Patterns of Yeast Diversity Distribution and its Drivers in Rhizosphere Soil of Hami Melon Orchards in Different Regions of Xinjiang

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Abstract

Background: Yeast is an essential type of microscopic fungus found in the soil. It is vital to develop the resources of yeast to gain a better understanding of its role and potential in maintaining soil ecological balance and providing microbial resources. A special ecological environment is required for the evolution of yeast species. Xinjiang in China has unique climatic conditions with abundant melon and fruit resources. Here, we aimed to evaluate the diversity, community structure, and relationship between yeast species and environmental factors in Hami melon orchards in different regions of Xinjiang, China.

Results: We used Illumina MiSeq high-throughput sequencing analysis to cluster 29,090 yeast sequences into 87 operational taxonomic units (OTUs) with 97% sequence similarity and 47 genera and 73 species. Most sequences (93.16%) belonged to the Basidiomycota; only a few (6.84%) belonged to Ascomycota. We detected 10 dominant genera and 11 dominant species with relative abundances > 1% in all sample sequences. We found that the yeast communities were significantly more diverse in the eastern Xinjiang region than in the southern and northern Xinjiang regions. The most dominant genera in the southern, eastern, and northern Xinjiang regions were *Pseudozyma* (54.77%), *Solicoccozyma* (28.6%), and *Filobasidium* (88.08%), respectively. Redundancy analysis (RDA) results indicated that the main factors influencing the structure of yeast in the study sites were CO, total phosphorus (TP), and total potassium (TK) of the soil.

Conclusion: Our results suggest the presence of diversity and structural differences in yeast species among the southern, eastern, and northern Xinjiang regions. Eastern Xinjiang had the highest community diversity with a more even distribution of species. Differences in the geographical environment and the physicochemical properties of soils were probably the key factors driving yeast diversity and community structure.

Background

Soil is a multifunctional ecosystem that supports the global exchange of materials and energy and is home to various microorganisms [1, 2]. Microorganisms perform diverse functions in the soil, such as participating in biogeochemical cycles, dissolving nutrients, stabilizing soil particles, and controlling pests and diseases [3, 4]. Yeast, a common species found in the soil, plays an important role in maintaining the ecological functioning of the soil, promoting plant growth, and protecting plants from pests and diseases [5]. For example, yeasts isolated from soil (e.g., *Filobasidium magnum*, *Naganishia albida*, and *Lipomyces spp.*) are known to produce extracellular polymeric substances that protect themselves from adverse environmental conditions, as well as promote the formation of soil aggregates to enhance the stability of the soil structure [6–8]. Plant roots support the survival of yeast species by secreting carbohydrates and organic acids (i.e., amino acids and carboxylic acids). Yeast, in turn, contributes to plant growth and development by producing substances, such as Indole-3-acetic acid (IAA), and by dissolving large amounts of nutrients, such as phosphorus and calcium [2, 9–11]. Some soil yeasts are also present as antagonists of pathogens, such as *Verticillium dahliae* and *Pythium aphanidermatum*, and thus protect the plant from diseases [11, 12]. Additionally, several functional yeasts, such as oleaginous yeast and producing high level of 3-hydroxypropionic acid yeast, which are widely used in agriculture, industry, and pharmaceutical production, can be isolated from the soil by culture-dependent methods [13–15]. The size, diversity, and structure of the soil yeast community are known to be influenced by factors, such as soil type, plant species, and geographic location [5]. Moreover, special ecological environments can help yeast species develop tolerance to conditions, such as high/low temperatures, drought, salinity, etc [16]. Therefore, it is vital to study the diversity, community structure, and adaptation strategies of yeast in soils in special environments, which can provide more information regarding yeast resources.

Xinjiang is located in the hinterland of Eurasia, a transition zone between the dry summer zone of Europe and the humid summer belt of East Asia [17]. The special climatic conditions of this region, such as large differences in temperature between day and night and its long hours of daylight, promote the richness of melon and fruit resources [18]. Rich sugar sources in orchard ecosystems promote yeast survival. Moreover, the harsh natural environment of dry summer and cold winter is known to drive yeast evolution, resulting in improved species diversity of yeast [17]. Some studies have used culturable methods to identify 12 genera and 26 species of yeast in the soils from 52 vineyards in 28 autonomous prefectures or counties in Xinjiang, and isolated and identified 12 genera and 17 species of yeast in the soils of peach orchards in northern Xinjiang, followed by the screening of 23 strains of yeast with selenium-rich and protease-producing functions [17, 19]. *Saccharomyces cerevisiae* with excellent fermentation properties was also isolated from pear orchards, pomegranate orchards, and several vineyards in Xinjiang [20–24]. However, little is known about the yeast species in the soil of melon crops in Xinjiang. Hami melons are popular worldwide and are considered to be a national geographic product and the king of melons in China due to their pleasant aroma, crisp taste, sweetness, and color [25]. The central production areas of Hami melon are the Turpan-Hami Basin, northwest and southwest of Tarim Basin, as well as the north slope of Tianshan Mountain. These areas provide more than 100 varieties of Hami melon [26, 27]. Currently, the research on Hami melon yeast is mainly focused on the screening of antagonistic yeast to prevent postharvest diseases and control the bacterial fruit blotch disease [28–32]. However, the diversity and composition of the yeast community in the soil of Hami melon

orchards in different areas of Xinjiang are unclear; this has created a bottleneck for the in-depth understanding of the adaptation mechanism of Hami melon soil yeast species, its beneficial functions, and consequently for the development of yeast resources in Xinjiang.

In recent years, research on the yeast species from orchard soils has been done using the culture-dependent method. This method is useful for isolating diverse yeast cultures, enriching the resources bank of yeast strains, screening of useful strains for food, industry, medicine, etc.; however, only a few yeast species have been identified in soil samples using culture-dependent methods, and the possibility for studying microbial population dynamics in an individual environment is limited compared with culture-independent methods [33, 34]. Illumina MiSeq high-throughput sequencing is an emerging technology, which allows comprehensive and accurate detection of the species composition, generates large data volume with greater coverage and detects low-abundance species in various habitats compared with traditional culture methods [35]. The aim of this study was to quantitatively analyze the diversity and structure of rhizosphere soil yeast communities in Hami melon orchards in different regions of Xinjiang using Illumina MiSeq high-throughput sequencing technique and to explore the factors that influenced the differences in the formation of yeast community structures in different regions. To the best of our knowledge, this is the first study to analyze the yeast diversity in the soil rhizosphere in Hami melon of Xinjiang using high-throughput sequencing. Our results offer new insights into the in-depth understanding of the diversity and structure of yeast communities in the soil of Hami melon orchards in different regions of Xinjiang, providing supplemental information on the yeast resources in Xinjiang orchards.

Results

Richness and diversity

After the removal of chimeras and sequences with low-quality reads, we obtained 2,556,240 high-quality sequences from 54 soil samples. Rarefaction curves for all sequences of most samples were flat (Fig. 2), indicating that sequencing depth per sample was generally reasonable in the study sites. After removal of non-yeast sequences, a total of 29,090 yeast sequences were retained and used for further analysis, which were clustered into 87 OTUs with 97% sequence similarity.

Figure 3 shows the results of the average community richness indices (including Ace index and Chao1 index) and community diversity indices (including Shannon index and Simpson index) in each group. Shannon index and Simpson index are based on inter-group levels, and they indicated that there were significant differences among the three groups; the highest community diversity was found in the EX group, while the lowest is found in the NX groups ($P < 0.05$); while the Ace and Chao1 indices provided opposite results for the community diversity index: the NX groups had the highest community richness, the EX groups had the lowest community richness. On the contrary, there was no significant difference between the Ace and Chao1 indices among the three groups ($P > 0.05$).

Yeast community composition

The numbers of yeast sequences and OTUs detected in samples from the SX, EX, and NX groups were 6600 and 55, 3610 and 59, and 18880 and 50, respectively. We found that 28 0TUs were shared by all three groups; 38 OTUs were shared between SX and EX groups; 35 OTUs were shared between SX and NX groups; 32 OTUs were shared between EX and NX groups (Fig. 4).

We identified 87 OTUs, 47 genera, and 73 species, which belonged to Ascomycota and Basidiomycota. Ascomycota contained 50 OTUs, 23 genera, and 40 species accounting for approximately 6.84% of all yeast sequences, while Basidiomycota had 37 OTUs, 24 genera, and 33 species accounting for approximately 93.16%, with 40 rare species (relative abundance < 0.1%) (Table 1, 2). The predominant genera with relative abundance > 1% were *Filobasidium* (60.37%), *Pseudozyma* (12.94%), *Sporobolomyces_f__Sporidiobolaceae* (4.86%), *Solicoccozyma* (3.61%), *Cutaneotrichosporon* (3.49%), *Naganishia* (2.27%), *Udeniomyces* (2.11%), *Pichia* (1.96%), *Mrakia* (1.32%), and *Wickerhamiella* (1.05%). The predominant species with relative abundance > 1% were *Filobasidium_magnum* (60.37%), *Pseudozyma_prolifica* (12.94%), *Solicoccozyma_aeria* (3.61%), *Sporobolomyces_carnicolor* (3.35%), *Naganishia_albida* (2.27%), *Udeniomyces_sp._1_AK-2015* (2.11%), *Cutaneotrichosporon_curvatus* (1.76%), *Cutaneotrichosporon_cutaneum* (1.72%), *Pichia_kudriavzevii* (1.41%), *Mrakia_robertii* (1.17%), and *Sporobolomyces_ficis* (1.06%). There were 10 genera and 11 species that accounted for > 93.98% and > 91.77% of all yeast sequences, respectively (Fig. 5).

Table 1
OTUs annotation and sequence reads of Ascomycota in different groups

No. taxon	No. OTU	Genus	Species	Sequence reads			Total
				NX groups			
				SX groups	EX groups	NX groups	
1	3097	*Pichia*	*Pichia_kudriavzevii*	2	0	409	1.41%
2	2017	*Pichia*	*Pichia_kluyveri*	29	6	36	0.24%
3	4786	*Pichia*	*Pichia_kluyveri*	0	2	0	0.01%
4	1634	*Pichia*	*[Candida]_ethanolica*	17	36	8	0.21%
5	215	*Pichia*	*[Candida]_rugopelliculosa*	0	10	0	0.03%
6	275	*Pichia*	*[Candida]_rugopelliculosa*	0	2	0	0.01%
7	1457	*Pichia*	*Pichia_barkeri*	0	6	0	0.02%
8	3970	*Pichia*	*Pichia_occidentalis*	0	0	6	0.02%
9	536	*Pichia*	*Pichia_terricola*	0	2	0	0.01%
10	392	*Wickerhamiella*	*Candida_cf._pararugosa_EVN_1238*	11	163	12	0.64%
11	3786	*Wickerhamiella*	*Candida_cf._pararugosa_EVN_1238*	21	6	26	0.18%
12	3567	*Wickerhamiella*	*Candida_cf._pararugosa_EVN_1238*	7	7	0	0.05%
13	2428	*Wickerhamiella*	*Candida_cf._pararugosa_EVN_1238*	0	0	13	0.04%
14	4534	*Wickerhamiella*	*Candida_cf._pararugosa_EVN_1238*	0	2	10	0.04%
15	804	*Wickerhamiella*	*Candida_cf._pararugosa_EVN_1238*	2	3	4	0.03%
16	4357	*Wickerhamiella*	*Candida_cf._pararugosa_EVN_1238*	0	0	2	0.01%
17	4363	*Wickerhamiella*	*[Candida]_pararugosa*	1	2	13	0.05%
18	2336	*Cephaloascus*	*Cephaloascus_fragrans*	230	0	0	0.79%
19	2509	*Candida_o__Saccharomycetales*	*Candida_tunisiensis*	55	20	41	0.40%
20	2476	*Candida_o__Saccharomycetales*	*Candida_tunisiensis*	17	36	5	0.20%
21	1525	*Candida_o__Saccharomycetales*	*Candida_sp._UFMG_DC_166*	12	18	8	0.13%
22	1692	*Candida_o__Saccharomycetales*	*Candida_sp._(Saccharomycetales)*	0	7	0	0.02%
23	1987	*Candida_o__Saccharomycetales*	*Candida_sake*	4	0	0	0.01%
24	3619	*Candida_o__Saccharomycetales*	*Candida_tunisiensis*	4	0	0	0.01%
25	4892	*Aureobasidium*	*Aureobasidium_melanogenum*	0	62	25	0.30%
26	3888	*Aureobasidium*	*Aureobasidium_sp.*	13	2	42	0.20%
27	1063	*Aureobasidium*	*Aureobasidium_pullulans*	7	0	22	0.10%
28	2483	*Exophiala_f__Herpotrichiellaceae*	*Exophiala_equina*	56	12	70	0.47%
29	211	*Schizosaccharomyces*	*Schizosaccharomyces_sp.*	9	72	0	0.28%
30	4907	*Schizosaccharomyces*	*Schizosaccharomyces_japonicus*	0	13	0	0.04%
31	4306	*Candida_f__Debaryomycetaceae*	*Candida_tropicalis*	7	9	34	0.17%
32	2555	*Starmerella*	*Starmerella_bacillaris*	0	3	20	0.08%
33	3015	*Starmerella*	*[Candida]_bombi*	0	0	16	0.06%
34	2865	*Starmerella*	*[Candida]_lactis-condensi*	0	0	3	0.01%

No. taxon	No. OTU	Genus	Species	Sequence reads NX groups			Total
				SX groups	EX groups	NX groups	
35	2477	*Saccharomyces*	*Saccharomyces_cerevisiae*	22	2	16	0.14%
36	1073	*Cyberlindnera*	*Cyberlindnera_jadinii*	11	14	7	0.11%
37	1174	*Hanseniaspora*	*Hanseniaspora_opuntiae*	4	7	5	0.06%
38	288	*Kazachstania*	*Kazachstania_humilis*	0	13	0	0.04%
39	1544	*Torulaspora*	*Torulaspora_delbrueckii*	1	11	0	0.04%
40	4605	*Saturnispora*	*Saturnispora_dispora*	3	0	4	0.02%
41	1538	*Saturnispora*	*Saturnispora_diversa*	3	1	0	0.02%
42	4094	*Meyerozyma*	*Meyerozyma_guilliermondii*	0	1	8	0.03%
43	2401	*Nakazawaea*	*Nakazawaea_ishiwadae*	5	0	0	0.02%
44	3333	*Wickerhamomyces*	*Wickerhamomyces_pijperi*	3	0	0	0.01%
45	2413	*Wickerhamomyces*	*Wickerhamomyces_hampshirensis*	2	0	0	0.01%
46	971	*Geotrichum*	*Geotrichum_sp._YM24346*	5	0	0	0.02%
`47	1178	*Ogataea*	*[Candida]_boidinii*	0	3	0	0.01%
48	2409	*Yamadazyma*	*[Candida]_membranifaciens*	3	0	0	0.01%
49	3046	*Metschnikowia*	*Metschnikowia_sp._JJW-2009a*	0	0	3	0.01%
50	1608	*Kodamaea*	*Kodamaea_ohmeri*	0	2	0	0.01%

Table 2
OTUs annotation and sequence reads of Basidiomycota in different groups

No. taxon	No. OTU	Genus	Species	Sequence reads			Total
				SX groups	EX groups	NX groups	
1	4412	*Filobasidium*	*Filobasidium_magnum*	761	170	16589	60.23%
2	4319	*Filobasidium*	*Filobasidium_magnum*	3	0	40	0.15%
3	1928	*Pseudozyma*	*Pseudozyma_prolifica*	3615	17	131	12.94%
4	731	*Sporobolomyces_f__Sporidiobolaceae*	*Sporobolomyces_carnicolor*	587	388	0	3.35%
5	4669	*Sporobolomyces_f__Sporidiobolaceae*	*Sporobolomyces_ficis*	0	307	0	1.06%
6	2348	*Sporobolomyces_f__Sporidiobolaceae*	*Sporobolomyces_roseus*	6	0	127	0.46%
7	4900	*Solicoccozyma*	*Solicoccozyma_aeria*	4	1029	18	3.61%
8	568	*Cutaneotrichosporon*	*Cutaneotrichosporon_curvatus*	159	142	210	1.76%
9	223	*Cutaneotrichosporon*	*Cutaneotrichosporon_cutaneum*	170	147	182	1.72%
10	616	*Cutaneotrichosporon*	*Cutaneotrichosporon_dermatis*	2	4	0	0.02%
11	4497	*Naganishia*	*Naganishia_albida*	12	404	245	2.27%
12	4935	*Udeniomyces*	*Udeniomyces_sp._1_AK-2015*	232	134	173	1.85%
13	2792	*Udeniomyces*	*Udeniomyces_sp._1_AK-2015*	0	0	74	0.25%
14	3266	*Mrakia*	*Mrakia_robertii*	336	3	0	1.17%
15	3899	*Mrakia*	*Mrakia_sp.*	31	1	7	0.13%
16	4615	*Mrakia*	*Mrakia_sp.*	0	0	6	0.02%
17	565	*Cryptococcus_f__Trichosporonaceae*	*Cryptococcus_sp._MB2*	0	135	0	0.46%
18	358	*Cryptococcus_f__Trichosporonaceae*	*Cryptococcus_sp._TSN-649*	0	18	0	0.06%
19	2651	*Vanrija*	*Vanrija_humicola*	0	0	113	0.39%
20	165	*Vanrija*	*Vanrija_nantouana*	0	3	0	0.01%
21	4952	*Vanrija*	*Vanrija_nantouana*	0	2	0	0.01%
22	3255	*Tausonia*	*Tausonia_pullulans*	20	0	31	0.18%
23	4262	*Tausonia*	*Tausonia_sp._KBP_4496*	5	8	13	0.09%
24	1382	*Hannaella*	*Hannaella_oryzae*	0	60	0	0.21%
25	2914	*Rhodotorula*	*Rhodotorula_mucilaginosa*	2	20	8	0.10%
26	2396	*Rhodotorula*	*Rhodotorula_sp.*	23	3	1	0.09%
27	3166	*Papiliotrema*	*Papiliotrema_fonsecae*	33	2	21	0.19%
28	369	*Kockovaella*	*Kockovaella_vietnamensis*	1	34	0	0.12%
29	1565	*Sterigmatomyces*	*Sterigmatomyces_elviae*	12	6	0	0.06%
30	5011	*Basidioascus*	*Basidioascus_persicus*	0	12	0	0.04%
31	1015	*Cryptococcus_f__Filobasidiaceae*	*Cryptococcus_sp._RP419_8*	6	5	0	0.04%
32	3986	*Dioszegia*	*Dioszegia_zsoltii*	0	0	11	0.04%
33	1010	*Trichosporon*	*Trichosporon_sp.*	7	0	0	0.02%
34	4215	*Kurtzmanomyces*	*Kurtzmanomyces_nectairei*	1	0	5	0.02%
35	4590	*Cystofilobasidium*	*Cystofilobasidium_infirmominiatum*	2	1	3	0.02%

No. taxon	No. OTU	Genus	Species	Sequence reads			Total
				SX groups	EX groups	NX groups	
36	3623	*Saitozyma*	*Saitozyma_aff._flava_DSM_101939*	4	0	0	0.01%
37	2661	*Cystobasidium*	*Cystobasidium_lysinophilum*	0	0	4	0.01%

The most predominant genus *Filobasidium* was detected in the NX groups (88.08%), with SX and EX groups having 11.58% and 4.71%, respectively; *Pseudozyma* was the second most predominant genera: SX groups (54.77%), EX groups (0.47%), and NX groups (0.69%). The relative abundance of *Sporobolomyces_f_Sporidiobolaceae* was 8.98%, 19.25%, and 0.67% in SX, EX, and NX groups, respectively. *Solicoccozyma* was the most dominant genera in the EX groups (28.6%). The most dominant species in SX, EX, and NX groups were *Pseudozyma_prolifica* (54.77%), *Solicoccozyma_aeria* (28.50%), and *Filobasidium_magnum* (88.08%), respectively (Fig. 5 and Table 1–2).

Based on the genus level, the results of abundance difference analysis of the top 10 dominant yeast genera in SX, EX, and NX groups (Fig. 6a) showed that there were 9 dominant genera with significant differences in abundance ($P < 0.05$) among the SX, EX, and NX groups, except for *Udeniomyces* ($P > 0.05$). The abundance of *Cutaneotrichosporon*, *Sporobolomyces_f__Sporidiobolaceae, Solicoccozyma, Wickerhamiella*, and *Naganishia* in EX groups was significantly higher than in the SX and NX groups ($P < 0.05$). At the phylum level, Basidiomycota was considered to be the dominant phylum; the relative abundance of Basidiomycota was significantly higher than that of Ascomycota among all soil samples from three groups, and the relative abundance of Ascomycota in the EX group was significantly higher than that in SX group and NX group (Fig. 6b).

Relationship between yeast communities in samples from different regions

We performed ordination by PCoA at the OTU level (Fig. 7a) to reveal the relationships among different samples. The first principal coordinates axis (PCo1) and the second principal coordinates axis (PCo2) alone explained 24.64% and 10.02% of the variance, respectively. Although there was a slight overlapping among the samples from the three groups on the score plots, most samples from each group were clustered together. Both the OTU level-based PCoA and genus level-based UPGMA clustering analysis (Fig. 7b) indicated that each group of samples had similar yeast community structures. In terms of inter-group analysis, the SX and EX groups were more similar in structure.

Relationship between yeast genus abundance and soil factors

For all three groups, the soil CO value of SX group was significantly higher than EX and NX groups ($P < 0.05$); the levels of OM and TP in EX group were significantly higher than SX and NX groups ($P < 0.05$); the pH, TK, and AK values from the NX group were significantly higher than SX and EX groups ($P < 0.05$); AN content of NX group was significantly lower than SX and EX groups ($P < 0.05$) (Table 3).

Table 3
The physicochemical properties of rhizosphere soil of Hami Melon in different regions

sample group	Sample number	pH	CO mS/cm	OM g/kg	TN g/kg	TP g/kg	TK g/kg	AN mg/kg	AP mg/kg	AK mg/kg
SX	KS1	7.99 ± 0.007ab	1.15 ± 1.732a	7.53 ± 0.087b	0.57 ± 0.002b	0.79 ± 0.011b	18.24 ± 0.168	42.20 ± 0.064b	18.80 ± 0.183b	96.47 ± 2.636ab
	KS2	7.85 ± 0.007ab	1.11 ± 1.732ab	10.07 ± 0.030ab	1.03 ± 0.241ab	0.94 ± 0.005ab	18.25 ± 0.179	71.72 ± 0.356ab	35.81 ± 0.206ab	103.73 ± 2.008ab
	KS3	7.92 ± 0.003ab	1.08 ± 2.963ab	10.08 ± 0.010ab	0.77 ± 0.013ab	0.82 ± 0.004ab	18.12 ± 0.089	62.66 ± 0.384ab	25.25 ± 3.153ab	102.77 ± 0.318ab
	AK1	8.16 ± 0.007a	0.47 ± 5.840ab	12.89 ± 0.079ab	0.97 ± 0.011ab	0.83 ± 0.012ab	19.48 ± 0.130	140.24 ± 0.670ab	31.50 ± 0.369ab	304.60 ± 1.484a
	AK2	8.04 ± 0.003ab	0.45 ± 0.333b	13.77 ± 0.056ab	0.87 ± 0.010ab	0.99 ± 0.011ab	19.12 ± 0.372	54.54 ± 0.557ab	57.25 ± 9.575ab	60.17 ± 0.517b
	AK3	7.51 ± 0.003b	0.65 ± 3.464ab	18.01 ± 0.194a	1.43 ± 0.030a	1.25 ± 0.00780a	19.79 ± 0.081	289.71 ± 4.556a	158.23 ± 1.295a	180.57 ± 0.696ab
	mean	7.91 ± 0.050**B**	0.82 ± 0.074**A**	12.06 ± 0.814**AB**	0.94 ± 0.073	0.94 ± 0.039**B**	18.83 ± 0.174**B**	110.18 ± 20.918**A**	54.47 ± 11.70846	141.38 ± 19.735**B**
EX	TL1	8.17 ± 0.003ab	0.17 ± 0.700ab	9.27 ± 0.240b	0.57 ± 0.010b	1.15 ± 0.013ab	19.19 ± 0.148ab	56.64 ± 0.819b	35.37 ± 0.182ab	136.60 ± 0.874ab
	TL2	7.96 ± 0.003ab	0.37 ± 2.186ab	11.09 ± 0.042ab	0.76 ± 0.011ab	1.13 ± 0.005ab	18.76 ± 0.284ab	75.12 ± 0.508ab	51.63 ± 0.518a	180.37 ± 1.812ab
	TL3	8.24 ± 0.009ab	0.19 ± 2.881ab	9.11 ± 0.027b	0.68 ± 0.014ab	0.90 ± 0.008b	22.88 ± 0.099ab	57.87 ± 0.407ab	16.83 ± 0.305b	172.87 ± 0.982ab
	HM1	8.24 ± 0.012ab	0.19 ± 0.657ab	22.20 ± 0.301ab	1.38 ± 0.011ab	1.06 ± 0.001ab	25.68 ± 0.164a	248.86 ± 4.012ab	25.10 ± 0.432ab	246.87 ± 0.617a
	HM2	7.76 ± 0.003b	1.10 ± 2.517a	43.73 ± 0.038a	2.40 ± 0.011a	1.02 ± 0.003ab	13.46 ± 0.135b	2795.73 ± 10.3201a	46.61 ± 0.143ab	240.07 ± 3.223ab
	HM3	8.25 ± 0.010a	0.09 ± 1.594b	18.72 ± 0.185ab	1.22 ± 0.036ab	1.22 ± 0.020a	21.55 ± 0.093ab	87.33 ± 0.154ab	40.27 ± 0.296ab	71.30 ± 1.386b
	mean	8.10 ± 0.044**B**	0.35 ± 0.083**B**	19.02 ± 2.933**A**	0.17 ± 0.151	1.08 ± 0.025**A**	20.25 ± 0.928**B**	553.59 ± 243.73**A**	35.97 ± 2.90898	174.68 ± 14.584**B**
NX	TC1	8.22 ± 0.003b	0.30 ± 1.764a	13.79 ± 0.165a	1.00 ± 0.007ab	0.91 ± 0.005a	25.41 ± 0.081ab	65.37 ± 0.202ab	30.77 ± 0.157ab	402.27 ± 2.204ab
	TC2	8.23 ± 0.003ab	0.24 ± 1.202ab	13.79 ± 0.152a	1.05 ± 0.005a	0.88 ± 0.009ab	25.47 ± 0.215ab	73.36 ± 0.511a	40.33 ± 0.395a	414.30 ± 1.217a
	TC3	8.46 ± 0.006ab	0.19 ± 3.075ab	9.44 ± 0.109ab	0.66 ± 0.007ab	0.74 ± 0.007ab	24.69 ± 0.098b	40.21 ± 0.293ab	29.89 ± 0.470ab	249.27 ± 1.157ab
	TS1	8.65 ± 0.012a	0.16 ± 7.169b	6.11 ± 0.032ab	0.39 ± 0.004ab	0.57 ± 0.002b	25.20 ± 0.174ab	29.40 ± 0.161b	17.47 ± 0.170b	170.87 ± 1.753ab
	TS2	8.56 ± 0.003ab	0.25 ± 0.882ab	5.23 ± 0.094b	0.35 ± 0.009b	0.60 ± 0.005ab	26.46 ± 0.135a	43.34 ± 0.136ab	26.85 ± 0.248ab	149.17 ± 1.525b
	TS3	8.32 ± 0.038ab	0.18 ± 0.809ab	10.35 ± 0.532ab	0.73 ± 0.017ab	0.69 ± 0.007ab	24.72 ± 0.078b	49.92 ± 0.202ab	20.35 ± 0.078ab	251.67 ± 0.940ab
	mean	8.41 ± 0.039**A**	0.22 ± 0.012**B**	9.76 ± 0.808**B**	0.70 ± 0.065	0.73 ± 0.031**C**	25.32 ± 0.151**A**	50.27 ± 3.634**B**	27.61 ± 1.810	272.92 ± 24.949**A**

Note: Samples abbreviations are as in Fig. 1. Soil physicochemical properties: pH, Conductivity (CO), Organic matter (OM), Total nitrogen (TN), Total phosphorus (TP), Total potassium (TK), Available nitrogen (AN), Available phosphorus (AP), Available potassium (AK). The values of mean ± SE (standard error) of three samples are shown in the table. The different lowercase letters are significantly difference within groups, the different capital letters are significantly difference among groups. (Kruskal-Wallis test, $P < 0.05$)

RDA was used to further identify the specific yeast genus that accounted for the difference observed among the soil samples from the SX, EX, and NX groups and was used to assessment the relationship between soil factors and genera abundance (Fig. 8). The results showed

that the soil samples of SX, EX, and NX groups were noticeably differentiated by the results. The first and second RDA components explained 43.6% of the total yeast genus variation. We screened for three major soil factors associated with yeast communities, including CO, TP, and TK. Amongst them, CO showed a significant positive correlation with the dominant genera *Psedozyma* and *Mrakia* in the SX group; TP showed a significant positive correlation with the dominant genera *Solicoccozyma* in the EX group; AP showed a significant positive correlation with the dominant genera *Filobasidium* and *Pichia* in the NX group.

Discussion

Yeast diversity in rhizosphere soils of Hami melon orchards

The results of this study indicated that Illumina MiSeq high-throughput sequencing technique dramatically accelerated the identification of yeast community in orchard soils; we identified 47 genera and 73 species of yeast using this technique. The yeast diversity in this study was higher than other studies that used culture-dependent methods to detect yeast diversity in orchard soils. Some studies identified only 21 species of 13 genera of yeast and 26 species of 13 genera of yeast in apple orchards of Beijing and Shandong, China, respectively; also, only 60 yeast species were identified from five types of soils (apple, pear, plum, peach, and apricot soils) [36, 37]. Moreover, 16 species of yeast were detected in Cameroon-based agricultural soils using the culture-dependent method [38]. Xinjiang region is characterized by a dry climate, high evaporation, and hot summer, which regulate the evolution of yeast adaptation and increase the overall diversity of yeast [39]. Moreover, tillage practices also partially impact the diversity and composition of soil yeast, such as crop rotation practices that are commonly used in agriculture tend to increase the diversity and abundance of soil microbial communities [40–42]. To avoid pests and diseases, and soil micronutrient deficiencies caused by continuous cropping, crop rotation is commonly used in the Hami melons fields of Xinjiang region [43]. Therefore, we hypothesized that the epiphytic yeast on various plants involved in the rotation increased yeast diversity in Hami melon orchard soils as it entered the soil along with decaying plant material during soil tillage [44]. In our study, we found that Ascomycota was the more diverse phylum, but its abundance was much lower than that of Basidiomycetes (Table 1, 2 and Fig. 6b), which challenged the traditional view that Ascomycetous yeasts were generally more frequent and abundant in agricultural soils, orchards, and grasslands [5, 45, 46]. Other studies revealed that Basidiomycetes were dominant in forest soils [8, 34, 45, 47]. This could have been due to the fact that previous studies that were based on culture methods could only be used to analyze fungi capable of growing on artificial media [48]. Moreover, other studies have shown that the rhizosphere of maize seedlings (20 d) was harbored only by yeasts of the phylum “Ascomycota,” whereas the rhizosphere of senescent plants (90 d) was inhabited by basidiomycetous yeasts [49]. The samples collected in this study were from rhizosphere soil at the ripening stage of Hami melon, which may also account for the higher abundance of basidiomycetous yeasts in this study. Additionally, the rare yeast found in this study accounted for approximately 54.79% of the yeast species in all soil samples of Hami melon, a value within the range of the proportion of rare yeast isolated by other studies from fruit trees, forests, grasslands, and shrub soils [37, 50, 51]. *Tausonia pullulans*, which was detected in this study, produces Indole-3-acetic acid (IAA), which could be developed for future applications in promoting plant growth [11, 52, 53]; *Filobasidium_magnum*, *Naganishia_albida*, and *Cutaneotrichosporon_curvatus* belong to three of the dominant species in this study. The first two are known to produce extracellular polymerase, which contributes to the stability of soil structure, and the last one belongs to the oleaginous yeast, which can be used as a biofuel [15, 54–56].

Differences in yeast diversity and community composition among regions

We found that the yeast community diversity differed significantly among groups based on the differential analysis of the α-diversity index of rhizosphere soil of Hami melon in all three regions of Xinjiang, China. Yeast diversity was highest in eastern Xinjiang and lowest in northern Xinjiang (Fig. 3). Additionally, we found that the distribution and composition of yeast among the three regions were significantly different. Overall, the community structure of samples from southern and eastern Xinjiang was more similar (Fig. 7). These observations might be attributed to the distinct differences between the topographical features of the three regions and their environmental climates. In our sample area, the temperature and precipitation considerably differed among all three regions. The southern (293–322 KJ/cm^2 per year) and eastern Xinjiang (304–307 KJ/cm^2 per year) had relatively similar climates; they received more solar radiation than the northern Xinjiang (262–277 KJ/cm^2 per year), and thus, they were warmer and more evaporative than the northern regions during the same season [57, 58, 59]. However, the precipitation situation was the opposite. Due to the influence of the warm and humid air currents from Siberia, the climate in northern Xinjiang is relatively humid, with a little more rainfall; while humid air currents cannot cross the towering Tianshan Mountains into southern Xinjiang, so the southern Xinjiang region has a more arid climate with little rainfall; for eastern Xinjiang, the complex topographical conditions of three basins is surrounded by four mountains creating a typical extreme arid climate with scarce precipitation and high evaporation [60, 61]. The high level of environmental heterogeneity in eastern Xinjiang also facilitates the generation of genetic mutations and the accumulation of genetic variation in yeast [62]. Additionally, the high quality and strong landrace of Hami melon in eastern Xinjiang also reflect the good interplay between rhizosphere yeast community and plants [26]. The abundance of

Filobasidium_magnum was highest in the northern Xinjiang region and lowest in the eastern Xinjiang region, which was probably related to the local precipitation conditions and soil moisture conditions. The fact that this species was isolated from other habitats with higher humidity and exists as a dominant species also confirms our hypothesis [63, 64]. On the contrary, the most dominant species in the genus *Solicoccozyma*, *Solicoccozyma_aeria*, has a preference for arid environments, mainly in the eastern Xinjiang region [65]. Thus, these two yeast species have the potential to serve as indicator species of ambient humidity in future studies.

Direct driving forces affecting yeast distribution in soil

Climatic factors limit the composition of the yeast community by influencing soil properties and above-ground vegetation properties, such as its biomass, and thus the degree of nutrients available to the substrate in the soil that can be used by the yeast community [47]. In addition to climatic causes that can lead to soil differences, mineral composition, organic matter characteristics, soil formation processes, and management practices can all contribute to soil heterogeneity [66]. Previous studies have shown that soils rich in organic matter generally produce higher yeast colony numbers. For example, yeast abundance is higher in fertilized agricultural soils [5, 8]. Similarly, another study showed the presence of a correlation between yeast abundance and soil factors, such as pH, organic nutrients, and organic phosphorus content [67]. Furthermore, soil yeast species not only respond to the previously described changes in soil pH, organic matter content, and organic phosphorus but also to conductivity and several nutrients, such as N, P, K, Na, and Mg [8, 44, 46, 51, 65]. In our study, soil physicochemical factors were closely related to the differences in yeast community composition in samples from different geographic regions and CO, TP, and TK were detected as the main soil factors that significantly affected yeast composition in different regions (Fig. 8). These three factors were positively correlated with the abundance of dominant yeast genus in the southern, eastern, and northern Xinjiang regions, respectively. This was consistent with the results of previous studies that soil factors were associated with yeast abundance, thus confirming our hypothesis that differences in soil properties among regions were also responsible for the differences in yeast community structure. Furthermore, these results indicated that we could indirectly optimize soil structure and improve the growing environment of Hami melon crops by adjusting the practices of field fertilization based on the relationship between yeast and soil factors. However, the interactions between biotic and abiotic factors in soil ecosystems are complex, and the optimal soil management model requires further investigation.

Conclusions

In this study, we used Illumina high-throughput sequencing technology to study yeast species in the rhizosphere soil of Hami melon orchards in Xinjiang and compared the diversity and structure of yeast communities in southern, eastern, and northern Xinjiang regions to identify the reasons for differences in yeast communities diversity and what stimulated the structural formation of yeast communities. Additionally, we aimed to explain the relationship between soil factors and yeast communities by RDA. Our results showed that yeast resources were abundant in the soil of Hami melon orchards, and there were noticeable differences in yeast diversity and community structure among southern, eastern, and northern Xinjiang. The results of this study provided interesting insights into the relationship between the yeast composition of rhizosphere soil in Hami melon orchards and their geographic regions. The results also demonstrated a strong relationship between soil physicochemical properties and the yeast community. The results of this study will provide a theoretical basis for better exploitation of soil yeast resources and understanding of their adaptive mechanisms.

Materials And Methods

Study sites and sampling

We collected rhizosphere soil samples from Hami melon orchards from six different localities within three regions of Xinjiang between July and August 2019. Study sites included the Kashgar and Aksu Prefecture (SX, Southern Xinjiang), the Turpan and Hami Prefecture (EX, Eastern Xinjiang), and the Shihezi and Changji Prefecture (NX, Northern Xinjiang). Three Hami melon orchards were selected from each prefecture, and soil samples were collected in triplicates from each orchard. In total, 54 rhizosphere soil samples were studied (Fig. 1).

The five-point sampling method was used for sample collection. Briefly, five Hami melons were randomly selected from each orchard to collect soil samples around their roots, at approximately 10 cm depth, using a shovel and sieved to remove plant residues and stones. These soil samples were then mixed and divided into three equal portions. Each sample was stored individually in sterile self-sealing bags and transported to the laboratory in an ice box (< 10 °C). After each soil sample was crushed and filtered using a 2 mm sieve, they were divided into two parts: one part was air dried and used for soil physicochemical analysis; the other part was stored in a -80 °C refrigerator for DNA extraction.

DNA extraction and Illumina MiSeq

E.Z.N.A.® soil DNA Kit (Omega Biotek, USA) was used to extract total DNA from soil samples (0.5 g) following the manufacturer's protocol. The final DNA concentration was detected using a NanoDrop 2000 UV-Vis spectrophotometer (Thermo Scientific, USA). The integrity of the DNA was assessed using 1% agarose gel electrophoresis. The yeast 26S rDNA was amplified with a pair of primers NL1F (forward primer) (5'-GCATATCAATAAGCGGAGGAAAAG-3') and NL2R (reverse primer) (5'-CTTGTTCGCTATCGGTCTC-3') [68]. The PCR reaction system (20 μL) contained 5 × Fast*Pfu* Buffer (4 μL), 2.5 mM dNTPs (2 μL), primer (5 μM; 0.8 μL each), Fast*Pfu* Polymerase (0.4 μL), BSA (0.2 μL), and template DNA (10 ng). The PCR reaction was performed using a thermocycler PCR system as follows: 5 min at 98 °C (denaturation), 30 cycles at 98 °C for 30 s, 52 °C for 30 s, and 72 °C for 45 s, and finally, at 72 °C for 5 min (elongation). The PCR products were analyzed using 2% agarose gel electrophoresis, purified using the AxyPrep DNA Gel Extraction Kit (Axygen Biosciences, USA). The DNA fragments were quantified using QuantiFluor™-ST (Promega, USA) [69]. Equimolar amounts of purified DNA fragments were pooled, and the Illumina MiSeq PE300 platform (Illumina, USA) was used to perform paired-end sequencing (2 × 300) following the protocol by Meiji Biomedical Technology Co. Ltd. (Shanghai, China).

Sequence processing

Raw sequence files were demultiplexed and quality filtered by Trimmomatic and merged by FLASH based on the following criteria: (i) reads with an average quality score < 20 over a 50-bp sliding window were truncated; (ii) sequences with an overlap longer than 10 bp were merged based on their overlapping sequences; (iii) the maximum mismatch ratio allowed in the overlap region of a spliced sequence was 0.2, and non-conforming sequences were screened; (iv) the samples were differentiated according to the barcode and primers at the beginning and end of the sequence; the sequence orientation was adjusted, the number of mismatches allowed by the barcode was 0, and the maximum number of primer mismatches was 2 [70, 71]. Next, we plotted the rarefaction curves to observe the community abundance of each sample and the sequencing data [69, 72]. The coverage estimator (ACE) index, bias-corrected Chao1 richness estimator, and the Shannon and Simpson diversity indices were calculated using the mothur (version v.1.30.2 https://mothur.org/wiki/chao/, https://mothur.org/wiki/ace/, https://mothur.org/wiki/shannon/, http://mothur.org/wiki/Simpson) index analysis with Operational Taxonomic Units (OTUs) at 0.97 level [70, 72]. OTUs were clustered with a 97% similarity cutoff using UPARSE (version 7.1 http://drive5.com/uparse/), and chimeric sequences were identified and removed using the UCHIME software [72, 73]. The classification of each 26S rRNA sequence was analyzed by the Ribosomal Database Project (RDP) Classifier algorithm (version 2.2 http://sourceforge.net/pro-jects/rdp-classifier/) [72]. The NCBI database (National Centre for Biotechnology Information, https://www.ncbi.nlm.nih.gov/public/) database using a confidence threshold of 0.7 [74]. RDA was performed using CANOCO for Windows to study the relationships among samples, soil factors, and genus abundance [69, 70, 72].

Determination of soil chemical properties

Here, we evaluated nine soil physicochemical factors. The soil water suspension was shook for 30 min, followed by measurement of pH using a glass electrode meter. A naturally dried soil sample was mixed with water at a ratio of 1:5 (M/V), and CO was determined using the electrode method. The organic matter (OM) was determined by titration with ferrous sulfate, using o-phenanthroline as the indicator, by adding a potassium dichromate-sulfuric acid solution to a test tube containing the soil samples. The available nitrogen (AN) and total nitrogen (TN) were determined by the Kjeldahl method. The available phosphorus (AP) in the soil was extracted with sodium bicarbonate and then determined using the molybdenum blue method [69]. The available potassium (AK) in the soil was extracted with ammonium acetate and determined by flame photometry. Total phosphorus (TP) and total potassium (TK) were measured by acid solubilization [75, 76].

Data analysis

SPSS Statistics v25.0 software (IBM, USA) was used to analyze the data. All values are presented as mean ± standard error (mean ± SE). Since the data were not normally distributed, Kruskal-Wallis test for independent samples was used to compare the physicochemical properties of the soil among different groups. Differences were taken statistically significant at $P < 0.05$. The dilution curve was drawn using the "vegan" and "ggplot2" packages in R (v4.0.2); Venn diagram using the "VennDiagram" package; community bar graph was plotted using "ggplot2" and "ggalluvial" packages in R (v4.0.2). Since the data did not follow a normal distribution, the Kruskal-Wallis test was used to detect whether there were significant differences in the α diversity index values among the groups. Using community abundance data from samples, we performed hypothesis tests to assess the significance of observed differences based on the Kruskal-Wallis rank-sum test to identify species that showed differences in abundance in different groups (samples) of microbial communities, and plots were drawn using the "ggplot2" package in R (v4.0.2). The UPGMA clustering was done based on the Bray-Curtis distance matrix at the genus level, which was conducted by QIIME (v1.9.1) and drawn by "vegan" and "phangorn" packages in R (v4.0.2). Principal co-ordinate analysis (PCoA) was done based on Bray-Curtis at OTU level to analyze similarities or differences in the community composition of samples using "vegan" and "ape" packages in R (v4.0.2). Redundancy analysis (RDA) was used to evaluate the relationship among soil factors, samples and yeast, and it was calculated using the software Canoco for Windows 5 (Microcomputer Power, USA).

Abbreviations

SX: Southern Xinjiang; EX: Eastern Xinjiang; NX: Northern Xinjiang; OTU: Operational Taxonomic Units; CO: Conductivity, OM: Organic matter, TN: Total nitrogen, TP: Total phosphorus, TK: Total potassium, AN: Available nitrogen, AP: Available phosphorus (AP), AK: Available potassium; RDA: Redundancy analysis.

Declarations

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Availability of data and materials

The datasets used and analyzed within the current study are available from the corresponding author on reasonable request.

Authors' contributions

ShanShan Zhu designed and performed the experiments, analyzed the data, and drafted the manuscript. YongHui Lei helped design experiments, analyzed the data and drafted the manuscript. Chong Wang performed sample collection, DNA extraction, PCR amplification and analyzed part of the data. YuMei Wei performed sample collection, and soil chemical property analysis. ChunCheng Wang performed sample collection, DNA extraction and PCR amplification. YanFei Sun designed and performed the experiments and analyzed data. All authors read and approved the final manuscript.

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Ethics approval and consent to participate

Ethical approval is not applicable in the case of the study. However, the collection of the soil samples from hami melon orchards was verbally permitted by each farm owner.

Consent for publication

Not Applicable.

Competing interests

The authors declare that they have no competing interests.

References

1. Welbaum G, Sturz A, Dong Z, Nowak J: Managing Soil Microorganisms to Improve Productivity of Agro-Ecosystems. Critical Reviews in Plant Sciences - CRIT REV PLANT SCI. 2004; 23:175–193. https://doi.org/10.1080/07352680490433295.
2. Amprayn K-o, Rose M, Kecskés M, Pereg L, Nguyen H, Kennedy I: Plant growth promoting characteristics of soil yeast (Candida tropicalis HY) and its effectiveness for promoting rice growth. Applied Soil Ecology. 2012; 61:295–299. https://doi.org/10.1016/j.apsoil.2011.11.009.
3. McCauley A, Jones C, Jacobsen J: Basic soil properties. Montana State Univ Extension Serv. 2005:1–12.
4. Turrini A, Agnolucci M, Palla M, Tomé E, Tagliavini M, Scandellari F, Giovannetti M: Species diversity and community composition of native arbuscular mycorrhizal fungi in apple roots are affected by site and orchard management. Applied Soil Ecology. 2017; 116. https://doi.org/10.1016/j.apsoil.2017.03.016.
5. Vadkertiová R, Dudášová H, Balaščáková M: Yeasts in Agricultural and Managed Soils. In.; 2017: 117–144. https://doi.org/10.1007/978-3-319-62683-3_4.
6. Deng J, Orner E, Chau J, Anderson E, Kadilak A, Rubinstein R, Bouchillon G, Goodwin R, Gage D, Shor L: Synergistic effects of soil microstructure and bacterial EPS on drying rate in emulated soil micromodels. Soil Biology and Biochemistry. 2015; 83:116. https://doi.org/10.1016/j.soilbio.2014.12.006.

7. Simulated in situ competitive ability and survival of a representative soil yeast, Cryptococcus albidus. Microbial ecology. 1995; 30:309–320. https://doi.org/10.1007/BF00171937.
8. Botha A: Yeasts in Soil. In: Biodiversity and Ecophysiology of Yeasts. Edited by Péter G, Rosa C. Berlin, Heidelberg: Springer Berlin Heidelberg; 2006: 221–240. https://doi.org/10.1007/3-540-30985-3_11.
9. Berendsen R, Pieterse C, Bakker P: The rhizosphere microbiome and plant health. Trends in plant science. 2012; 17:478–486. https://doi.org/10.1016/j.tplants.2012.04.001.
10. Fu S-F, Sun P-F, Lu H-Y, Wei J-Y, Xiao H-S, Fang W-T, Cheng B-Y, Chou J-Y: Plant Growth–Promoting Traits of Yeasts Isolated from the Phyllosphere and Rhizosphere of Drosera spathulata Lab. Fungal Biology. 2016; 120. https://doi.org/10.1016/j.funbio.2015.12.006.
11. Mestre M, Fontenla S, Bruzone M, Fernández N, Dames J: Detection of plant growth enhancing features in psychrotolerant yeasts from Patagonia (Argentina): Plant growth promoter yeasts from Patagonia. Journal of Basic Microbiology. 2016; 56. https://doi.org/10.1002/jobm.201500728.
12. Azcón R, Perálvarez M, Roldán A, Barea J-M: Arbuscular Mycorrhizal Fungi, Bacillus cereus, and Candida parapsilosis from a Multicontaminated Soil Alleviate Metal Toxicity in Plants. Microbial ecology. 2009; 59:668–677. https://doi.org/10.1007/s00248-009-9618-5.
13. Tanimura A, Takashima M, Sugita T, Endoh R, Kikukawa M, Yamaguchi S, Sakuradani E, Ogawa J, Ohkuma M, Shima J: Cryptococcus terricola is a promising oleaginous yeast for biodiesel production from starch through consolidated bioprocessing. Scientific reports. 2014; 4:4776. https://doi.org/10.1038/srep04776.
14. Li W, Wang T, Dong Y, Li T: Screening, identification, and low-energy ion modified breeding of a yeast strain producing high level of 3-hydroxypropionic acid. MicrobiologyOpen. 2019; 9. https://doi.org/10.1002/mbo3.956.
15. Sitepu I, Garay L, Sestric R, Levin D, Block D, German B, Boundy-Mills K: Oleaginous yeasts for biodiesel: Current and future trends in biology and production. Biotechnology Advances. 2014; 32. https://doi.org/10.1016/j.biotechadv.2014.08.003.
16. Wei D. Significance and recommendation of Xinjiang special environmental microorganism resources research and exploitation. Xingjiang Agricultural Sciences. 2004;41(s1):1–4. https://doi.org/10.3969/j.issn.1001-4330.2004.z1.001.
17. Wang QG. Studies on Species Diversity and Application of Wild Yeast in Xinjiang. Shandong Institute of Light Industry, Jinan, China, 2007.
18. Chen YL. Melon and Fruit Plant Resources in Xinjiang. Jiangxi Forestry Science and Technology. 1996;(01):45. https://doi.org/CNKI:SUN:JXLI.0.1996-01-016.
19. Qiqi W, Yao Z, Yonghui L, Li F, Jie X, Yanfei SJBR: Diversity of culturable yeast and screening of functional yeast in soils of flat peach trees of different ages in Shihezi. 2019. https://doi.org/10.14188/j.ajsh.2019.01.007.
20. Jun-Hu W, Li-Juan Y, Zuo-Shan FJL-m: Breeding of the First-rated Kuerle Pear Wine Yeast. 2003. https://doi.org/10.3969/j.issn.1002-8110.2003.06.010.
21. Xiaoji Z, Shunli W, Xuewei S, Chunhui SJJoFS, Biotechnology: Screening, Identification and Fermentation Characteristics of Yeast from the Vineyard of the Sixth Division in Xinjiang Province. 2015. https://doi.org/10.3969/j.issn.1673-1689.2015.10.017.
22. Wei Y, Zou W, Wang W, Zhang Y, Wang D, Yun WU, Xue J, University XA. Screening of High-Quality Yeast Strains in Xinjiang Wine-Producing Regions. Liquor-Making Science & Technology. 2017;(05):42–47. https://doi.org/10.13746/j.njkj.2015442.
23. Jin ZZ, Wang N, Bao HF, Hou M, Chen FQ. Screening and Performance Testing of Saccharomyces cerevisiae for High Ethanol Production. Gansu Agriculture. 2017;(01):34–37. https://doi.org/10.15979/j.cnki.cn62-1104/f.2017.01.010.
24. Liu YQ, Huo XD, Shi CW, Lou K. Screening, Identification and Fermentation Performance of Yeast Used for Production of Pomegranate Wine. Food science. 2009;30(11):211–215. https://doi.org/10.3321/j.issn:1002-6630.2009.11.047.
25. Zhao XX, Ning M, Zhang Q, Cai WC, Shan CH, Tang FX. Isolation and identification of pathogenic microorganisms causing post-harvest spoilage in Hami melo. Food Science. 2020;1–20. https://doi.org/10.7506/spkx1002-6630-20200102-023.
26. Wang J, Jiang M, Yuchao LI, Guangjun LIJAAR: Influence of Climatic Conditions on Planting of Hami Melon. 2018; v.10(02):86–90. https://doi.org/10.19601 /j.cnki.issn1943-9903.2018.2.019.
27. Lim D: Cucumis melo L. (Reticulatus Group) 'Hami melon'. In.; 2012: 231–234. https://doi.org/10.1007/978-94-007-1764-0_36.
28. Pei SQ, Tong JM, Kou XT, Wang XT. Biological Control of Postharvest Diseases of Postharvest Hami-melon Using Antagonistic Yeasts. Anhui Agricultural Science Bulletin. 2009;15(01):134-5,75. https://doi.org/10.16377/j.cnki.issn1007-7731.2009.01.076.
29. Zhi-Hao W, Chun-Hui S, Jian W, Cai B, Li-Fang Z, Jing-Yun W, Pei-Pei FJAPoFPP: Antagonistic Yeast Adding Method on Preservation Effect of Cantaloupe. 2013. https://doi.org/10.3969/j.issn.1671-9646(X).2013.03.009.
30. Li BK, Mao XY, Chen J, Zhang J. Identification of Yeast From the Melon Juice of Spontaneous Fermentation. Liquor-making Science & Technology. 2009;36(01):41–43. https://doi.org/10.3969/j.issn.1002-8110.2009.01.015.

31. Shen T, Chen HZ, Yang J. Selection of Aroma-producing Yeast for Hami Melon Wine and Its Properties. Liquor-making Science & Technology. 2004;(03):36–8. https://doi.org/10.3969/j.issn.1001-9286.2004.03.008.
32. Wang X, Li G, Jiang D, Huang H-C: Screening of plant epiphytic yeasts for biocontrol of bacterial fruit blotch (Acidovorax avenae subsp. citrulli) of hami melon. Biological Control. 2009; 50:164–171. https://doi.org/10.1016/j.biocontrol.2009.03.009.
33. Hrynkiewicz K: Belowground Microbiota and the Health of Tree Crops. Frontiers in Microbiology. 2018; 9. https://doi.org/10.3389/fmicb.2018.01006.
34. Yurkov A: Yeasts in Forest Soils. In.; 2017: 87–116. https://doi.org/10.1007/978-3-319-62683-3_3.
35. Chen Z, Xia T, Wang D, Wu G, Liu J, Zhang Y, Ren Z, Jin S, Peng S, Niu, Y. Diversity Analysis of Endophytic Fungi in Mentha Using Illumina MiSeq High-throughput Sequencing Technology. Medicinal Plant. 2016;7(Z1):46–50. https://doi.org/CNKI:SUN:MDPT.0.2016-Z1-015.
36. Chen R, Jang YM, Wei SC, Wang QM. Species diversity of yeasts in Fuji apple orchards. Mycosystema. 2012;31(06):837–844. https://doi.org/10.13346/j.mycosystema.2012.06.004.
37. Vadkertiová R, Dudášová H, Stratilová E, Balaščáková M: Diversity of yeasts in the soil adjacent to fruit trees of the Rosaceae family. Yeast (Chichester, England). 2019; 36(10):617–631. https://doi.org/10.1002/yea.3430.
38. Aljohani R, Samarasinghe H, Ashu T, Xu J: Diversity and relationships among strains of culturable yeasts in agricultural soils in Cameroon. Scientific reports. 2018; 8(1):15687. https://doi.org/10.1038/s41598-018-34122-2.
39. Ding YH, Wang SR. Overview of Climate and ecological environment in Northwest China. Xinjiang Meteorologia. 2001;(02):16. https://doi.org/CNKI:SUN:XJQX.0.2001-02-005.
40. Yurkov AM: Yeasts of the soil - obscure but precious. Yeast (Chichester, England). 2018; 35(5):369–378. https://doi.org/10.1002/yea.3310.
41. Singh B, Dawson L, Macdonald C, Buckland S: Impact of biotic and abiotic interaction on soil microbial communities and functions: A field study. Applied Soil Ecology. 2009; 41:239–248. https://doi.org/10.1016/j.apsoil.2008.10.003.
42. Spehn E, Joshi J, Schmid B, Alphei J, Körner C: Plant diversity and soil heterotrophic activity in experimental grassland systems. Plant and Soil. 2000; 224:217–230. https://doi.org/10.1023/A:1004891807664.
43. He X. Study on Standardization Production Base Model of Hami Melon in Xinjiang. Xinjiang Agricultural University. 2012. https://doi.org/10.7666/d.D236888.
44. Botha A: The importance and ecology of yeasts in soil. Soil Biology & Biochemistry - SOIL BIOL BIOCHEM. 2011; 43:1–8. https://doi.org/10.1016/j.soilbio.2010.10.001.
45. Yurkov A, Kemler M, Begerow D: Assessment of yeast diversity in soils under different management regimes. Fungal Ecology. 2012; 5:24–35. https://doi.org/10.1016/j.funeco.2011.07.004.
46. Sláviková E, Vadkertiová R: The diversity of yeasts in the agricultural soil. J Basic Microbiol. 2003; 43(5):430–436. https://doi.org/10.1002/jobm.200310277.
47. Yurkov AM, Röhl O, Pontes A, Carvalho C, Maldonado C, Sampaio JP: Local climatic conditions constrain soil yeast diversity patterns in Mediterranean forests, woodlands and scrub biome. FEMS yeast research. 2016; 16(1):fov103. https://doi.org/10.1093/femsyr/fov103.
48. Di Menna ME: The isolation of yeasts from soil. Journal of general microbiology. 1957; 17(3):678–688. https://doi.org/10.1099/00221287-17-3-678.
49. Gomes NC, Fagbola O, Costa R, Rumjanek NG, Buchner A, Mendona-Hagler L, Smalla K: Dynamics of fungal communities in bulk and maize rhizosphere soil in the tropics. Applied and environmental microbiology. 2003; 69(7):3758–3766. https://doi.org/10.1128/aem.69.7.3758-3766.2003.
50. França L, Sannino C, Turchetti B, Buzzini P, Margesin R: Seasonal and altitudinal changes of culturable bacterial and yeast diversity in Alpine forest soils. Extremophiles: life under extreme conditions. 2016; 20(6):855–873. https://doi.org/10.1007/s00792-016-0874-2.
51. Vishniac HS: A multivariate analysis of soil yeasts isolated from a latitudinal gradient. Microb Ecol. 2006; 52(1):90–103. https://doi.org/10.1007/s00248-006-9066-4.
52. Limtong S, Kaewwichian R, Yongmanitchai W, Kawasaki H: Diversity of culturable yeasts in phylloplane of sugarcane in Thailand and their capability to produce indole-3-acetic acid. World journal of microbiology & biotechnology. 2014; 30(6):1785–1796. https://doi.org/10.1007/s11274-014-1602-7.
53. Streletskii R, Kachalkin A, Glushakova A, Demin V, Chernov I: Quantitative determination of indole-3-acetic acid in yeasts using high performance liquid chromatography—tandem mass spectrometry. Microbiology. 2016; 85:727–736. https://doi.org/10.1134/S0026261716060187.

54. Vishniac HS: Simulated in situ competitive ability and survival of a representative soil yeast, Cryptococcus albidus. Microb Ecol. 1995; 30(3):309–320. https://doi.org/10.1007/bf00171937.
55. Pan L-X, Yang D-F, Shao L, Li W, Chen G-G, Liang Z-Q: Isolation of the Oleaginous Yeasts from the Soil and Studies of Their Lipid-Producing Capacities. Food Technology and Biotechnology. 2009; 47. https://doi.org/10.1016/j.fm.2008.11.001.
56. García-Martos P, Marín P, Hernández-Molina JM, García-Agudo L, Aoufi S, Mira J: Extracellular enzymatic activity in 11 Cryptococcus species. Mycopathologia. 2001; 150(1):1–4. https://doi.org/10.1023/a:1010868223582.
57. Li HB, Suo FY. Progress in the research on microorganism resources in special ecological environments of Xinjiang. Agricultural Research in the Arid Areas. 2004;22(4):198–202. https://doi.org/10.3321/j.issn:1000-7601.2004.04.039.
58. Liao XP, He YP, Qin R. Influence of climatic conditions on the quality of cantaloupe in Numao Lake, Xinjiang. Science and Technology Innovation Herald. 2010;(26):124. https://doi.org/10.3969/j.issn.1674-098X.2010.26.105.
59. Lin C, Qin Y, Chen QJ, Lin CY. Climate Characteristics and Protected Area Vegetable Production in Xinjiang. Chinese Vegetables. 1994;1(4): 16–20. http://www.cnveg.org/CN/Y1994/V1/I4/16.
60. Xu GQ, Wei WS: Climate change of Xinjiang and its impact on eco-environment. Arid Land Geography. 2004; 27:14–18. https://doi.org/10.13826/j.cnki.cn65-1103/x.2004.01.003.
61. Wang WT, Tian B, Li J. Climate Change in Eastern Region of Xinjiang in the Past 50 Years and Its Effects on the Local Ecological Environment. Research of Soil and Water Conservation. 2014;21(05):249–54. https://doi.org/10.13869/j.cnki.rswc.2014.05.045.
62. Pan HX, Chen ZM, Wang LX. Studies on the Micro-Organisms Resources in Special Ecological Environment in Xinjiang Turpan Basin. Journal of Arid Land Resources & Environment. 2002;16(4):91–94. https://doi.org/10.3969/j.issn.1003-7578.2002.04.019.
63. Guo XF, De J, Long QW, Bai BJ, Wang HJ, Zeng YP. Spatial dynamics of yeast community and its relationship with environmental factors in Lhalu Wetland, Tibet. Acta Microbiologica Sinica. 2018;58(07):1167–1181. https://doi.org/10.13343/j.cnki.wsxb.20170311.
64. Han L. Diversity and spatial distribution of fungi in Dianchi Lake of Yunnan plateau. Yunnan University. 2018.
65. Chernov I: [The latitude-zonal and spatial-successional trends in the distribution of yeasts]. Zhurnal obshchei biologii. 2005; 66(2):123–135.
66. Lag J, Hadas A, Fairbridge R: History of Soil Science. In.; 2008: 307–312. https://doi.org/10.1007/978-1-4020-3995-9_268.
67. Turchetti B, Goretti M, Branda E, Diolaiuti G, D'Agata C, Smiraglia C, Onofri A, Buzzini P: Influence of abiotic variables on culturable yeast diversity in two distinct Alpine glaciers. FEMS microbiology ecology. 2013; 86(2):327–340. https://doi.org/10.1111/1574-6941.12164.
68. Liu KP, Wei YM, Xiong J, Sun YF, Lei YH. Analysis of diversity of endobiotic yeasts isolated from Locusta migratoria manilensis and Ischiodon scutellaris Fabricius. Guangdong Agricultural Sciences. 2018;45(09):90–95. https://doi.org/10.16768/j.issn.1004-874X.2018.09.015.
69. Zhang H, Wang Y, Chen S, Zhao Z, Feng J, Zhang Z, Lu K, Jia J: Water Bacterial and Fungal Community Compositions Associated with Urban Lakes, Xi'an, China. International Journal of Environmental Research and Public Health. 2018; 15:469. https://doi.org/10.3390/ijerph15030469.
70. Zhang H, Feng J, Chen S, Li B, Raju S, Zhao Z, Jia J, Wang Y, Kang P: Disentangling the Drivers of Diversity and Distribution of Fungal Community Composition in Wastewater Treatment Plants Across Spatial Scales. Frontiers in Microbiolo.gy. 2018; 9:1291. https://doi.org/10.3389/fmicb.2018.01291
71. Magoč T, Salzberg SL: FLASH: fast length adjustment of short reads to improve genome assemblies. Bioinformatics (Oxford, England). 2011; 27(21):2957–2963. https://doi.org/10.1093/bioinformatics/btr507.
72. Zhang H, Jia J, Chen S, Huang T, Wang Y, Zhao Z, Feng J, Hao H, Li S, Ma X: Dynamics of Bacterial and Fungal Communities during the Outbreak and Decline of an Algal Bloom in a Drinking Water Reservoir. Int J Environ Res Public Health. 2018; 15(2). https://doi.org/10.3390/ijerph15020361.
73. Edgar RC, Haas BJ, Clemente JC, Quince C, Knight R: UCHIME improves sensitivity and speed of chimera detection. Bioinformatics (Oxford, England). 2011; 27(16):2194–2200. https://doi.org/10.1093/bioinformatics/btr381.
74. Li J, Hu W, Huang X, Xu Y: Investigation of yeast population diversity and dynamics in spontaneous fermentation of Vidal blanc icewine by traditional culture-dependent and high-throughput sequencing methods. Food research international (Ottawa, Ont). 2018; 112:66–77. https://doi.org/10.1016/j.foodres.2018.06.011.
75. Sanguin H, Sarniguet A, Gazengel K, Moënne-Loccoz Y, Grundmann GL: Rhizosphere bacterial communities associated with disease suppressiveness stages of take-all decline in wheat monoculture. The New phytologist. 2009; 184(3):694–707. https://doi.org/10.1111/j.1469-8137.2009.03010.x.
76. Bao SD. Soil agro-chemistrical analysis. Beijing: China Agriculture Press. 2007; 268–270, 389–391.

Figures

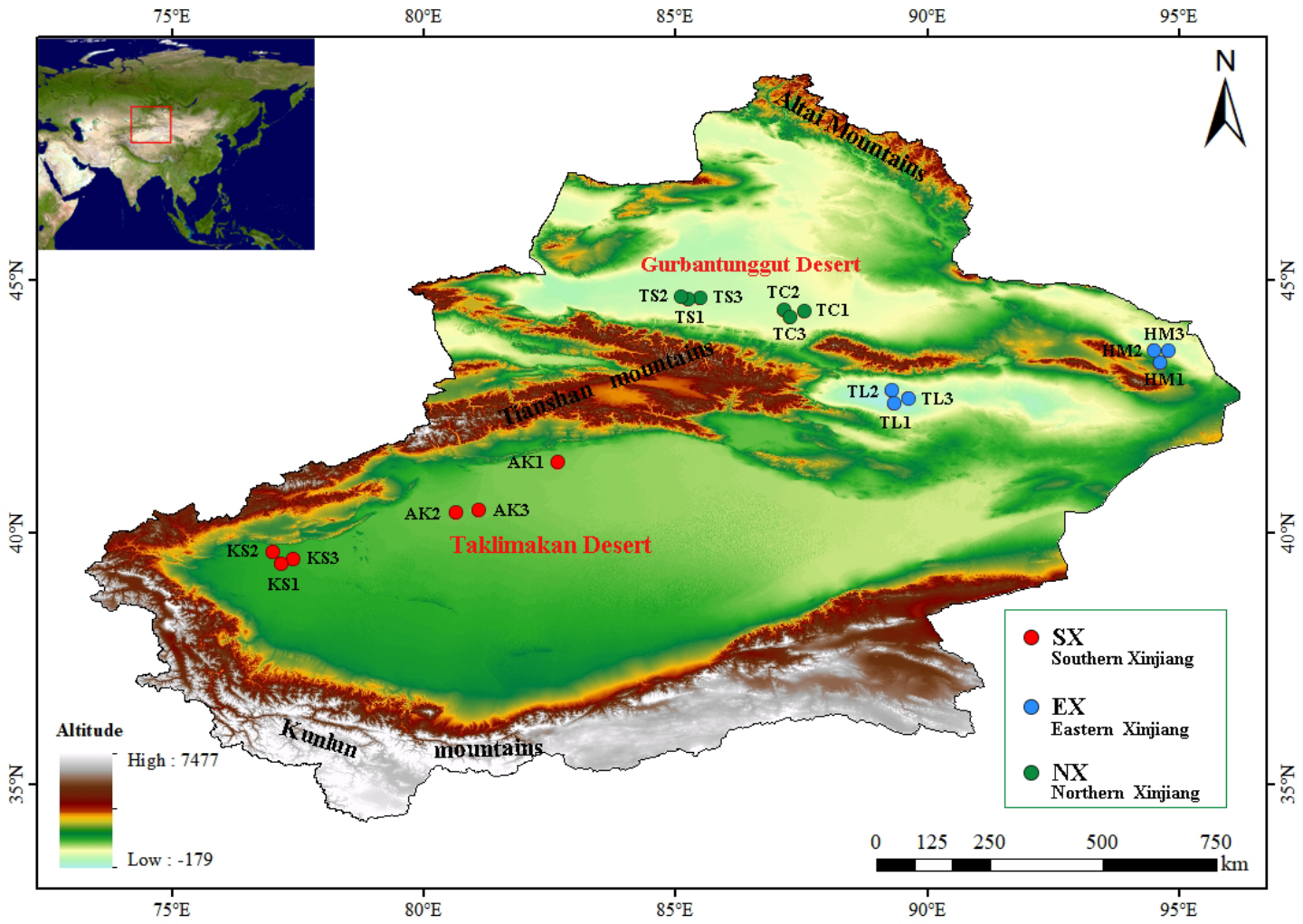

Figure 1

Sampling locations and geographic distribution of all rhizosphere soil samples of Cucumis melo var. saccharinus in Xinjiang, China. Here, SX, EX, and NX represent the sampled areas of Cucumis melo var. saccharinus in Southern Xinjiang, Eastern Xinjiang, and Northern Xinjiang respectively; KS, AK, TL, HM, TC and TS represents the sampled locations in Kashgar and Aksu Prefecture of Southern Xinjiang, Turpan and Hami Prefecture of Eastern Xinjiang, Changji and Shihezi Prefecture of Northern Xinjiang, respectively. Note: The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.

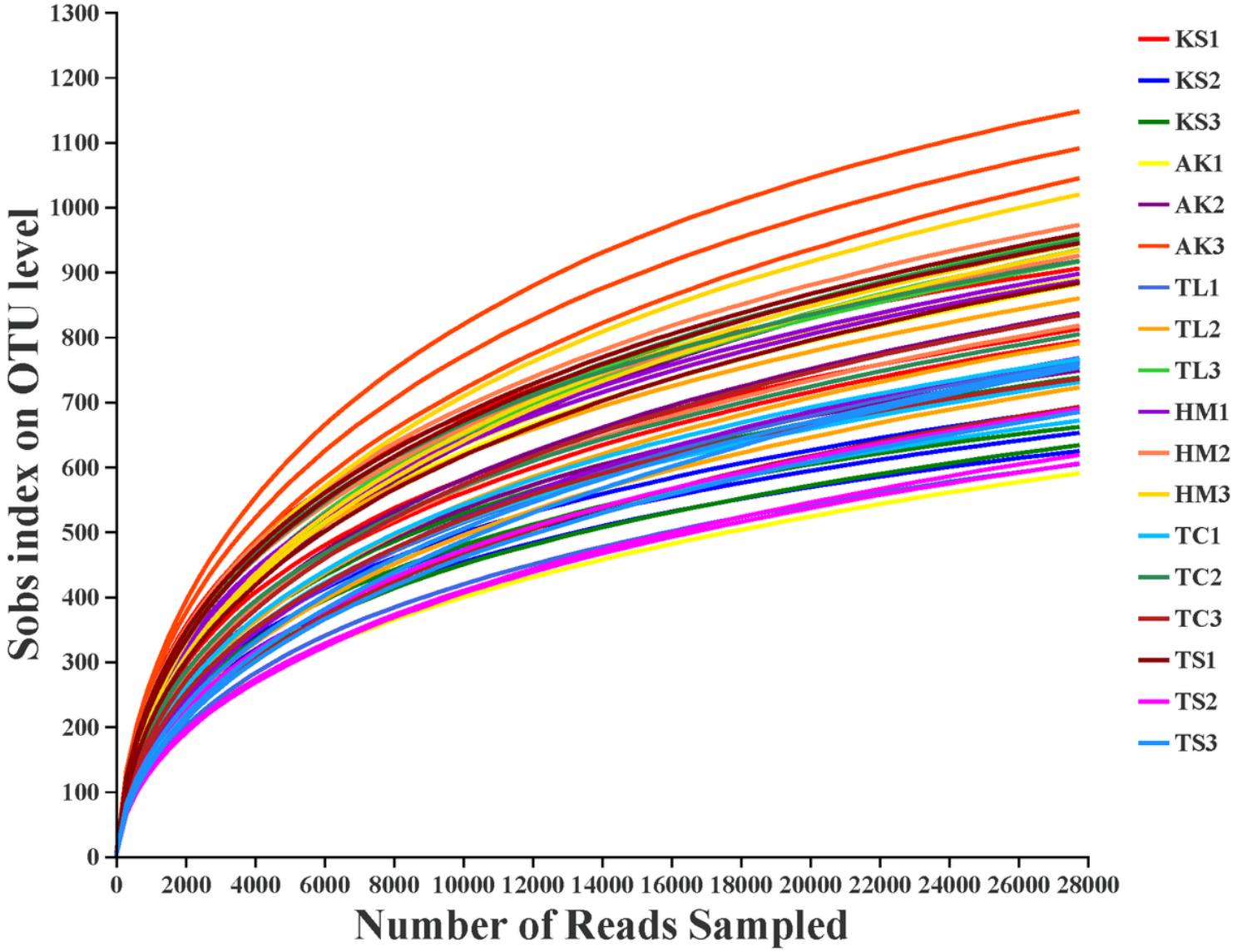

Figure 2

The rarefaction analysis of all samples. Rarefaction curves of OTUs were clustered for a dissimilarity threshold of 3%. Each sample had three replicates. Sample abbreviations are same as presented in Fig. 1

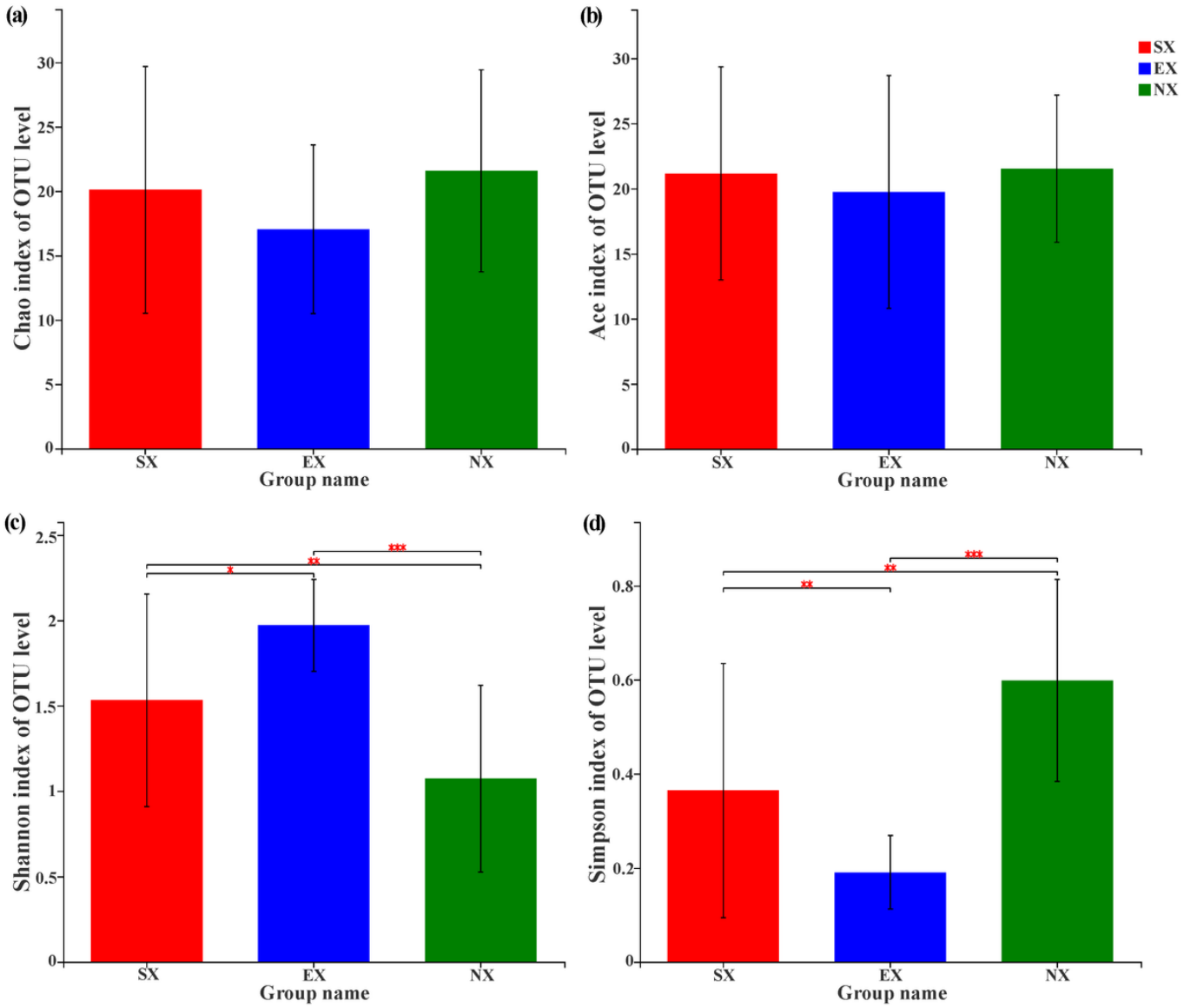

Figure 3

Alpha-diversity index differences in yeast species in rhizosphere soil samples of SX, EX, and NX groups. (a) Ace index and (b) Chao1 index were used to evaluate community richness, (c) Shannon index and (d) Simpson index were used to assess community diversity. The higher the Simpson index value, lower was the community diversity. The Wilcoxon rank-sum test was used to represent significant differences (*: 0.01 < P < = 0.05, **: 0.001 < P < = 0.01, ***: P < = 0.001)

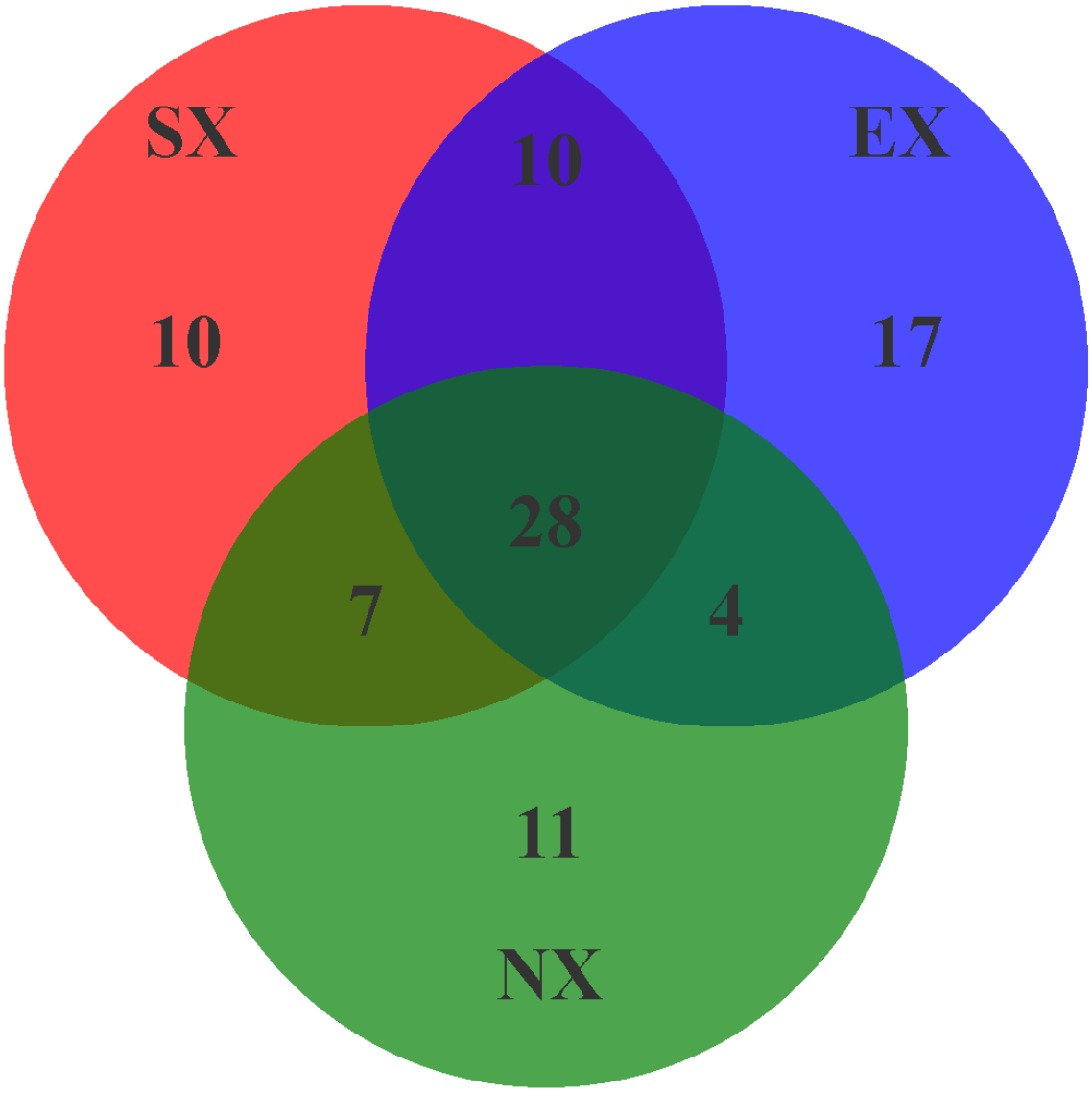

Figure 4

Venn diagram at the OTU level of soil samples in SX, EX, and NX groups. Each circle with different colors in the diagram represents a group; middle core numbers represent the number of OTUs common to all groups. The shared and unique yeast OTUs were shown at a 0.03 dissimilarity distance after removing singletons.

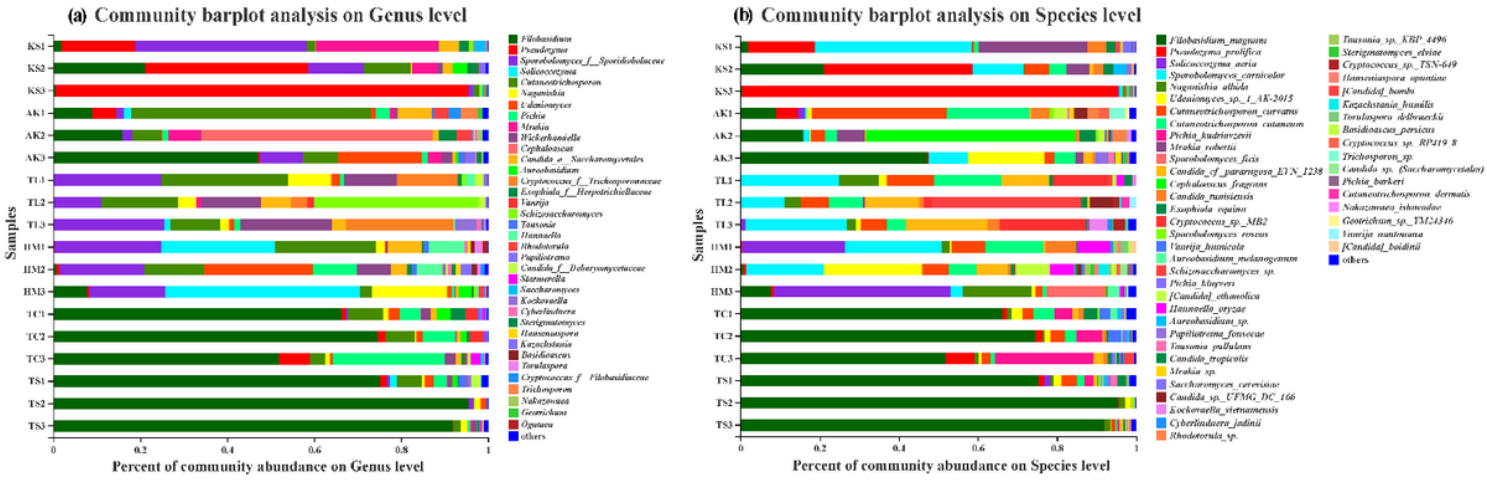

Figure 5

Relative abundance of predominant yeasts in all samples. (a) at the genus level; (b) at the species level. Others indicate the abundance of < 0.1% of genus. Sample abbreviations are same as presented in Fig. 1.

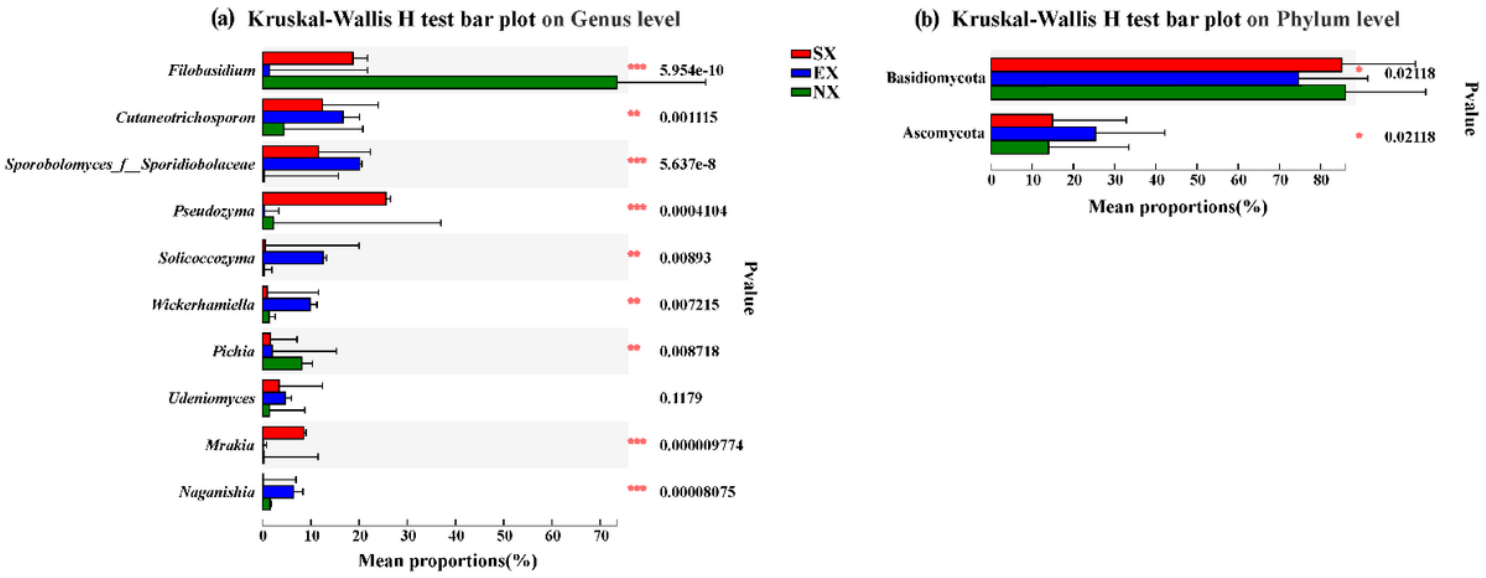

Figure 6

Relative abundance analysis of at the level of genus and phylum of the samples in the southern Xinjiang (SX), eastern Xinjiang (EX), and northern Xinjiang (NX): (a) at the genus level; (b) at the phylum level. The y-axis represents the classification levels of species, and the x-axis represents the percentage of species abundance in each sample group. The red, blue, and green columns represent the average results in the SX, EX, and NX soil samples, respectively. The Kruskal-Wallis rank-sum test was used to show significant differences (*: 0.01 < P < = 0.05, **: 0.001 < P < = 0.01, ***: P < = 0.001)

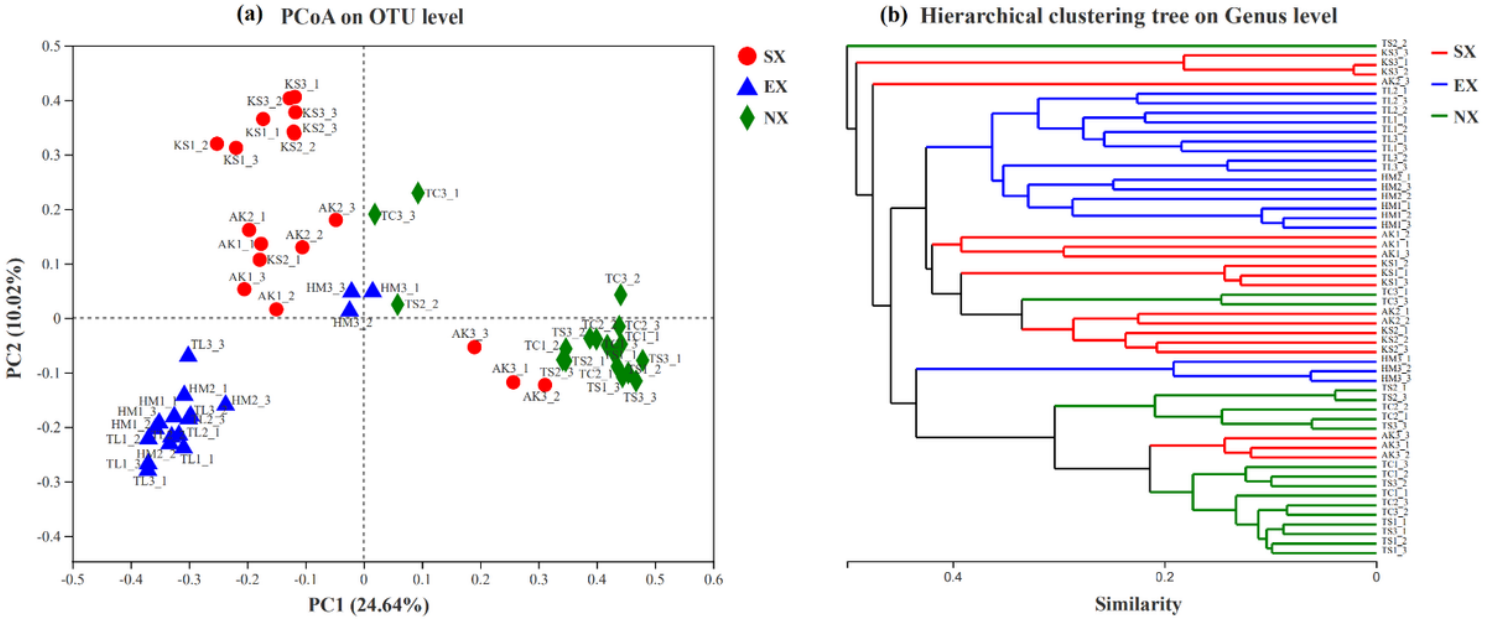

Figure 7

Comparative analysis of the different samples from SX, EX, and NX groups. (a) Principal Coordinates Analysis (PCoA) based on Bray-Curtis distance method at the OTU level; (b) UPGMA clustering analysis based on Bray-Curtis distance matrix at the genus level. Red, blue, and green symbols or lines represent samples from SX, EX, and NX groups, respectively. Each sample had three replicates. Sample abbreviations are same as presented in Fig. 1

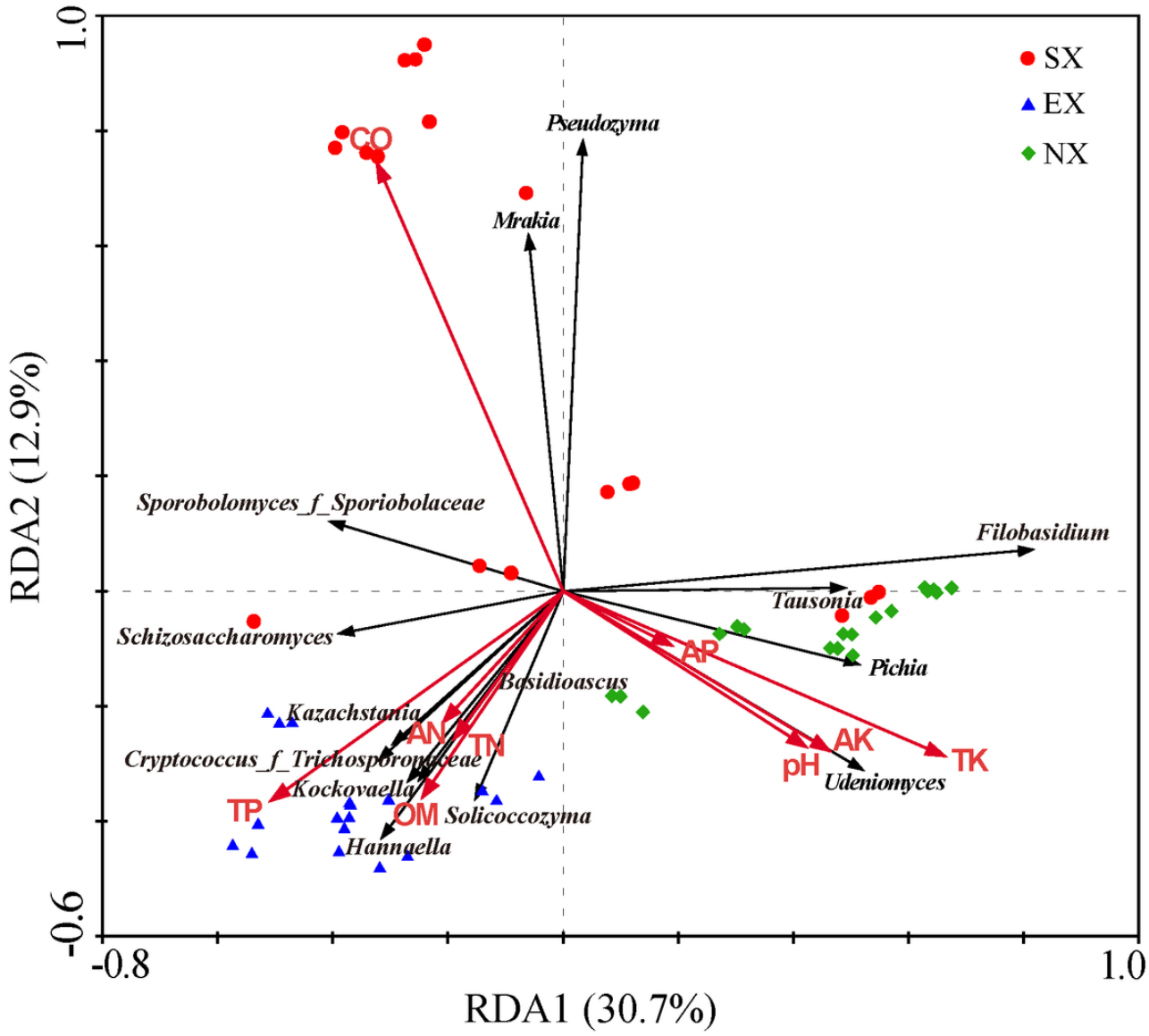

Figure 8

Redundancy analysis (RDA) of the correlation between yeast community and soil physicochemical properties in all samples from three regions in Xinjiang at the genus level. Red, blue, and green symbols represent samples from SX, EX, and NX groups, respectively. Red and black arrows represent the soil parameters and genera, respectively. Soil parameters: pH, Conductivity (CO), Organic matter (OM), Total nitrogen (TN), Total phosphorus (TP), Total potassium (TK), Available nitrogen (AN), Available phosphorus (AP), Available potassium (AK). Each sample had three replicates