Model accuracy was evaluated using the root mean square error (RMSE) and coefficient of determination (R^2) to assess the accuracy of the simulation results.

Statistical analyses and visualizations were performed using RStudio, IBM SPSS Amos 28, and Origin 2021. One-way ANOVA and Pearson's correlation analyses were conducted using SPSS 25.0.

3. Results

3.1. Effect of Drip Irrigation Tape Burial Depth on Soil Physicochemical Properties and Soil Desalination in Primary Root Zone

Figure 3 illustrates the changes in the soil physicochemical properties within the primary root zone across different treatments during the sunflower growth cycle. At the budding stage, the average soil water content increased by 6.10%, 7.78%, 8.03%, and 8.81% in the D10, D15, D20, and D25 treatments, respectively, compared to the CK treatment. No significant difference in soil pH was observed in the primary root zone between treatments as the sunflower plants progressed through their growth stages. During the rapid growth phase from flowering to pustulation, the soil NO_3^- -N content in the main root zone declined sharply. The maximum NO_3^- -N content dropped from 20.35~24.39 $\text{mg}\cdot\text{kg}^{-1}$ to 13.06~17.27 $\text{mg}\cdot\text{kg}^{-1}$. As the fertility period advanced, crop growth continued to absorb nutrients, and the soil NO_3^- -N content reached its minimum during the maturity period. The soil salinity content, an indicator of soil salinization, was assessed using soil EC measurements, which indirectly reflect soil salinity levels. In the main root zone, soil salinity was in the range of 0.54~1.99 $\text{mS}\cdot\text{cm}^{-1}$, and the EC values of the treatments exhibited a fluctuating trend: it initially increasing, and then decreased, and subsequently increased as the fertility period progressed. Among the treatments, soil salinity in the main root zone decreased in the following order: CK > D10 > D20 > D15 > D25. When analyzing the changes in soil salinity after irrigation at the budding stage, it was found that the CK treatment displayed the most significant salinity increase from the budding stage to the flowering stage, followed by D10, D15, and D20, with D25 showing the smallest increase.

The soil desalination rate is a key measure of the effectiveness of irrigation for soil salt removal. The soil desalination rate was calculated as the ratio of the difference between the initial soil salt content and that at the end of irrigation to the initial soil salt content. As shown in Table 2, subsurface drip irrigation treatments achieved soil desalination rates ranging from 15.33% to 26.96% within the main root zone soil layer. Among the treatments, the D25 treatment showed the highest desalination rate in this root zone layer, with rates 82.01%, 43.35%, 13.43%, and 24.89% higher than those observed in the CK, D10, D15, and D20 treatments, respectively. This indicated that D25 provided the most effective desalination under the same water and fertilizer conditions. The CK treatment exhibited the lowest desalination rate owing to the limited irrigation water volumes during the reproductive phase, which was insufficient to effectively flush the salts. Consequently, the salts could not wash the surface soil salts at the deep soil layer but stayed in the tillage layer; the subsurface drip irrigation was more conducive to maintaining a higher water content and low salt environment in the main root zone due to the fact that the water washed salts from the vicinity of the drip head to the edges of the wadding body, resulting in a reduction in salt within the wadding body. Therefore, subsurface drip irrigation in the study area was more effective in desalting the soil in the main root zone compared to surface drip irrigation.

Table 2. Effect of different treatments on soil desalination rate at 20–40 cm soil depth.

Soil Depth	CK	D10	D15	D20	D25
20–40 cm	12.06%	15.33%	19.36%	17.59%	21.96%

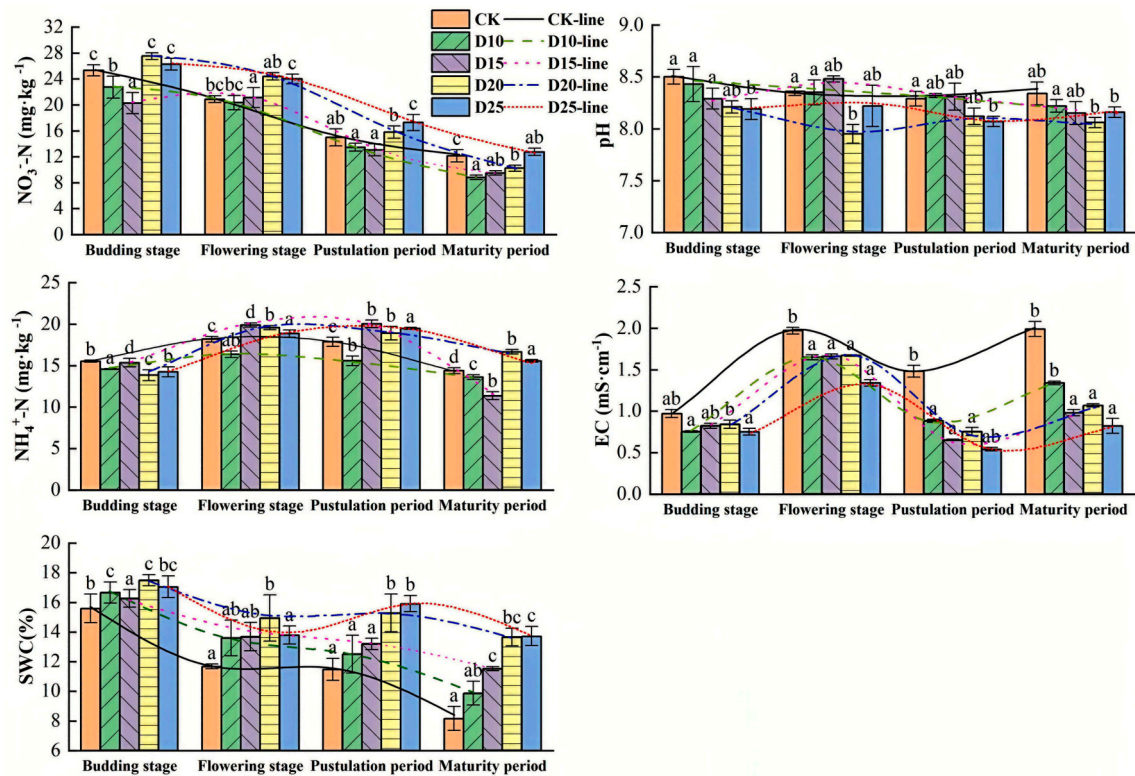


Figure 3. Effect of different treatments on soil physical and chemical properties during reproductive period (different lowercase letters indicate that differences between treatments reached significance ($p < 0.05$)).

3.2. Effect of Drip Irrigation Tape Burial Depth on Soil Fungal Community Diversity in Main Root Zone of Sunflower

The OTUs identified in the sunflower root zone represented over 80% of the total soil fungal population, providing a comprehensive overview of the soil fungal community diversity (Table 3). Compared to the control (CK), the Chao1 index for treatments D10, D15, D20, and D25 increased by 12.7%, 9.3%, 17.4%, and 21.2%, respectively. The Simpson index values for the D10, D15, D20, and D25 treatments increased by 2.5%, 7%, 7%, and 6.3%, respectively, compared with CK. The Shannon indices of the D10, D15, D20, and D25 treatments increased by 1.4%, 8.1%, 12.3%, and 0.5%, respectively, compared to CK. These increases in the Simpson, Shannon, and Chao1 indices across the subsurface drip irrigation treatments indicated enhanced soil fungal community diversity and richness, suggesting that subsurface drip irrigation positively affects soil fungal communities. Spearman's correlation analysis further revealed that the Simpson index was positively correlated with SWC, NO_3^- -N, and NH_4^+ -N (Table 4), indicating the potential influence of soil moisture and nutrient availability on fungal diversity.

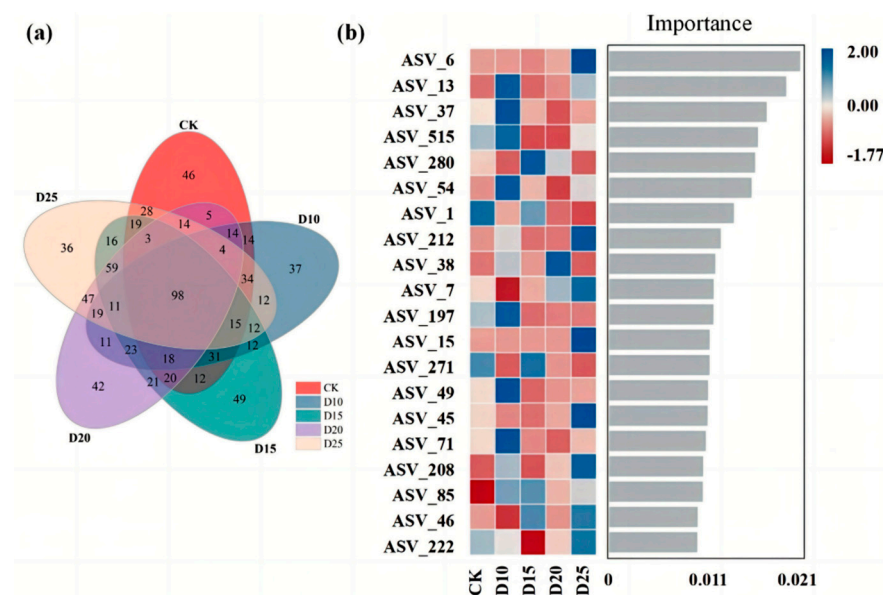
Table 3. Statistics on diversity index of soil fungi under different treatments. (Data are shown as mean $\pm$ standard deviation, and different lowercase letters after values in same column indicate significant differences ($p < 0.05$)).

Treatment	Chao1 Index	Simpson Index	Shannon Index	Coverage Index
CK	314.00 $\pm$ 5.32a	0.80 $\pm$ 0.005c	4.32 $\pm$ 0.044c	86%
D10	292.00 $\pm$ 5.38ab	0.82 $\pm$ 0.003c	4.38 $\pm$ 0.039c	90%
D15	283.67 $\pm$ 5.67b	0.86 $\pm$ 0.000a	4.67 $\pm$ 0.044b	84%
D20	304.53 $\pm$ 5.85ab	0.86 $\pm$ 0.001a	4.85 $\pm$ 0.045a	81%
D25	259.74 $\pm$ 5.34c	0.85 $\pm$ 0.004b	4.34 $\pm$ 0.059c	80%

Table 4. Correlation between soil physicochemical properties and diversity indices (* indicates $p < 0.05$; ** indicates $p < 0.01$).

Item	pH	EC	NH ₄ ⁺ -N	NO ₃ ⁻ -N	SWC
Chao1 Index	0.173	0.745 **	−0.0268	−0.533	−0.706 **
Simpson Index	0.036	−0.021	0.711 **	0.479 *	0.593 *
Shannon Index	0.238	0.036	0.045	0.246	0.321

Across the five treatments, 210 OTUs were detected, with 98 OTUs being shared among the treatments, accounting for 46.67% of the total OTUs (Figure 4). The CK treatment had 46 unique OTUs, primarily ASV100, ASV391, ASV42, ASV675, ASV676, ASV687, and ASV73, comprising 21.90% of the total OTUs. There were 37 D10 treatment-specific OTUs, predominantly consisting of ASV1002, ASV1068, ASV1093, ASV1096, ASV1097, ASV1098, ASV1099, ASV1113, ASV1233, and ASV1234, representing 17.62% of the total OTUs. The D15 treatment displayed 449 unique OTUs, including ASV1453, ASV1457, ASV1458, ASV1459, ASV1462, ASV1464, ASV1468, ASV1470, and ASV1471, comprising 23.33% of the total OTUs. D20 contained 42 unique OTUs, including ASV2011, ASV2012, ASV2014, ASV2016, ASV2019, ASV2021, ASV2026, and ASV2028, representing 20% of the total OTUs. The T4 treatment included 36 OTUs, predominantly ASV2615, ASV2618, ASV2633, ASV2648, ASV3720, ASV3723, ASV3725, and ASV5300, accounting for 17.14% of the total OTUs.

**Figure 4.** Venn diagram of OTUs of soil fungal communities. ((a) shows the number of OUTs for the five treatments, and (b) shows the key ASVs and their importance for the five treatments obtained from the random forest model).

As shown in Figure 5, the principal component analysis (PCA) highlighted the influence of the drip irrigation tape burial depth on the soil fungal community structure. An analysis revealed that the first and second principal components accounted for 23.2% and 17.7% of the variance, respectively, with a cumulative contribution of 40.9%. Notably, the fungal communities in the subsurface drip irrigation treatments exhibited significant separation from those of their CK counterparts, suggesting that subsurface drip irrigation can substantially alter the structure of soil fungal communities compared with surface drip irrigation. PERMANOVA demonstrated that the variations in fungal communities between treatments with varying drip tape burial depths were statistically significant ($p < 0.05$).

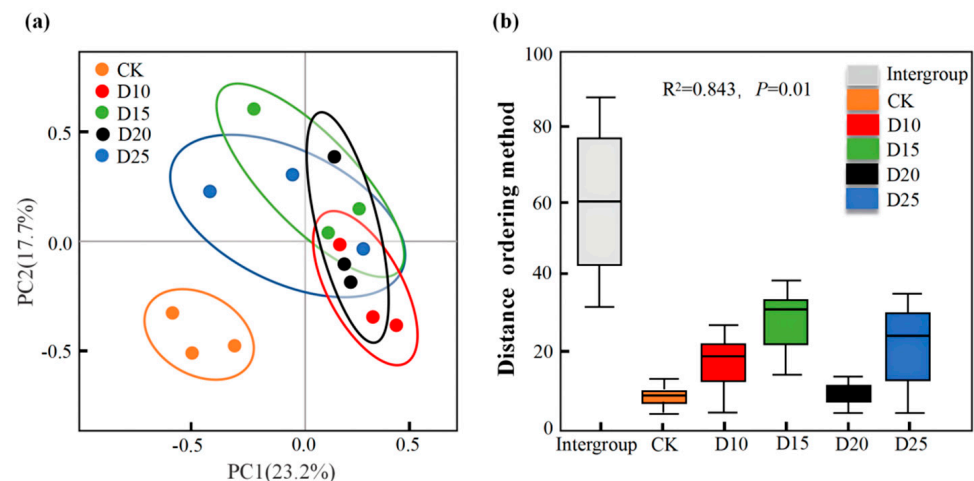


Figure 5. Principal component analysis (PCA) and PERMANOVA analysis of soil fungal community. ((a) shows the effect of drip irrigation tape burial depth on soil fungal community structure using PCA, and (b) shows the differences in fungal communities among different drip irrigation tape burial depth treatments analysed using PERMANOVA).

3.3. Effect of Drip Irrigation Tape Burial Depth on Soil Fungal Community Composition and Structure

The horizontal community composition of soil fungal phyla in the main root zone is shown in Figure 6a. The dominant phylum was Ascomycetes ($87.85\% \pm 5.07\%$), with additional major phyla including Tephritobacterium ($5.64\% \pm 3.92\%$) and Staphylococcus ($1.38\% \pm 0.91\%$). The relative abundance of Ascomycota increased significantly by 5.25% under the D15 treatment compared with the CK treatment. Notably, the relative abundance of *Aspergillus niger* increased by 118.80% under the D20 treatment compared to that in CK. At the fungal genus level, as shown in Figure 6b, the D15 treatment significantly enhanced the relative abundance of several genera within the phylum Ascomycetes, including *Alternaria*, *Lophotrichus*, *Fusarium*, *Plectosphaerella*, *Mycosphaerella*, *Lectera*, and *Nectria*, compared with the CK and D10 treatments. Additionally, the relative abundance of the genus *Plectosphaerella* in the horizontal community, particularly *Mortierella*, increased by 63.32% and 118.42% under the D20 treatment relative to CK. Figure 6c presents the fungal community at the species level, where the D25 treatment significantly increased the relative abundances of *Cladprrhinum_foecundissimu*, *Mortierella foecundissimu*, and *Pseudo gymnoascusroseus* compared to the CK treatment.

3.4. Correlation Analysis Between Soil Physicochemical Properties and Community Structure of Dominant Fungi in Saline–Alkaline Soils

A redundancy analysis (RDA) of soil physicochemical properties and the fungal community structure at the phylum level in the 20–40 cm soil layer conducted during the budding stage revealed that the first and second axes explained 55.31 and 18.76% of the variation in the dominant fungal phylum, respectively. Together, these axes accounted for 74.07% of the observed variation in the fungal phyla (Figure 7). In this study, the soil fungal community structure was primarily influenced by EC, SWC, and NO_3^- -N. A positive correlation was observed between NH_4^+ -N and NO_3^- -N, as indicated by the acute angle between them. The phylum Ascomycetes exhibited a positive correlation with the SWC and soil NH_4^+ -N and a negative correlation with the soil EC and soil NO_3^- -N. Similarly, the phylum Tephritidium was positively correlated with the SWC, NH_4^+ -N, and NO_3^- -N but negatively correlated with the soil EC.

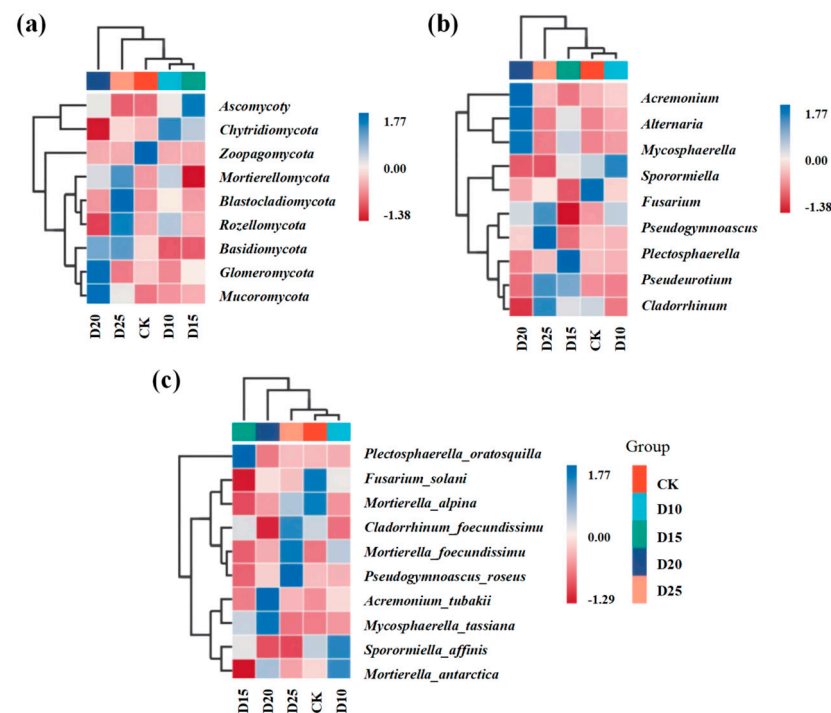


Figure 6. Relative abundance of fungal phylum and genus levels in different treatments ((a) top 10 at phylum level; (b) top 10 at genus level; (c) top 10 at species level).

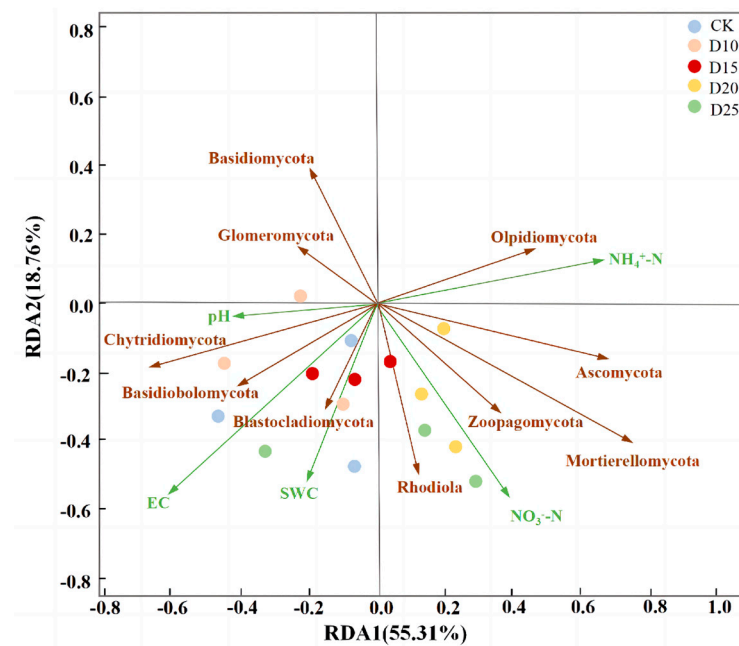


Figure 7. Redundancy analysis between soil fungal communities and physicochemical properties. (RDA of dominant fungal phyla and physicochemical properties, where red arrows indicate soil physicochemical properties, and green arrows indicate dominant fungal phyla).

To elucidate the primary factors affecting the dominant fungal genera, Pearson correlation analyses were performed between the top five dominant fungal genera and the soil physicochemical properties within the main root zone layer during the budding stage. As illustrated in Figure 8, *Alternaria* and *Fusarium* exhibited significant negative correlations with the soil pH, the soil EC demonstrated a significant negative correlation with *Mortierella*, the soil $\text{NH}_4^+\text{-N}$ showed a highly significant positive correlation with *Alternaria*,

and the soil NO_3^- -N displayed a significant positive correlation with *Lophotrichus* and a significant negative correlation with *Botryotrichum*. In conclusion, EC, soil NH_4^+ -N, and soil NO_3^- -N were identified as key environmental factors influencing the diversity of fungal communities.

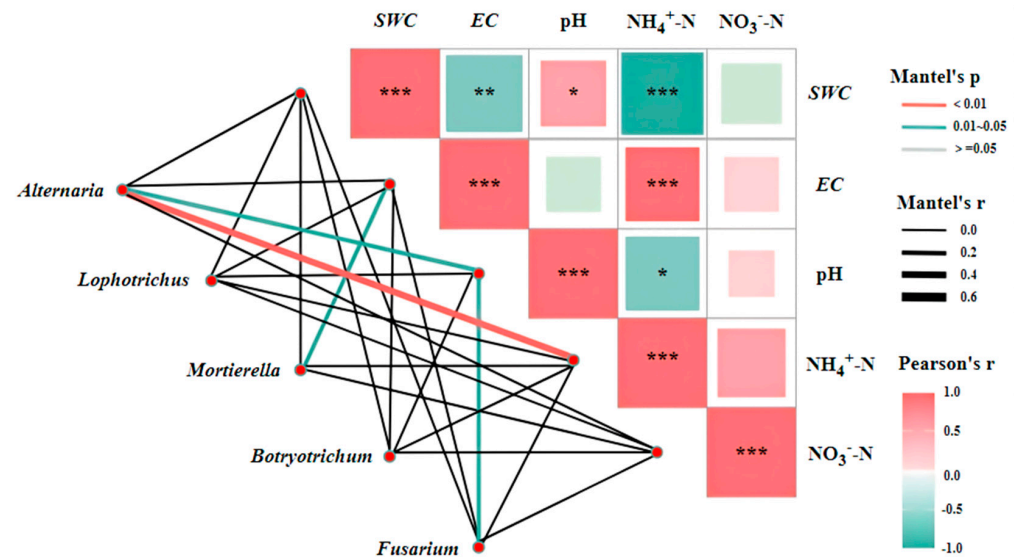


Figure 8. Correlation analysis between soil physical and chemical properties and dominant genera of soil fungi. (* indicates a highly significant correlation at $p < 0.05$; ** indicates a significant correlation at $p < 0.01$; *** indicates a highly significant correlation at $p < 0.001$).

3.5. Structural Equation Modeling of Soil Physicochemical Factors and Soil Fungi

To further analyze the effects of soil physicochemical properties on the soil fungal diversity and community structure at a 20–40 cm depth during the budding stage, five indices were used for model evaluation: the goodness-of-fit index (GFI), adjusted goodness-of-fit index (AGFI), comparative fit index (CFI), canonical fit index (NFI), and root mean square of approximation error (RMSEA) (Table 5). The chi-square degree of freedom ratio was 2.103, falling below the threshold of 3, indicating a good model fit. The RMSEA value was 0.075 under the 0.08 benchmark, and both the CFI and NFI values exceeded 0.9. Additionally, the GFI and AGFI values approached 0.9, indicating that the model was well constructed, and the model results were reliable. Discriminant and convergent validity tests confirmed the adequacy of the model.

Table 5. Fitting index of structural equation model.

Fitting Index	Model Index Value	Standard
Chi square/degree of freedom	2.103	<3
GFI	0.874	>0.9
AGFI	0.884	>0.9
CFI	0.924	>0.9
NFI	0.931	>0.9
RMSEA	0.075	<0.08

The structural equation model SMC yielded an R^2 value of 0.94, indicating that 94% of the variation in the soil fungal composition and diversity was explained by the model (Figure 9). Within the model, the soil NO_3^- -N exhibited a significant direct positive effect on the soil fungal diversity (path coefficient = 0.44) and a direct negative effect on the soil fungal community structure. The soil EC also showed a strong direct positive impact on the soil fungal community composition and diversity with path coefficients of 0.26 and 0.53, respectively. Additionally, subsurface drip irrigation treatments were found to have a substantial indirect positive influence on the soil fungal diversity via changes in the SWC,

soil NO_3^- -N, and soil EC. In contrast, the same irrigation treatment had a weaker indirect positive effect on fungal diversity through modifications in the soil pH and bulk weight.

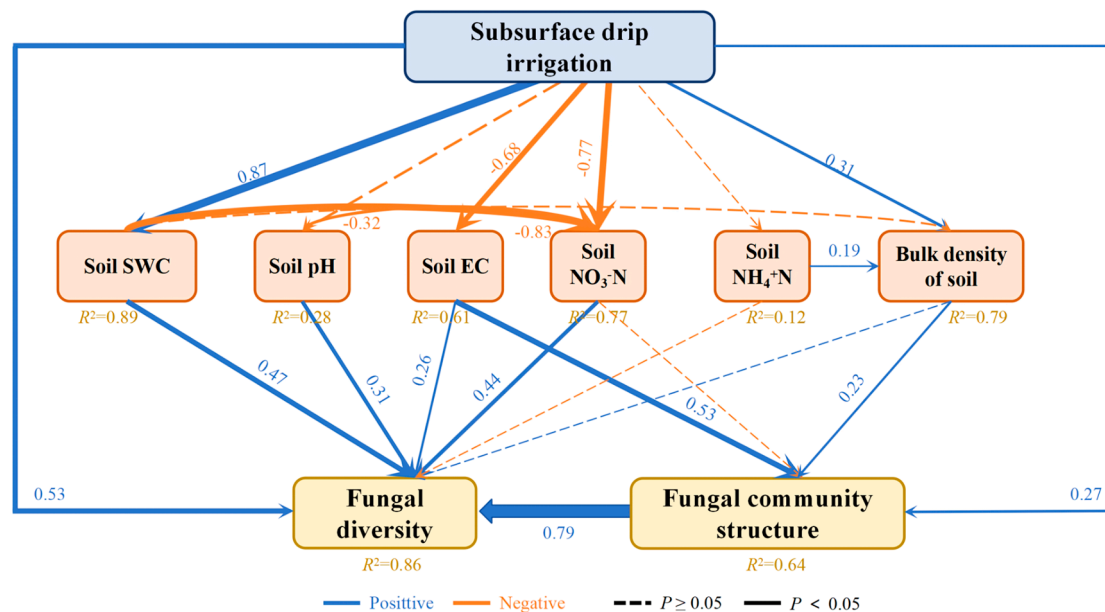


Figure 9. Structural equation model of soil physicochemical factors and soil fungal communities.

4. Discussion

4.1. Effect of Subsurface Drip Irrigation on Soil Physicochemical Properties and Soil Desalination in Main Root Zone of Saline–Alkaline Fields

In subsurface drip irrigation, a drip tape is installed below the soil surface, creating a water distribution pattern that is significantly distinct from that of surface drip irrigation [22]. Soil water distribution and transport also vary considerably depending on the depth of the drip tape [23], and soil water distribution has a substantial impact on environmental factors such as water, nutrients, pH, and temperature in the crop root zone [24,25]. Research has demonstrated that shallowly buried drip irrigation belts are more susceptible to nutrient leaching and secondary soil salinization [26]. Conversely, if the drip irrigation tape is buried too deeply, nutrient dissolution and release may be compromised, hindering thorough leaching and resulting in salinity stress in crops [27]. The optimal burial depths have shown promising results. For example, burying drip irrigation tape at a depth of 20 cm significantly enhances the soil water-holding capacity, thus improving water use efficiency [28]. Similarly, a depth of 30 cm was found to optimize the root-to-crown ratio, boost root vitality [29], facilitate nutrient uptake [30], and improve crop yield and water use efficiency [31]. Changes in soil physicochemical properties also affect soil microbial community dynamics and interactions within the root zone microenvironment, ultimately influencing crop growth and development. Therefore, by examining the effects of subsurface drip irrigation on the physicochemical properties within the main root zone (20–40 cm depth) of sunflowers, we can determine the optimal depth for drip irrigation belt installation. This approach aims to create a favorable water, salt, and nitrogen environment in the main root zone, thereby enhancing sunflower growth.

In the present study, the average soil water content of the D10, D15, D20, and D25 treatments increased by 6.10, 7.78, 8.03, and 8.81%, respectively, at the budding stage compared with the surface drip irrigation treatment (CK). Throughout crop growth, these treatments maintained nutrient absorption, leading to a minimal soil NO_3^- -N content during the maturity period. The EC values for each treatment showed a cyclical pattern: it initially increased, and then decreased, and finally increased again as fertility progressed. Notably, after irrigation at the budding stage, the soil EC in the main root zone of the CK treatment increased the most significantly, with the D10, D15, and D20 treatments exhibiting

greater increases than the D25 treatment. Compared with surface drip irrigation, subsurface drip irrigation effectively reduced soil salinity, with the soil desalination rate in the main rooting zone soil layer ranging from 15.33% to 26.96%. In the 20–40 cm soil layer, the D25 treatment exhibited 82.01%, 43.35%, and 13.43% higher desalination rates than the CK, D10, D15, and D20 treatments, respectively (24.89%). CK showed the lowest soil desalination effect, whereas the most effective soil salt leaching occurred at the drip irrigation depth of 25 cm. These findings suggest that subsurface drip irrigation offers notable advantages over the conventional method of drip irrigation. However, research on the effects of subsurface drip irrigation on soil fungal communities within the main root zone remains limited. Further studies are required to evaluate the influence of subsurface drip irrigation on soil fungi, refine soil management practices, enhance irrigation strategies, and contribute to sustainable water conservation and ecological stability in saline–alkaline fields.

4.2. Effects of Subsurface Drip Irrigation on Soil Fungal Community Structure and Its Diversity in Main Root Zone of Saline–Alkaline Fields

As an important component of soil microorganisms, fungi play essential roles in degrading soil apoplasts, driving nutrient cycling, facilitating energy flow, reflecting soil change processes, and maintaining symbiotic relationships with plants and bacteria [32–34]. Drip irrigation measures directly influence fungal cell permeability by modifying soil moisture conditions [35,36] and indirectly affect fungi by improving soil physicochemical properties [37]. In this study, subsurface drip irrigation decreased the abundance and increased the diversity of soil fungal communities compared to CK. Using high-throughput macrogenomic sequencing, the diversity and abundance of fungal communities across different burial depths in the drip irrigation lines were investigated. The results indicated that subsurface drip irrigation significantly decreased the number of soil fungal OTUs as well as the Chao1 and ACE indices while increasing the Shannon index. This suggests that subsurface drip irrigation enhanced the diversity of the soil fungal community, whereas the abundance of the fungal community was relatively reduced.

Notably, Ascomycetes emerged as the dominant phylum in these soils. The relative abundance of the phylum Ascomycetes was 5.25% higher than that at a surface drip irrigation tape depth of 15 cm and 118.8% higher than that at a surface drip irrigation tape depth of 25 cm. At the genus level, the dominant fungal genera identified were *Fusarium*, *Pollenosporium*, *Pythium*, and *Oleococcus*, which comprised 75.65% of the total relative abundance. Among the dominant genera, *Fusarium* and *Oleococcus* spp. are pathogenic. *Fusarium* spp. are one of the pathogens of soil-borne diseases [38], whereas *Oleococcus* spp. function as transmission media for fungi [39] and are capable of transmitting numerous viruses, and both can cause plant diseases and economic losses. A further analysis revealed that the relative abundance of *Fusarium* spp. was significantly reduced in the drip irrigation line buried at depths of 10–25 cm. Although the difference in *Fusarium* abundance between the 20 and 25 cm depths was not statistically significant, both depths had a markedly lower abundance than that at a 10 cm depth, suggesting that deeper burial of subsurface drip irrigation lines may mitigate the prevalence of pathogenic fungi in saline–alkaline soils.

4.3. Analysis of Factors Affecting Soil Fungi in Main Root Zone of Saline–Alkaline Fields

The physicochemical properties of soil are closely associated with the fungal community structure and diversity. Numerous studies have demonstrated that soil fungal diversity is significantly influenced by factors such as soil salinity, water content, pH, and nutrient levels [40–44]. However, it is challenging to elucidate the complex relationships between these factors using conventional analyses. In this study, structural equation modeling (SEM) was employed to establish connections among soil physicochemical properties, fungal communities, and diversity. The results indicate that the physical and chemical properties of the soil environment significantly affected the structure and diversity of soil fungal communities. These findings identified soil EC as a critical factor affecting fungal

communities in saline soils. RDA further indicated that under subsurface drip irrigation treatments, soil fungal communities were primarily influenced by the soil EC, $\text{NH}_4^+\text{-N}$, and $\text{NO}_3^-\text{-N}$. Correlation analyses demonstrated that the principal factors driving changes in the soil fungal community structure were the soil EC, SWC, and soil $\text{NO}_3^-\text{-N}$. Subsurface drip irrigation notably increased the soil $\text{NO}_3^-\text{-N}$ and $\text{NH}_4^+\text{-N}$ contents, enriching the soil with substrates conducive to microbial growth. Nitrogen availability in soil directly affects crop health, growth, and development [45–48]. Soil organic matter and nutrients are essential for crop growth [49,50], and subsurface drip irrigation not only improves the soil nutrient content [51] but also enhances the soil structure and physicochemical properties, thereby increasing fertilizer efficiency [52,53]. It should be noted that this study only analyzed the overall changes in soil fungal communities without focusing on microorganisms from special functional groups. Future research should explore the unique metabolic pathways, expression pathways, and functional contributions of these specialized microbial groups. In summary, subsurface drip irrigation has demonstrated significant capacity to improve soil physicochemical properties, enhance fungal diversity, and support crop growth and productivity.

5. Conclusions

1. Soil desalination in the primary root zone (20–40 cm soil layer) of sunflower ranged from 15.33% to 26.96% for each treatment of subsurface drip irrigation. When the drip irrigation tape was buried at a depth of 25 cm, the desalination rate in the main root zone of the sunflower increased by 82.01% compared with surface drip irrigation. This depth exhibited the most pronounced desalination effect under consistent water and fertilizer management. Additionally, throughout the reproductive phase, subsurface drip irrigation treatments increased the soil $\text{NO}_3^-\text{-N}$ and $\text{NH}_4^+\text{-N}$ contents and reduced the soil EC in the primary root zone compared to the surface drip irrigation treatments.
2. Subsurface drip irrigation significantly improved the diversity and abundance of soil fungal communities compared to surface drip irrigation. Shannon's index increased by 8.1% and 12.3%, whereas Chao1's index increased by 21.2% and 17.4% when the drip tape was buried at depths of 15 cm and 20 cm, respectively. The dominant phyla identified in the sunflower root zone in the saline–alkaline soils of the experimental site were Ascomycetes, Aspergillus, and Alternaria. The relative abundance of Ascomycetes was 118.8% higher at a burial depth of 25 cm than under surface drip irrigation. Furthermore, subsurface drip irrigation substantially altered the soil fungal community structure, with the soil EC, water content, and $\text{NO}_3^-\text{-N}$ content emerging as key factors influencing the soil fungal community structure and diversity.
3. To improve soil physicochemical properties, enhance soil desalination, and support fungal diversity in the main root zone of sunflower, we recommend the use of subsurface drip irrigation in mildly to moderately saline–alkaline soils of the Tumochuan Plain irrigation area in China. Based on the experimental results, a drip irrigation tape burial depth of 25 cm is optimal for achieving these benefits.

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