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Original Article

Analysis of pathogen spectrum changes and epidemiological characteristics of superficial mycosis in the Shantou region of China from 2022 to 2024

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Abstract: Objective: The etiological spectrum of superficial mycoses varies regionally. This retrospective study investigated the clinical type composition and pathogen distribution shifts in Shantou from 2022-2024 to inform localized diagnosis and treatment. Methods: A total of 2,635 patients with positive fungal cultures from the Shantou Institute of Dermatology and Venereology were enrolled. Categorical data were compared using Chi-square or Fisher's exact tests; non-normally distributed continuous data were expressed as median (IQR). Advanced visualizations (Sankey diagrams, heatmaps) were generated using Python. P < 0.05 was considered significant. Results: The cohort comprised 1,488 males (56.47%) and 1,147 females (43.53%), with a median age of 31.0 years (IQR: 18.0-48.0). The five most common diagnoses were pityrosporum folliculitis (463, 17.57%), tinea pedis (286, 10.85%), tinea cruris (284, 10.78%), onychomycosis (273, 10.36%), and tinea corporis (243, 9.22%). Predominant pathogens were Malassezia (1,112, 42.20%), yeast-like fungi (784, 29.75%), Trichophyton rubrum (273, 10.36%), and T. mentagrophytes (252, 9.56%). Significant gender differences were observed for tinea cruris, tinea corporis, onychomycosis, and seborrheic dermatitis (all P < 0.05), but not for pityrosporum folliculitis (P = 0.754). Gender-based variations were also significant for Malassezia (P = 0.002) and T. rubrum (P < 0.001). Pathogen distribution differed significantly across age groups (all P < 0.001). Conclusions: The etiological spectrum in Shantou has shifted, with Malassezia now the leading pathogen. Distinct gender- and age-specific patterns warrant increased clinical vigilance and targeted prevention strategies.

Keywords: Superficial mycoses, epidemiology, pathogen distribution, *Malassezia*, *Trichophyton rubrum*, statistical analysis, data visualization

Introduction

Superficial mycoses are infectious dermatological conditions caused by fungi - including dermatophytes, yeasts, and molds - that invade the superficial layers of the skin, hair, nails, and mucous membranes [1-3]. These infections are characterized by high incidence rates, a tendency to recur, and ease of transmission [4, 5]. Globally, the prevalence of superficial mycoses has been steadily increasing, particularly in warm and humid regions, making it a significant public health concern [6, 7]. Such diseases not only cause uncomfortable symptoms like pruritus, scaling, and erythema - severely impairing patients' quality of life - but can also lead to secondary bacterial infections that exacerbate the condition [8-10].

The growth and spread of pathogenic fungi are influenced by multiple factors, including climate, environment, host immune status, and lifestyle habits, resulting in substantial differences in the spectrum of causative agents and disease profiles across geographic regions [11-13]. For instance, Malassezia infections are more common in tropical and subtropical areas, whereas dermatophytes (such as *Trichophyton rubrum* and *Trichophyton mentagrophytes*) remain predominant in temperate zones [14-17].

Given China's vast territory and marked regional variations in climate, economic development, and hygiene conditions, conducting region specific epidemiological surveillance is crucial for understanding the distribution patterns of fungal diseases within the country and for guiding clinical diagnosis and treatment [4, 18-21].

Shantou City, located on the eastern coast of Guangdong Province, features a southern subtropical maritime climate characterized by year-round warmth and humidity-conditions highly conducive to fungal proliferation [22-24]. The region's rapid economic development and rising living standards, increased bathing frequency, widespread use of personal care products, and evolving clothing habits may further alter the skin microbiome, potentially shifting the etiological profile of superficial mycoses. Previous studies have indicated that *Trichophyton rubrum* and *Trichophyton mentagrophytes* were the predominant causative agents of superficial mycoses in Shantou, with *Malassezia* species ranking only third. However, recent reports from multiple regions across China - including Changchun and Shanghai - have consistently shown a significant rise in the detection rate of *Malassezia*, which is gradually becoming the dominant pathogen in certain clinical conditions such as pityrosporum folliculitis and seborrheic dermatitis [12, 14, 25]. Whether a similar shift has occurred in Shantou remains unclear due to the lack of systematic, up-to-date data.

Therefore, this retrospective study aimed to investigate the clinical type composition and shifts in pathogen distribution of superficial mycoses in Shantou between 2022 and 2024, and to explore their associations with gender and age. The findings are expected to provide evidence for localized precision diagnosis and treatment, offer updated epidemiological evidence to guide prevention strategies in Shantou and similar regions, and inform ongoing pathogen surveillance and control measures.

Materials and methods

General information

A total of 2,635 patients who visited the Shantou Institute of Dermatology and Venereology between January 2022 and December 2024 and tested positive for fungal culture were included in this study. All patients had a clinical diagnosis of superficial mycosis and complete clinical records. This study was approved by the Ethics Committee of the Shantou Institute of Dermatology and Venereology. All procedures performed in this study involving human participants were in accordance with the Declaration of Helsinki (as revised in 2013).

Inclusion criteria

Age ≥ 1 year; Clinical diagnosis of superficial mycosis (including tinea corporis, tinea cruris, tinea pedis, tinea manuum, onychomycosis, tinea capitis, tinea versicolor, pityrosporum folliculitis, cutaneous candidiasis, etc.); Positive fungal culture results from specimens collected at the lesion site; Complete documentation in the medical record system of gender, age, clinical diagnosis, and fungal identification results.

Exclusion criteria

Negative or contaminated fungal culture results; Missing key clinical information (such as age, diagnosis, pathogen species); Patients with severe immunodeficiency diseases (e.g., HIV infection, long-term use of immunosuppressants, hematological malignancies) or those who had systemic antifungal treatment within 4 weeks prior to admission were excluded to avoid interference with the natural pathogen spectrum. During the study period, if a patient had multiple visits, only the first visit record was retained.

Mycological examination and data extraction methods

This study retrospectively extracted relevant data from electronic medical records and laboratory test records archived in the Hospital Information System (HIS) and Laboratory Information System (LIS). During the study period, all patients clinically diagnosed with superficial mycoses underwent the following standardized mycological examination process: Specimen Collection and Documentation: According to electronic medical records, clinicians collected specimens (such as scraping skin scales, plucking affected hairs, collecting nail debris, etc.) from suspected lesions according to standard operating procedures and submitted them to the laboratory.

Culture and identification process review: Laboratory records indicated that all specimens were processed according to the hospital's clinical laboratory operating procedures.

Media and culturing: Specimens were routinely inoculated on Chromagar Candida medium, modified Sabouraud chloramphenicol slant medium, Sabouraud chloramphenicol slant medium with olive oil, and modified Sabouraud chloramphenicol plate medium. Culturing conditions were set at dual temperatures of 26°C and 35°C for 10-14 days of continuous observation.

Species identification: Species identification was summarized based on descriptions in archived identification reports in the LIS. Identification primarily relied on colony morphology and microscopic characteristics (lactophenol cotton blue staining). For yeast-like fungi, the reports mentioned initial screening using Chromagar Candida medium; for difficult-to-identify dermatophytes, small culture methods were used for auxiliary identification. The final species identification results (e.g., *Malassezia*, *Trichophyton rubrum*, etc.) were directly extracted from the database.

Data extraction: Members of the research team queried the HIS and LIS to extract and record the following information for each positive patient: anonymized unique identifier, gender, age, clinical diagnosis, type of specimen submitted for testing, final fungal culture identification result, and report date. All data extraction was performed using a uniformly designed data collection form.

Statistical analysis

A standardized database was established using Microsoft Excel 2019 for data entry and cleaning. To ensure data accuracy, all entries were independently input by two individuals and subsequently cross-checked. Statistical analyses were performed using IBM SPSS Statistics 25.0. Categorical data were presented as frequencies (n) and percentages (%), while measurement data were first assessed for normality using the Shapiro-Wilk test. Normally distributed continuous data were described as mean ± standard deviation, whereas non-normally distributed data were expressed as median and interquartile range (IQR). For multiple-group comparisons of non-normally distributed measurement data, the Kruskal-Wallis H test was employed, followed by pairwise comparisons with Bonferroni correction when overall differences were significant. For comparisons of categorical variables (e.g., disease or pathogen distribution across gender and age groups), the Chi-square test or Fisher's exact test was used instead. For pairwise comparisons between multiple age groups or disease groups, the Bonferroni method was used to adjust the significance level. The Mann-Whitney U test was used for two-group comparisons of non-normally distributed data. To visually illustrate associations between major pathogens and various diseases, a many-to-many relational data matrix was constructed. Advanced data visualization was carried out using Python version 3.0 with Matplotlib 3.5.0 and Seaborn 0.11.2 libraries: grouped bar charts and cluster heatmaps were generated to display gender differences and pathogen-disease patterns; Sankey diagrams were drawn to show the flow from pathogens to clinical manifestations; and line graphs were plotted to depict pathogen distribution trends across age groups. All hypothesis tests were two-tailed, and a P-value < 0.05 was considered statistically significant.

Results

Baseline characteristics of the study population

A total of 2,635 patients with positive fungal cultures were ultimately included in this study. As shown in **Table 1**, there were 1,488 male patients (56.47%) and 1,147 female patients (43.53%), yielding a male-to-female ratio of 1.30:1. The age range was broad, spanning from 1 to 95 years, with a median age of 31.0 years (IQR: 18.0-48.0 years) and a mean age of 34.0 ± 19.7 years. When stratified by age group, the majority of patients were in the young adult group aged 19-45 years (1,173 cases, 44.52%), followed by those aged 0-17 years (620 cases, 23.53%) and 18-30 years (631 cases, 23.95%). Disease spectrum analysis (**Figure 1**) revealed that the top five clinical conditions were: pityrosporum folliculitis (463 cases, 17.57%), tinea pedis (286 cases, 10.85%), tinea cruris (284 cases, 10.78%), onychomycosis (273 cases, 10.36%), and tinea corporis (243 cases, 9.22%). Together, these

Table 1. Baseline demographic and clinical characteristics of the study population (n = 2,635)

Characteristic	Value
Total cases	2635
Gender	
Male	1488 (56.47%)
Female	1147 (43.53%)
Age (years)	
Range	1-95
Mean ± SD	34.0 ± 19.7
Median (IQR)	31.0 (18.0-48.0)
Age group	
0-17	620 (23.53%)
18-30	631 (23.95%)
31-45	636 (24.14%)
46-60	403 (15.29%)
> 60	345 (13.09%)
Top 5 diagnoses	
Pityrosporum folliculitis	463 (17.57%)
Tinea pedis	286 (10.85%)
Tinea cruris	284 (10.78%)
Onychomycosis	273 (10.36%)
Tinea corporis	243 (9.22%)

Abbreviations: SD, standard deviation; IQR, interquartile range.

five diseases accounted for 58.78% of all cases.

Etiological spectrum and leading pathogens

Among the 2,635 positive specimens, 14 pathogenic fungal species were identified. The etiological spectrum was dominated by Malassezia spp., which accounted for 1,112 strains (42.20%), making it the most prevalent pathogen. This was followed by yeast-like fungi (784 strains, 29.75%), Trichophyton rubrum (273 strains, 10.36%), and Trichophyton mentagrophytes (252 strains, 9.56%). These four pathogens constituted 91.87% of all isolates. The correspondence between different diseases and pathogens exhibited significant specificity (**Table 2**). Pityrosporum folliculitis was almost exclusively caused by Malassezia (433/463, 93.52%) (**Figure 2A**). The pathogens responsible for tinea pedis were mainly yeast-like fungi (134/286, 46.85%), T. mentagrophytes (86/286, 30.07%), and T. rubrum (57/286, 19.93%) (**Figure 2B**). For tinea cruris, the primary pathogens were T. rubrum (101/284, 35.56%), yeast-like fungi (89/284, 31.34%), and T. mentagrophytes (52/284, 18.31%) (**Figure 2C**). In onychomycosis, yeast-like fungi predominated absolutely (182/273, 66.67%) (**Figure 2D**). The etiological composition of tinea corporis was relatively diverse but still mainly consisted of yeast-like fungi (81/243, 33.33%), T. rubrum (64/243, 26.34%), and T. mentagrophytes (43/243, 17.70%) (**Figure 2E**). Notably, the detection rate of Malassezia in seborrheic dermatitis (214/229, 93.45%) and tinea versicolor (178/188, 94.68%) patients was extremely high. Tinea capitis was primarily caused by zoophilic Microsporum canis (48/84, 57.14%). A small number of cases were attributed to other fungi, including Candida tropicalis, Aspergillus spp., and Fusarium spp., which collectively accounted for less than 1% of all isolates (**Table 2**).

Gender distribution differences among common diseases

A gender distribution analysis was conducted for five common diseases with higher case numbers (**Table 3**). The χ^2 test results indicated that there were statistically significant differences in the gender distribution of tinea cruris, tinea corporis, onychomycosis, and seborrheic dermatitis (all $P < 0.05$). Specifically, the proportion of male patients was significantly higher than females for tinea cruris (male 227 vs. female 57, $\chi^2 = 70.20$, $P < 0.001$) and tinea corporis (male 157 vs. female 86, $\chi^2 = 6.85$, $P = 0.009$). Conversely, the proportion of female patients was significantly higher than males for onychomycosis (female 164 vs. male 109, $\chi^2 = 33.16$, $P < 0.001$) and seborrheic dermatitis (female 119 vs. male 110, $\chi^2 = 6.89$, $P = 0.009$). No significant gender difference was observed for pityrosporum folliculitis (male 265 vs. female 198, $\chi^2 = 0.10$, $P = 0.754$).

Association of major pathogens with superficial mycoses

To gain a deeper understanding of the complex relationships between the four major pathogens (Malassezia, yeast-like fungi, Trichophyton rubrum, and Trichophyton mentagrophytes) and various types of superficial mycoses, we conducted visualization modeling. The heatmap in **Figure 3** visually demonstrates the relative proportions of each pathogen across different diseases, with color intensity representing

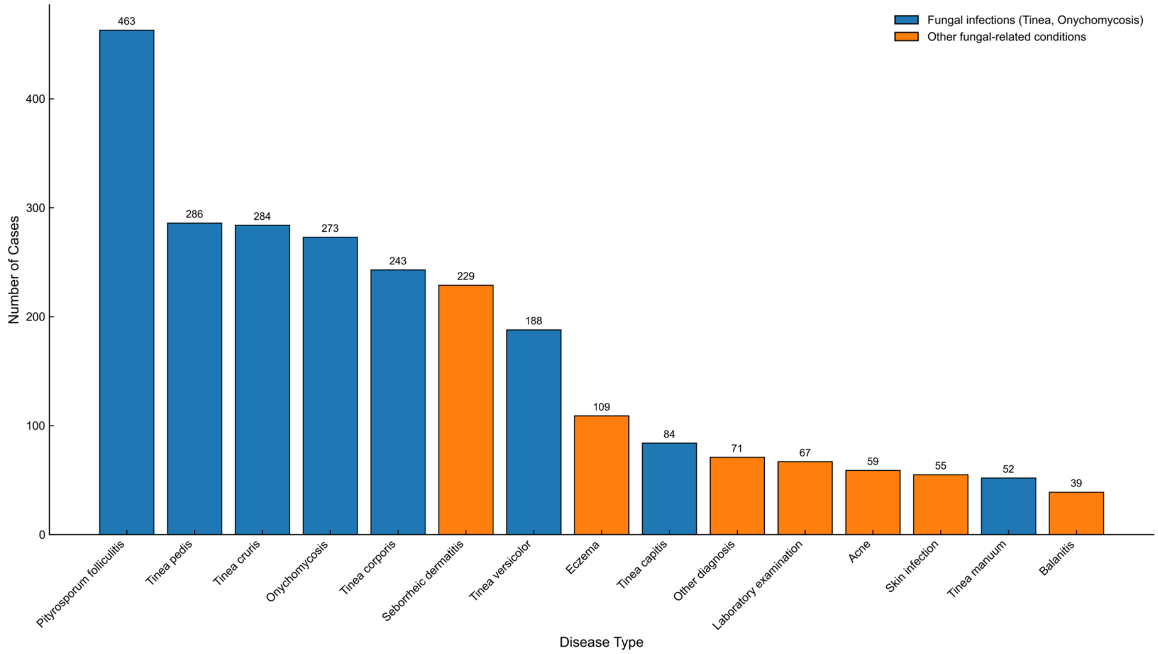

Figure 1. Spectrum of superficial fungal diseases in Shantou (2022-2024).

the strength of association. The Sankey diagram in **Figure 4** dynamically presents the flow and volume of cases from specific pathogens to various clinical diagnoses, clearly revealing: 1) Malassezia predominantly flows to pityrosporum folliculitis, tinea versicolor, and seborrheic dermatitis; 2) Yeast-like fungi are widely distributed across multiple diseases such as onychomycosis, tinea pedis, and eczema; 3) T. rubrum and T. mentagrophytes hold significant positions in tinea cruris, tinea pedis, and tinea corporis.

Age and gender distribution of major pathogens

Further analysis of the demographic distribution of the four major pathogens is presented in **Table 4**. The age and gender composition of the patient population is illustrated in **Figure 5A**, which shows that males outnumbered females in most age groups, particularly in the 0-17 and > 60 years groups, while the gender distribution was more balanced in the 18-45 years range. Regarding the age-specific prevalence of the four major pathogens (**Figure 5B**), the proportion differences across age groups were highly statistically significant (all $P < 0.001$). The detection peaks for both Malassezia and T. rubrum were observed in the young adult group aged 19-45 years, accounting for 41.9% and 12.8% of cases in this age group, respectively. The detection rate of yeast-like fungi increased progressively with age, peaking in the > 60 years group at 68.3%. The distribution of T. mentagrophytes was relatively uniform across age groups, ranging from 6.7% to 13.4%, with a slight predominance in the 31-45 years group (13.0%).

Discussion

Our data reveal a significant shift in the etiological spectrum of superficial mycoses in the Shantou region, with *Malassezia* (42.20%) now identified as the predominant pathogen, surpassing traditional dermatophytes such as *Trichophyton rubrum* (10.36%) and *Trichophyton mentagrophytes* (9.56%). This finding aligns with reports of an evolving global epidemiological profile for these infections [7, 10, 22]. While dermatophytes like *T. rubrum* and *T. mentagrophytes* have traditionally been considered the primary agents in subtropical regions [1, 5, 26, 27], recent studies indicate a rising prevalence of yeasts-notably *Malassezia* spp. - as dominant pathogens in certain settings, a change attributed to climatic, lifestyle, and therapeutic factors [25, 28-30].

Our findings confirm a significant shift in the etiological spectrum of superficial mycoses in

Table 2. Distribution of major pathogenic fungi across different superficial fungal diseases

Disease	Total	Malassezia	Yeast-like fungi	Trichophyton rubrum	Trichophyton mentagrophytes	Candida albicans	Microsporum canis	Microsporum gypseum	Epidermophyton floccosum	Red yeast	Candida tropicalis	Other fungi
Pityrosporum folliculitis	463	433 (93.52%)	29 (6.26%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	1 (0.22%)	0 (0.00%)	0 (0.00%)
Tinea pedis	286	0 (0.00%)	134 (46.85%)	57 (19.93%)	86 (30.07%)	5 (1.75%)	1 (0.35%)	0 (0.00%)	1 (0.35%)	2 (0.70%)	0 (0.00%)	0 (0.00%)
Tinea cruris	284	2 (0.70%)	89 (31.34%)	101 (35.56%)	52 (18.31%)	25 (8.80%)	0 (0.00%)	3 (1.06%)	8 (2.82%)	1 (0.35%)	2 (0.70%)	1 (0.35%)
Onychomycosis	273	1 (0.37%)	182 (66.67%)	33 (12.09%)	49 (17.95%)	4 (1.47%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	4 (1.47%)	0 (0.00%)	0 (0.00%)
Tinea corporis	243	17 (7.00%)	81 (33.33%)	64 (26.34%)	43 (17.70%)	8 (3.29%)	13 (5.35%)	9 (3.70%)	3 (1.23%)	1 (0.41%)	1 (0.41%)	3 (1.23%)
Seborrheic dermatitis	229	214 (93.45%)	13 (5.68%)	1 (0.44%)	0 (0.00%)	0 (0.00%)	1 (0.44%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)
Tinea versicolor	188	178 (94.68%)	10 (5.32%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)
Eczema	109	24 (22.02%)	67 (61.47%)	6 (5.50%)	7 (6.42%)	1 (0.92%)	0 (0.00%)	1 (0.92%)	1 (0.92%)	2 (1.83%)	0 (0.00%)	0 (0.00%)
Tinea capitis	84	12 (14.29%)	13 (15.48%)	2 (2.38%)	5 (5.95%)	0 (0.00%)	48 (57.14%)	1 (1.19%)	1 (1.19%)	0 (0.00%)	0 (0.00%)	2 (2.38%)
Other diagnosis	71	46 (64.79%)	16 (22.54%)	1 (1.41%)	1 (1.41%)	6 (8.45%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	1 (1.41%)

Among the 2,635 positive specimens, a total of 14 distinct fungal species were identified. The predominant pathogen was Malassezia spp., isolated from 1,112 cases (42.20%), followed by yeast-like fungi (784 cases, 29.75%), Trichophyton rubrum (273 cases, 10.36%), and Trichophyton mentagrophytes (252 cases, 9.56%). The remaining fungi accounted for 8.13% of isolates and included: Candida albicans (80 cases, 3.04%), Microsporum canis (72 cases, 2.73%), Microsporum gypseum (16 cases, 0.61%), Epidermophyton floccosum (14 cases, 0.53%), Rhodotorula (red yeast) (13 cases, 0.49%), Candida tropicalis (8 cases, 0.30%), Trichophyton violaceum (5 cases, 0.19%), Candida glabrata (4 cases, 0.15%), Aspergillus niger (1 case, 0.04%), and Trichophyton tonsurans (1 case, 0.04%). The category "yeast-like fungi" represents non-speciated yeasts other than the Candida species listed above. For a complete breakdown of all fungal species (including their original diagnostic names), refer to Supplementary Table 1 in the supporting information. Note: Values are presented as n (%). Percentages are calculated within each disease row. "Other fungi" includes species such as Aspergillus niger, Fusarium spp., Trichophyton violaceum, and other rare isolates.

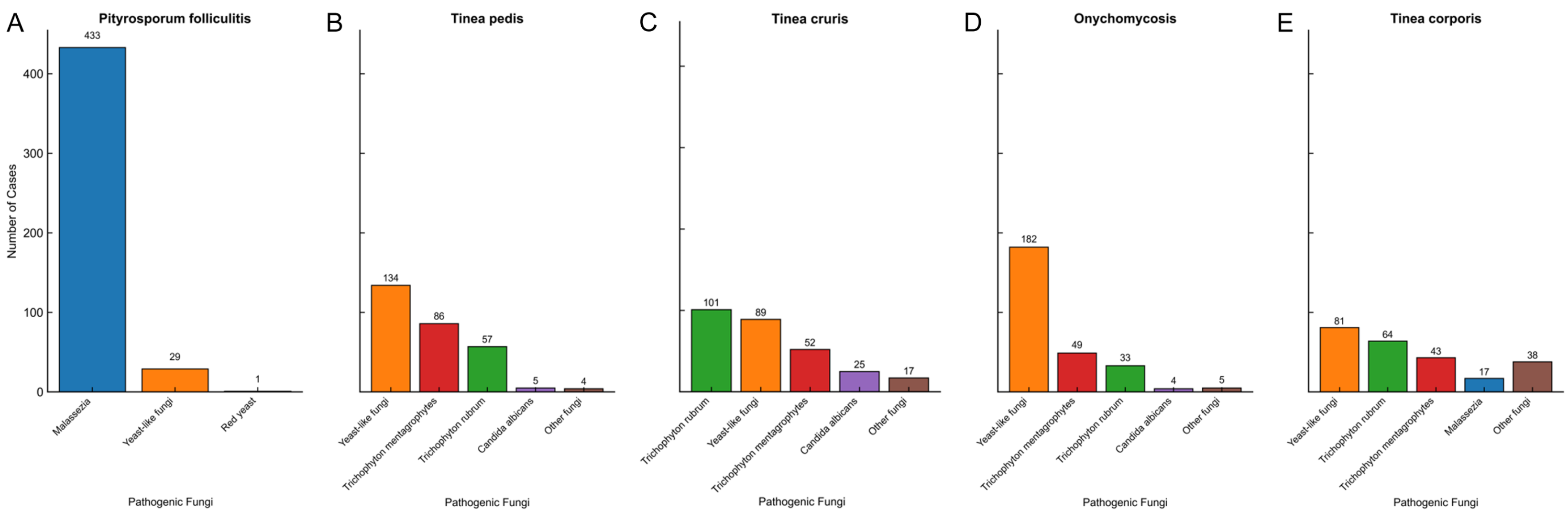

Figure 2. Etiological composition of the top 5 superficial fungal diseases. A. Pityrosporum folliculitis: Dominated by Malassezia (93.5%), with a small proportion of yeast-like fungi (6.3%). B. Tinea pedis: Mainly caused by yeast-like fungi (46.9%), Trichophyton mentagrophytes (30.1%), and Trichophyton rubrum (19.9%). C. Tinea cruris: Predominantly Trichophyton rubrum (35.7%), followed by yeast-like fungi (31.5%) and Trichophyton mentagrophytes (18.4%). D. Onychomycosis: Overwhelmingly yeast-like fungi (66.7%), with Trichophyton mentagrophytes (17.9%) and Trichophyton rubrum (12.1%) as secondary pathogens. E. Tinea corporis: Diversified pathogens, mainly yeast-like fungi (33.8%), Trichophyton rubrum (26.7%), and Trichophyton mentagrophytes (17.9%). Abbreviations: T. rubrum, Trichophyton rubrum; T. mentagrophytes, Trichophyton mentagrophytes; C. albicans, Candida albicans; M. canis, Microsporum canis; M. gypseum, Microsporum gypseum; E. floccosum, Epidermophyton floccosum; C. tropicalis, Candida tropicalis.

Table 3. Association between common diseases and patient gender

Disease	Male, n (%)	Female, n (%)	Total	χ^2	*P*-value
Pityrosporum folliculitis	265 (57.24%)	198 (42.76%)	463	0.10	0.754
Tinea cruris	227 (79.93%)	57 (20.07%)	284	70.20	< 0.001
Tinea corporis	157 (64.61%)	86 (35.39%)	243	6.85	0.009
Onychomycosis	109 (39.93%)	164 (60.07%)	273	33.16	< 0.001
Seborrheic dermatitis	110 (48.03%)	119 (51.97%)	229	6.89	0.009

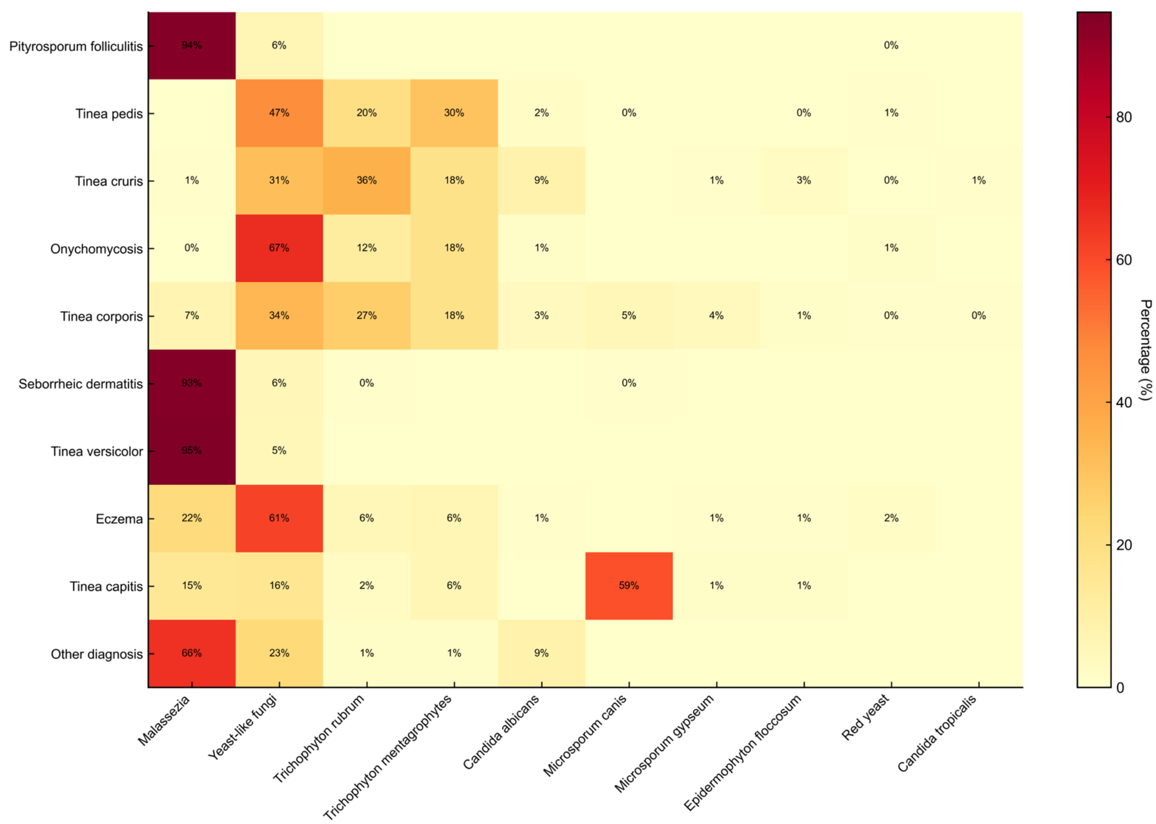

Figure 3. Association between major pathogenic fungi and superficial fungal diseases. Abbreviations: T. rubrum, Trichophyton rubrum; T. mentagrophytes, Trichophyton mentagrophytes; C. albicans, Candida albicans; M. canis, Microsporum canis; M. gypseum, Microsporum gypseum; E. floccosum, Epidermophyton floccosum; C. tropicalis, Candida tropicalis.

the Shantou region. *Malassezia* has now surpassed traditional dermatophytes to become the most frequently isolated pathogen, accounting for 42.20% of all positive cultures. This represents a notable departure from the epidemiological profile documented in Southern China a decade ago, where a study in Guangzhou (2004-2014) reported dermatophytes as the

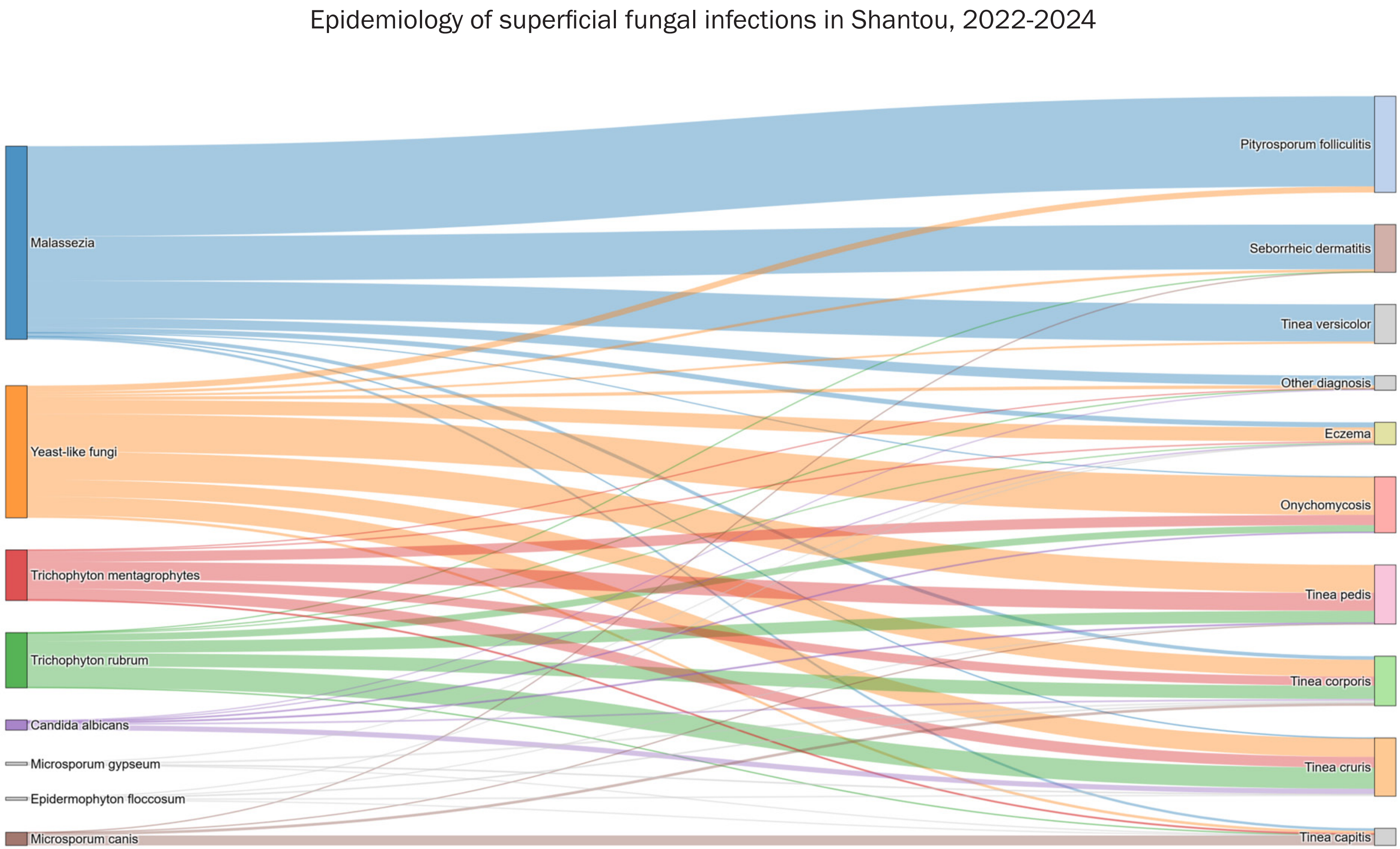

Figure 4. Flow of major pathogenic fungi to clinical disease manifestations. Abbreviations: T. rubrum, Trichophyton rubrum; T. mentagrophytes, Trichophyton mentagrophytes; C. albicans, Candida albicans; M. canis, Microsporum canis; M. gypseum, Microsporum gypseum; E. floccosum, Epidermophyton floccosum; C. tropicalis, Candida tropicalis.

Table 4. Distribution of the four major pathogenic fungi by age group and gender

Fungus	Age group	Male, n	Female, n	Total	Male%	Female%
Malassezia	0-17	209	138	347	60.23%	39.77%
Malassezia	18-30	205	188	393	52.16%	47.84%
Malassezia	31-45	125	130	255	49.02%	50.98%
Malassezia	46-60	53	39	92	57.61%	42.39%
Malassezia	> 60	16	9	25	64.00%	36.00%
Yeast-like fungi	0-17	58	43	101	57.43%	42.57%
Yeast-like fungi	18-30	57	55	112	50.89%	49.11%
Yeast-like fungi	31-45	97	99	196	49.49%	50.51%
Yeast-like fungi	46-60	74	94	168	44.05%	55.95%
Yeast-like fungi	> 60	124	83	207	59.90%	40.10%
Trichophyton rubrum	0-17	26	13	39	66.67%	33.33%
Trichophyton rubrum	18-30	50	11	61	81.97%	18.03%
Trichophyton rubrum	31-45	52	26	78	66.67%	33.33%
Trichophyton rubrum	46-60	46	18	64	71.88%	28.12%
Trichophyton rubrum	> 60	21	10	31	67.74%	32.26%
Trichophyton mentagrophytes	0-17	18	17	35	51.43%	48.57%
Trichophyton mentagrophytes	18-30	29	19	48	60.42%	39.58%
Trichophyton mentagrophytes	31-45	47	32	79	59.49%	40.51%
Trichophyton mentagrophytes	46-60	28	22	50	56.00%	44.00%
Trichophyton mentagrophytes	> 60	24	16	40	60.00%	40.00%

Note: Percentages are calculated within each fungus-age group stratum and represent the proportion of male or female patients among total cases for that specific fungus and age group.

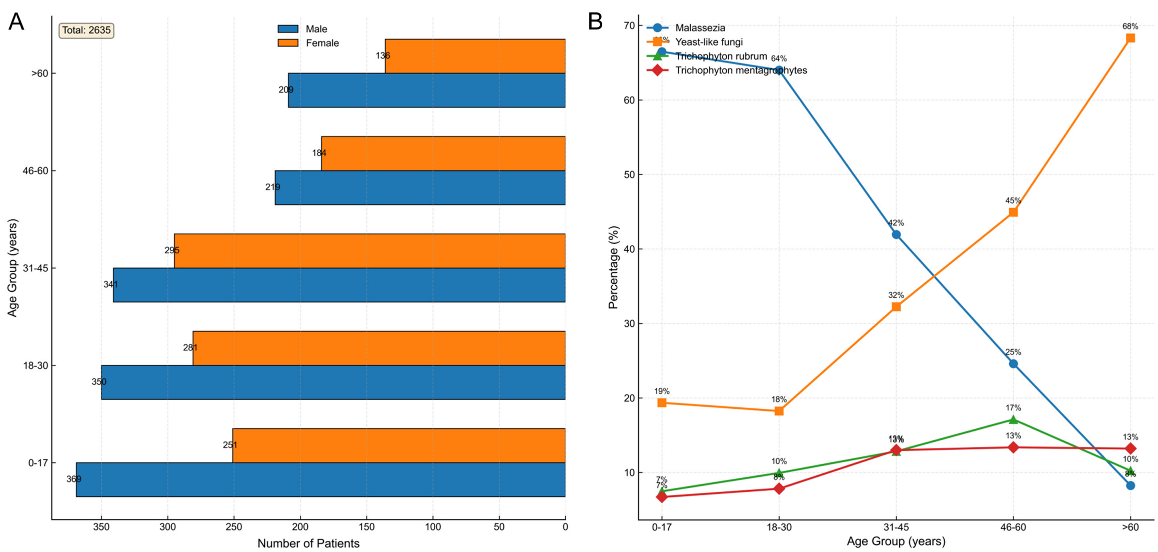

Figure 5. Age-specific distribution of the four major pathogenic fungi. A. Patient gender by age group (total n = 2635): Bar chart showing the number of male (blue) and female (orange) patients across 5 age groups; males are more numerous in most groups. B. Pathogen prevalence across age groups: Line chart of four major pathogens' percentage by age group; yeast-like fungi rise sharply (to 68%) in the > 60 years group, while Malassezia declines. Abbreviations: T. rubrum, Trichophyton rubrum; T. mentagrophytes, Trichophyton mentagrophytes.

predominant isolates (84.36%), with yeasts (including *Malassezia* spp.) constituting only 14.92% [31].

This shift may be attributed to both the biological characteristics of the pathogen and local environmental factors. Malassezia species are lipophilic yeasts whose growth is highly dependent on fatty acids in sebum, predisposing them to colonize sebum-rich areas [32]. Shantou's coastal, warm, and persistently humid climate provides an ideal external environment for its proliferation. This shift mirrors trends observed in other Chinese cities. For instance, a recent study in Changchun reported a marked increase in Malassezia-associated dermatoses, accounting for over 30% of superficial fungal infections in 2019 [12]. Similarly, data from Chinese mainland showed that Malassezia species have become the predominant pathogens in pityrosporum folliculitis and seborrheic dermatitis, with detection rates exceeding 40% [25]. In contrast, studies from temperate regions such as Europe and North America continue to report dermatophytes - particularly Trichophyton rubrum - as the leading cause of tinea infections. These geographic variations underscore the influence of climate and local practices on fungal epidemiology [33]. Furthermore, the extensive clinical use of broad-spectrum antifungal agents such as terbinafine may have selectively suppressed dermatophytes while allowing Malassezia to persist, as terbinafine exhibits higher minimum inhibitory concentrations against Malassezia species compared to dermatophytes [34].

Moreover, rising living standards in the region have led to increased bathing frequency and widespread use of personal care products containing oily ingredients, which may further alter the skin's surface lipid composition and microecological balance, thereby promoting *Malassezia* overgrowth. Additionally, the extensive clinical use in recent years of broad-spectrum antifungal agents - such as terbinafine and itraconazole - has effectively suppressed dermatophyte growth, potentially creating an "ecological release" opportunity for *Malassezia*, which is relatively less susceptible to these drugs, allowing it to gain a competitive advantage in the pathogen landscape.

This epidemiological shift underscores the need for heightened clinical vigilance regarding *Malassezia*-associated conditions-such as *Pityrosporum folliculitis*, *Tinea versicolor,* and *Seborrheic dermatitis*-particularly in warm, humid regions and among individuals with active sebaceous gland activity. This study further clarifies the gender- and age-related distribution patterns of superficial mycoses, differences that are likely closely linked to physiological, behavioral, and immunological factors.

Regarding gender, Tinea cruris and Tinea corporis were significantly more common in males, while Onychomycosis and Seborrheic dermatitis showed a significant female predominance. No significant gender difference was observed for Pityrosporum folliculitis. Higher androgen levels in men stimulate sebaceous gland activity, creating a favorable environment for lipophilic *Malassezia* and dermatophytes that thrive in moist conditions. Additionally, men are more likely to engage in physical labor or sports activities and often wear less breathable clothing, which can lead to localized moisture and sweating-further promoting fungal infection. In contrast, onychomycosis was markedly more prevalent among females, possibly due to frequent manicures (causing microtrauma to the nail plate), prolonged exposure to water and detergents during household chores, and the habitual use of tight or non-breathable footwear - all of which may compromise local barrier integrity and increase susceptibility to fungal colonization.

In terms of age distribution, young adults (19-45 years) emerged as the high-risk group for multiple types of superficial mycoses. This population is highly socially active, experiences diverse occupational and environmental exposures, and maintains an active immune system - but often under chronic stress, which may impair cutaneous immune function and heighten infection susceptibility. Among children, tinea capitis was predominantly caused by *Microsporum canis*, indicating pet contact as a key source of infection; thus, improved pet hygiene management and health education for children are warranted. In older adults, the detection rate of yeast-like fungi - particularly *Candida* species - was elevated, likely attributable to age-related declines in skin barrier function and immunity, comorbidities such as diabetes, and long-term use of antibiotics or corticosteroids. Candida albicans, although accounting for only 3.04% of cases in our cohort, exhibits a propensity for recurrent infection due to its immune evasion mechanisms [35]. The management of Candida infections, particularly in elderly or immunocompromised patients, necessitates continuous surveillance of antifungal resistance and the exploration of novel therapeutic approaches [36].

Notably, our study found high detection rates of *Malassezia* in inflammatory skin disorders, including seborrheic dermatitis (93.4%), acne (88.1%), alopecia areata (90.9%), and eczema (22.0%). Although this does not establish causality, it strongly suggests that *Malassezia* may play a significant role in the pathogenesis or exacerbation of these conditions. Current evidence indicates that *Malassezia* may contribute to inflammation through several mechanisms: (1) its metabolic products (e.g., free fatty acids, lipases) can stimulate keratinocytes to release pro-inflammatory cytokines; (2) it can act as an allergen, triggering host immune responses; and (3) its ability to form biofilms may enhance colonization, persistence, and antifungal resistance, leading to chronic or refractory disease. Therefore, in cases of inflammatory dermatoses unresponsive to conventional therapy, clinicians should consider possible co-infection with *Malassezia* and perform mycological testing to guide comprehensive treatment.

The main strengths of this study include its large sample size, recent data collection period (2022-2024), the use of standardized mycological protocols (including dual-temperature culture and multiple media), and the integrated application of advanced statistical and visualization techniques to clearly illustrate the complex interrelationships among pathogens, diseases, and patient populations. Nevertheless, several limitations must be acknowledged. First, as a single-center retrospective study conducted at a specialized dermatology hospital, selection bias may exist, potentially limiting the generalizability of our findings to the broader community. Second, pathogen identification relied primarily on conventional culture and morphological methods without molecular typing, precluding differentiation of specific Malassezia species. Given that different Malassezia species (e.g., M. globosa, M. restricta) exhibit varying pathogenic potentials and antifungal susceptibility profiles [37], future studies incorporating molecular techniques - such as PCR sequencing or MALDI-TOF MS - are warranted to clarify their specific roles in superficial mycoses. Third, detailed information on patients' lifestyle habits, occupational exposures, and concomitant medications was not collected, which limited our ability to perform a deeper analysis of these potential confounding or contributing factors.

Conclusion

In summary, this study documents a notable shift in the etiological spectrum of superficial mycoses in Shantou, with *Malassezia* now established as the dominant pathogen, and delineates clear gender- and age-specific distribution patterns. These findings call for heightened clinical awareness and tailored strategies. Specifically, we recommend: (1) clinicians enhance vigilance and diagnostics for *Malassezia*-associated conditions; (2) laboratories strengthen mycological testing, incorporating molecular methods where feasible; and (3) public health initiatives utilize these data for targeted education, such as guiding adolescents in preventing pityrosporum folliculitis or advising on nail and pet hygiene. Consequently, our findings serve as a timely evidence base for shaping localized prevention and control measures. Ongoing regional surveillance remains crucial to monitor this evolving epidemiological landscape.

Disclosure of conflict of interest

None.

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Supplementary Table 1. Fungal species identified in superficial mycoses patients (Shantou, 2022-2024): original diagnostic names, simplified names, counts, and percentages

Fungal species (original)	Count	Simplified name	Percentage (%)
Malassezia growth	1112	Malassezia	42.20
Yeast-like growth	784	Yeast-like fungi	29.75
Trichophyton rubrum growth	273	Trichophyton rubrum	10.36
Trichophyton mentagrophytes growth	252	Trichophyton mentagrophytes	9.56
Candida albicans growth	80	Candida albicans	3.04
Microsporum canis growth	72	Microsporum canis	2.73
Microsporum gypseum growth	16	Microsporum gypseum	0.61
Epidermophyton floccosum growth	14	Epidermophyton floccosum	0.53
Rhodotorula growth	13	Red yeast	0.49
Candida tropicalis growth	8	Candida tropicalis	0.30
Trichophyton violaceum growth	5	Trichophyton violaceum	0.19
Candida glabrata growth	4	Candida glabrata	0.15
Aspergillus niger growth	1	Aspergillus niger	0.04
Trichophyton tonsurans growth	1	Other fungi	0.04