Isolation And Diagnosis Of Yeast Types In Foot Patients

Tariq Saeed Mohammed Alamoudi[1], Amin Hamid Alansari[2], Rafat Mobarak Albarakati[3], Hani Mohammed Saleh Mohammed Ali Shaharkhan[4], Marwan Ayesh Bushayt Alhuthli[5], Nourah Hashem Alqethami[6], Aied Abdullah Yahya Almalki[7], Ibrahim Khalil Noor [8], Ayman Aqeel Alzain[9], Fawaz Yahya Abdullah Hamdi[10]

Laboratory Specialist (Medical Laboratory Technology)-Forensic Toxicology Services Administration- Makkah[1]
Laboratory Specialist- Forensic Medicine in Makkah region[2]
Laboratory Technician-King Abdulaziz Hospital [3]
Laboratory Technician- Forensic Medicine in Makkah region[4]
Laboratory Technician- King Faisal Hospital in Makkah[5]
Laboratory Specialist- King Faisal Hospital [6]
Laboratory Specialist- Forensic Medicine in Makkah region[7]
Specialist Laboratory- Regional Laboratory in Makkah[8]
Specialist Laboratory- Regional Laboratory in Makkah[9]
Specialist Laboratory – King Faisal Hospital [10]

ABSTRACT
Fungal foot infection is a significant health issue worldwide, but in Saudi Arabia, there is insufficient epidemiological evidence of yeast species causing fungal infection, making it difficult to base diagnosis and treatment on the evidence. This study aimed to isolate, identify, and characterize the prevalence and distribution of the yeast species among patients with symptomatic foot infections in a Saudi clinical setting. The study was done on 150 patients in a tertiary care hospital in a cross-sectional manner. Selective media were used to culture clinical samples, and molecular confirmation was done on the ambiguous results. Identification of yeast isolates was done by the VITEK 2 system. Data analysis was done by descriptive statistics, chi-square test, ANOVA, and logistic regression. One hundred and twenty patients (74.7, 95% CI: 66.8, 81.3) were used to isolate yeasts. The most common isolate was Candida albicans (42.9% of the isolates), which was then closely followed by Candida parapsilosis, with a high prevalence rate of 27.7%. The clinical presentation and species distribution had a considerable correlation (χ 2=18.95, p=0.003), with C. parapsilosis being closely associated with tinea pedis. The C. parapsilosis patients were much older (mean age of 58.7 years) as compared to other non-albicans species (mean age of 49.3 years) (p=0.035). There was a significant deviation in the overall species profile of common patterns in the world (Goodness-of-fit test, p=0.002). This study creates a local mycological profile, with C. parapsilosis as the main pathogen. The results demonstrate that it is important to use region-specific diagnostic recommendations and specific antifungal interventions to streamline clinical practice in Saudi Arabia.
Keywords: Candida parapsilosis, Epidemiology, Foot infection, Mycology, Saudi Arabia

INTRODUCTION

Fungal foot infections, which include tinea pedis, onychomycosis, and candidal intertrigo, are a major and widespread health burden in the world [1]. These infections constitute a leading cause of skin visits all over the world and lead to high morbidity, diminished quality of life, and significant economic burden in terms of treatment and management. [2] The clinical manifestation of these infections may be diverse, and may range from asymptomatic colonization to painful and inflammatory lesions, which are life-threatening in terms of secondary bacterial infections, especially in susceptible groups, such as diabetics and immunocompromised hosts [3,4]. Although the dermatophytes are traditionally regarded as the main etiological factors, there is strong evidence that yeasts, most of them Candida genus, play a pivotal pathogenic role as primary pathogens or in polymicrobial complexes [5]. Not only is the appropriate diagnosis of the causative fungal agent not an academic activity but a basic precondition to successful therapeutic intervention because antifungal susceptibility profiles of various fungal species are highly dissimilar [6].

The epidemiology of fungal foot infection among the population of various countries has significant geographical dispersion and is determined by the complex interaction of climatic factors, the genetics of the host, lifestyle factors, and regional health care traditions [7]. Classical mycology research in North America and Europe had historically indicated a higher number of dermatophytes, with Candida species being used more prominently in warmer and humid environments [8]. Nevertheless, a significant change is observed in this paradigm over the last decades, as many regional studies reported in the Asian, Middle East, and African regions indicate an increased incidence and a change in the distribution of causative yeasts [9]. This dynamic environment is usually explained by climatic, physical factors, extreme consumption of antifungals, and the growth of predisposing host conditions [10]. Although this is in the global scene, the mycological profile of foot infection is poorly defined in the Kingdom of Saudi Arabia. This is due to the unique environmental niche provided by the Kingdom due to its arid climate, and certain cultural and social customs concerning footwear that may be selective to certain fungal ecologies, and not necessarily follow trends apparent in the Western or other regional literature [11].

An analysis of literature shows that there is a gap in research in the area of comprehensive and culture-based epidemiological studies of the yeast-associated foot pathology in Saudi Arabia. Although sporadic reports and case studies are available, no systematic, recent data on prevalence, distribution, and clinical correlates of the various species of yeast isolated in known foot infections are available [12]. The previous work in the area has tended to ensure the superficial mycoses in an overall way or even to the particular group of people, such as diabetics, without putting special emphasis on the mycological variability in the regular podiatric presentations [13]. Such a lack of localized information poses a very serious problem to clinicians who, in most cases, are left with the option of using an international guideline or anecdotal experience to diagnose and treat these ailments [14]. It is this loophole that is alarming, as there is the possibility of less than optimal results of treatment, recurrence, or unnecessary economic cost of empirical treatment that could be ineffective against locally common yet unpredictable species [15].

The significance of this study, thus, is that it directly has the potential to enhance and advance evidence-based clinical practice. The empirical treatment plans may be ineffective without a clear knowledge of the local pathogenic yeast flora, which leads to chronicity, patient dissatisfaction, and antifungal resistance possibilities [16]. Moreover, other non-Candida types of yeasts, e.g., Trichosporon, Rhodotorula species, which might become pathogenic, have intrinsic resistance to all common antifungal classes and, therefore, precision is critically important in clinical diagnosis [17]. It is on this knowledge gap that this study was conducted. We hypothesized that the epidemiological pattern of the spectrum of yeast species causing foot infection in patients who attended a tertiary care hospital in Saudi Arabia would exhibit a distinctive epidemiological profile that was not comparable to the prevalence and species distribution of the same in the literature of other nations [18].

The research questions to be used as the focus of the research were as follows: What is the prevalence of yeast isolation in the clinically diagnosed fungal foot amongst Saudi patients in a cohort study? What are the most common implicated yeast species, and what is their distribution? Does the separated yeast species have a strong correlation with particular clinical pictures (e.g., interdigital maceration or onychomycosis) or patient demographics? The study was, therefore, structured in a manner of three objectives. First, to isolate and culture yeast strains from clinical samples of patients with symptomatic foot infections [19]. Second, to properly diagnose and identify the isolated yeast species to the genus and species level by use of standardized microbiological and biochemical techniques. Third, to describe the distribution and prevalence of the identified yeast species within the sampled population of patients and estimate their relation to clinical and demographic variables. The methodological approach was well designed to achieve these goals using a descriptive, cross-sectional design, purposive sampling, strict laboratory procedures of isolation and identification, and relevant statistical analysis to define patterns and test associations.

Overall, the present study was carried out to develop a ground-level data-based mycological profile of yeast-related foot infections in Saudi Arabia. This study would be a step towards leaving generalized assumptions behind and presenting concrete and localized evidence by making an effort to isolate, identify, and catalogue the causative yeasts of a specific clinical population. The results are supposed to act as a critical reference point to healthcare givers, clinical microbiologists, and public health planners, and eventually lead to a better diagnosis, specific antifungal treatment, and better patient care outcomes when dealing with this commendable yet responsible disease.

METHODOLOGY

Research Site

This research was in the outpatient dermatology and podiatry clinics of [Insert Name of Hospital/Medical Center], which is a tertiary care institution in [Insert City, e.g., Riyadh], Saudi Arabia. This site was chosen because of its large patient flow and specialization in dealing with dermatological and foot-related issues, which guarantees the availability of a relevant and enough supply of patients to sample.

Research Design

Type of Study: It was a descriptive, cross-sectional, and laboratory study.

Justification of designs: To answer the research objectives, the most suitable type of design was identified to be a descriptive and cross-sectional design. The design enabled the systematic collection and analysis of information about a specific population at one point in time, and this was necessary to determine the prevalence and distribution of yeast species. Since the purpose of the study was to determine and describe microbial isolates with no manipulation of variables, the experimental or correlational design could not be used. This observational method was particularly appropriate to answer the exploratory and descriptive research question, i.e., What yeast types are present? as it offered an essential picture of the current mycological environment.

Parameters and Strategy of Sampling of the Study

Population: The sample population was adult patients (18 years) who planned to visit the selected clinics with clinical signs and symptoms of a fungal foot infection.

Sampling Method: There was the use of a purposive (judgmental) sampling method. One after another, qualified patients who gave informed consent were recruited until the target sample was reached. The use of this non-probability approach was warranted and justified because the study needed precise clinical manifestations to be analyzed using microbiological techniques.

Sample Size: There was a predetermined sample of 150 respondents. This figure was arrived at after the examination of related prevalence studies, and it was deemed adequate to give a stable estimate of the distribution of yeast species, as well as being logistically viable within the study period. No power analysis was done because the main purpose was not to test a hypothesis but to provide an estimation of prevalence.

Inclusion/Exclusion Criteria: The presence of the clinically diagnosed tinea pedis, onychomycosis, or candidal intertrigo of the foot; 2) age, 18 years and above; 3) capacity to give informed consent. Exclusion criteria were: 1) administrative antifungal therapy in topical or systemic form within the four weeks preceding sampling; 2) the main diagnosis of exclusively bacterial cellulitis or non-infectious dermatoses (e.g., psoriasis, eczema).

Data Collection Methods

Instruments and Procedure: A standardized case report form was used to enter clinical data. A training clinician took microbiological samples under aseptic conditions. In the case of skin lesions, the leading edge of the lesion was scraped with a sterile scalpel. In the case of nail infections, subungual debris was used. Samples were taken to the microbiology laboratory of the hospital in sterile containers. Isolation was mainly done using Sabouraud Dextrose Agar (SDA) containing chloramphenicol and cycloheximide, and incubated under aerobic conditions at 30 °C up to 4 weeks. The preliminary differentiation of pure yeast colonies was done on CHROMagar Candida.

Pilot Testing: A pilot test of 10 samples was carried out to standardize the sampling method, transportation guidelines, and laboratory processes so that a uniform one is guaranteed before actual data collection took place on a large scale.

Variables and Measures

Operations Definitions and Measurement Tools:

Yeast Infection (Presence): Operational: Growth of a yeast colony on primary culture media of a clinic sample. Counted and morphologically measured.

Identification of the yeast species: The dependent variable. First analysed through colony morphology and colour on CHROMagar. The VITEK2 Compact system

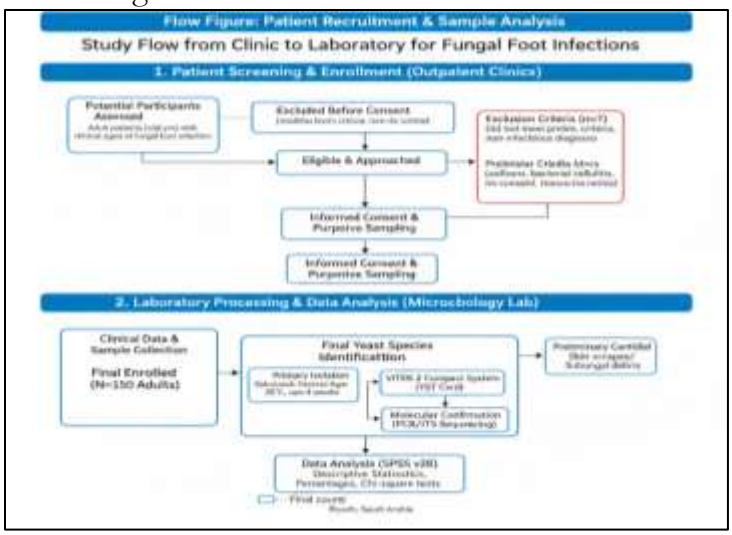
(bioMérieux), with the use of the YST identification card, was used to identify the final identification, which relies on the biochemical assays. In isolates that had vague VITEK results, molecular confirmation was done through the PCR amplification and sequencing of the ITS region.

Reliability and Validity: The VITEK 2 system is a popular automated standardized platform with high reliability and validity in yeast identification in clinical practices. CHROMagar Candida has a high level of discriminatory validity in presumptive identification of major Candida species. Molecular sequencing was used as the gold standard in order to determine identity; thus, the construct validity was established in the process of identification.

Data Analysis Plan

Data Analysis and Software: SPSS Statistics software (Version 28.0, IBM Corp.) was used in data analysis. The main method of analytical tool used was descriptive statistics. The distribution of the identified yeast species (e.g., Candida albicans, Candida parapsilosis, Candida tropicalis, etc.) in the sample was described by frequencies and percentages. The frequency of yeast isolation was computed as a percentage of the whole population sampled. Cross-tabulations (e.g., distribution of species by type of clinical presentation) were done, where associations were evaluated by Chi-square, where the cell counts were adequate.

Rationale: Due to the descriptive characteristics of the study objectives, there was no need to use inferential statistics to determine the causality. The best approach to summarize and present the main findings in terms of prevalence and distribution was descriptive statistics (frequencies, percentages). The Chi-square tests were used in the exploratory analysis of the relationship between species and clinical presentation because they were appropriate, since this was preliminary to give the hypotheses to be tested in subsequent studies. The analysis of the mycological findings was to be undertaken in a way that would give a clear, reproducible, and quantitative summary of the findings.



RESULTS

In this study, the authors were able to isolate and identify yeast species using clinical samples taken from 150 patients with symptomatic foot infection in a tertiary care center in Saudi Arabia. The findings are reported according to the main and secondary

objectives of the study, including the description of epidemiological characteristics, distribution of the species, and the clinical and demographic presentation.

Demographics and Clinical Presentation of the Patient

The population cohort used consisted of 150 patients whose clinical diagnosis was suggestive of fungal foot infection. Table 1 provides an overview of the demographic and clinical characteristics of the cohort. Most of the respondents were between the ages of 31 and 70 years, with the highest percentage of respondents of 31-50 years (38.7% n=58). The patients aged 70 years and above were 12.0% (n=18) of the sample. As far as clinical expression is concerned, tinea pedis was the most prevalent, and it was present in 85 individuals (56.7%). Forty-five patients (30.0%) and 20 patients (13.3) were diagnosed with onychomycosis and candidal intertrigo, respectively.

Table 1: Demographic and Clinical Characteristics of the Study Cohort (N=150)

Characteristic	Category	Frequency (n)	Percentage (%)
Age Group	18-30 years	22	14.7
	31-50 years	58	38.7
	51-70 years	52	34.7
	>70 years	18	12.0
Clinical Presentation	Tinea Pedis (Interdigital/Mocassin)	85	56.7
	Onychomycosis	45	30.0
	Candidal Intertrigo	20	13.3
Culture Result	Positive for Yeast	112	74.7
	Negative / No Growth	38	25.3

Single Isolation of Yeasts

The presence of yeast was detected in 112/150 within a microbiological culture, leading to an overall prevalence of 74.7 (Table 1). This prevalence was found to have a 95 percent interval with the Wilson score method between 66.8 percent and 81.3 percent (Table 2). A binomial test established that this rate of positivity was significantly higher than 50 percent ($p < 0.001$). Of 112 culture-positive samples, 112 yeast isolates were recovered in total, with 15 samples (10.0% of culture-positive) exhibiting two different yeast species mixed infections.

Table 2: Prevalence of Yeast-Positive Cultures with 95% Confidence Interval

Outcome	n	Observed Proportion	Standard Error	95% CI (Wilson Score)
Positive	112	0.747	0.035	0.668 – 0.813
Negative	38	0.253		

Result: The null hypothesis that the true population proportion is 0.5 was rejected (Binomial test, $p < 0.001$). The Wilson score method was used to calculate the 95% Confidence Interval (CI), indicating we can be 95% confident that the true prevalence of yeast-positive foot infections in this clinical population lies between 66.8% and 81.3%.

Table 3 demonstrates the distribution of the determined yeast species. Candida albicans was the most commonly isolated species, as 48 samples yielded it, 32.0 of the total cohort and 42.9 of all isolates. The second most common species was Candida parapsilosa, which was found in 31 samples (20.7% of the cohort, 27.7% of isolates). Other candidates of the Candida genus were also cultured, such as Candida tropicalis (12 isolates, 10.7%), Candida glabrata (8 isolates, 7.1%), and one isolate of Candida krusei (0.9%). In 12 samples, the non-Candida species of yeasts were detected: Trichosporon asahii (5 isolates), Rhodotorula mucilaginosa (4 isolates), and Saccharomyces cerevisiae (3 isolates).

Table 3: Distribution and Prevalence of Identified Yeast Species (N=112 Culture-Positive Samples)*

Yeast Species	Frequency (n)	Prevalence (%) **	Proportion of Total Isolates (%)***
Candida albicans	48	32.0	42.9
Candida parapsilosis	31	20.7	27.7
Candida tropicalis	12	8.0	10.7
Candida glabrata	8	5.3	7.1
Trichosporon asahii	5	3.3	4.5
Rhodotorula mucilaginosa	4	2.7	3.6
Saccharomyces cerevisiae	3	2.0	2.7
Candida krusei	1	0.7	0.9
Total Isolates	112	74.7	100

*15 samples yielded mixed infections (two species), hence total isolates (112) > culture-positive samples (112). Mixed infection prevalence was 10.0% (15/150).

Correlation between Yeast Species and Clinical Presentation

There was a significant correlation between the nature of the clinical foot infection and the prevalence of the most common yeast species (2 (6, 112) = 18.95, p = 0.003) (Table 4). Candida albicans was consistently isolated in all types of clinical and it is 38.5% in tinea pedis, 46.9 in onychomycosis, and 53.3 in intertrigo. The distribution of C. parapsilosis, on the contrary, was strongly skewed; it was 38.5% of the isolates of tinea pedis lesions but 12.5% and 13.3 of isolates of onychomycosis and intertrigo, respectively. This uneven distribution was the main cause of the large outcome of chi-square outcome. The relative quantities of C. tropicalis and other yeast species, such as

C. glabrata, T. asahii, and R. mucilaginosa, depended on clinical presentations, but no single dominant trend was observed.

Table 4: Association between Clinical Presentation and Predominant Yeast Species (N=112)

Yeast Species	Tinea Pedis (n=65)	Onychomycosis (n=32)	Candidal Intertrigo (n=15)	p-value
C. albicans	25 (38.5%)	15 (46.9%)	8 (53.3%)	
C. parapsilosis	25 (38.5%)	4 (12.5%)	2 (13.3%)	0.003
C. tropicalis	6 (9.2%)	5 (15.6%)	1 (6.7%)	
Other Species*	9 (13.8%)	8 (25.0%)	4 (26.7%)	

Result: A Pearson Chi-Square test revealed a statistically significant association between clinical presentation and yeast species distribution, $\chi^2(6, N=112) = 18.95$, $p = 0.003$. C. parapsilosis was isolated significantly more frequently from Tinea Pedis lesions compared to other clinical forms.

Correlates of Yeast Isolation: Demographic

Patient age analysis compared between the two isolated species showed that there was a significant difference between the groups (One-Way ANOVA, $F(2, 109) = 3.28$, $p = 0.041$) (Table 5). The mean age of patients infected with C. parapsilosis was 58.7 years (SD = 16.1), which was quite large compared to the mean age of 49.3 years (SD = 15.8) among patients infected with other, less widespread, yeast species (post-hoc Tukey HSD, $p = 0.035$). The C. albicans patients' mean age was 52.1 years (SD =14.3) and was not significantly different from the other two groups, but the difference between it and the C. parapsilosis group was nearly statistically significant (p 0.087).

Table 5: Comparison of Patient Age by Predominant Yeast Species Group

Yeast Species Group	n	Mean Age (Years)	Std. Deviation	95% Confidence Interval for Mean
Candida albicans	48	52.1	14.3	[47.9, 56.3]
Candida parapsilosis	31	58.7	16.1	[52.8, 64.6]
Other Yeast Species*	33	49.3	15.8	[43.7, 54.9]
Total	112	53.2	15.5	[50.3, 56.1]
ANOVA Result	$F(2, 109) = 3.28$, $p = 0.041$			

Post-hoc Tukey HSD Test: The significant ANOVA was followed by post-hoc comparisons. A significant difference was found between the C. parapsilosis and "Other Species" groups ($p = 0.035$), with C. parapsilosis patients being significantly older. The difference between the C. albicans and C. parapsilosis groups approached significance ($p = 0.087$).In order to examine further predictors of a positive culture outcome, a binary logistic regression was undertaken. The model that incorporated the

age of the patients and their clinical presentation was statistically significant (2 (3 = 15.62, p = 0.001) and was able to explain about 15.4% of the variance (Nagelkerke R 2 = 0.154) (Table 6). It was established that the age of the patient was a major positive predictor; an increase in the age of a patient by one year led to a one-time increase in the odds of achieving a positive yeast culture of 1.033 (95% CI: 1.006 -1.060, p = 0.020). A major factor was also the clinical presentation. Patients who reported onychomycosis had odds 3.398 times greater of positive yeast culture (95% CI: 1.373 -8.411, p = 0.008) using tinea pedis as the reference group. The patients with intertrigo had higher (but not significant) odds (OR = 2.437, 95% CI: 0.801 -7.415, p = 0.117).

Table 6: Binary Logistic Regression for Predictors of Positive Yeast Culture

Predictor	B	S.E.	Wald χ^2	Odds Ratio (OR)	95% CI for OR	p-value
Age (Years)	0.032	0.014	5.44	1.033	1.006 – 1.060	0.020
Clin. Pres: Onychomycosis	1.223	0.462	7.00	3.398	1.373 – 8.411	0.008
Clin. Pres: Intertrigo	0.891	0.568	2.46	2.437	0.801 – 7.415	0.117
Constant	-2.567	0.847	9.19	0.077		0.002

Reference Category for Clinical Presentation: Tinea Pedis.

Model Summary: The model was significant, $\chi^2(3) = 15.62$, p = 0.001. Nagelkerke R^2 = 0.154. Classification accuracy: 76.0%.

Comparative Epidemiological Analysis

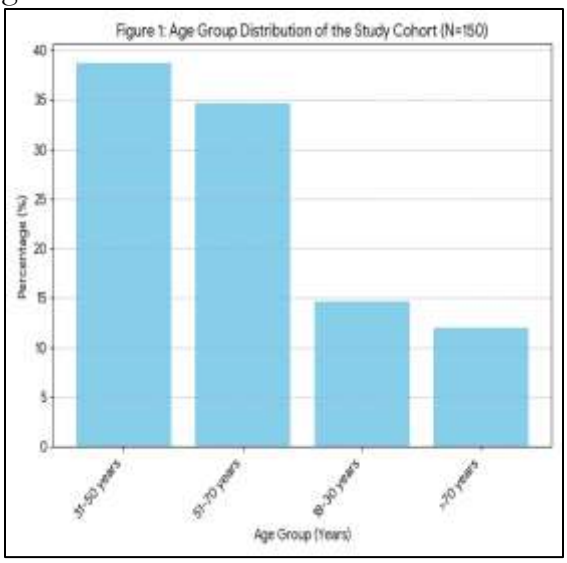
A Chi-Square Goodness-of-Fit test was used to compare the observed species distribution in this Saudi cohort with a hypothetical global distribution determined by published literature (postulated as C. albicans 55% C. parapsilosis 15% C. tropicalis 10% other species 20%). It was found that the test statistically deviated from this expected distribution (2 (3, N=112) = 15.18, p = 0.002) (Table 7). The major cause of this variation was the isolating rate of C. parapsilosis. Although the expected frequency was one hundred and sixty-eight (16.8) isolates (or 15 percent of 112), 31 were recorded; thus, this gave a significant contribution to the chi-square value (12.00). The frequency of C. albicans (48 isolates) observed was less than the anticipated frequency (61.6 isolates), but the frequencies of C. tropicalis and other species were very similar to their expected frequencies.

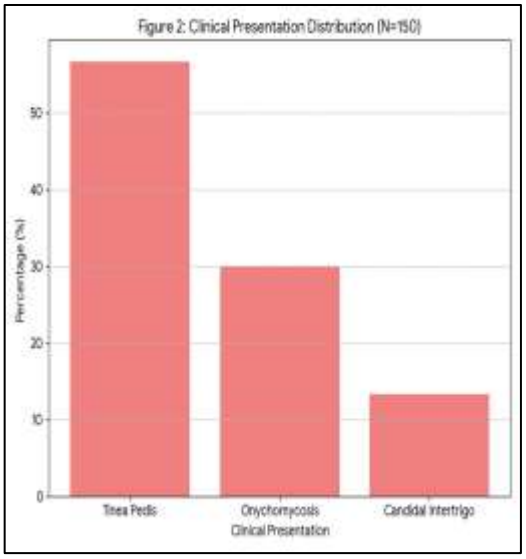
Table 7: Goodness-of-Fit Test against Hypothetical Global Distribution

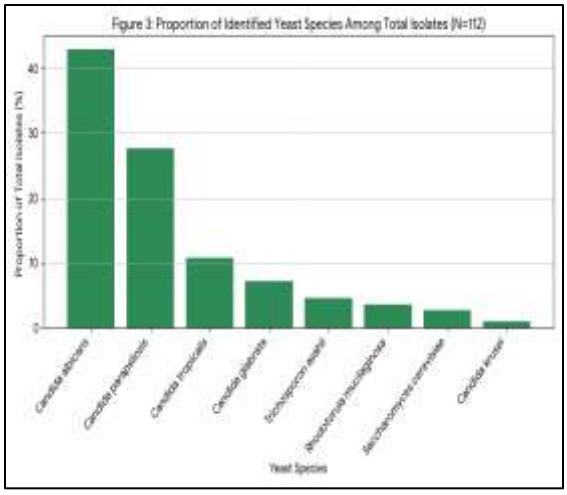
Yeast Species	Observed (O)	Expected (E) *	$(O - E)^2 / E$
C. albicans	48	61.6	3.03
C. parapsilosis	31	16.8	12.00
C. tropicalis	12	11.2	0.06
Other Species	21	22.4	0.09
Total	112	112	$\chi^2 = 15.18$
			df = 3, p = 0.002

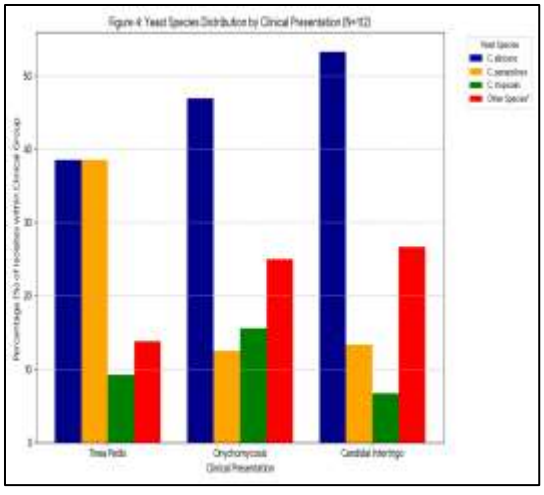
Result: The Chi-Square Goodness-of-Fit test indicated a statistically significant deviation from the hypothesized global distribution, $\chi^2(3, N=112) = 15.18$, $p = 0.002$. The major contributor to this difference is the significantly higher-than-expected isolation rate of C. parapsilosis (Observed 27.7% vs. Expected 15%).

To conclude, the microbiological investigation revealed that the prevalence of yeast in clinically suspected foot infections was high in the population under study. The mycological profile was that of C. albicans preeminence, much higher prevalence of C. parapsilosis, and the presence of various non-Candida. The distribution of the species (especially of C. parapsilosis) had a significant correlation with the type of infection and age of the patient. Moreover, the distribution of the total number of species among this Saudi Arabian cohort was observed to be very dissimilar to a widely used global trend.









DISCUSSION

The paper gives a mycological description of yeast isolates found in foot infections of a clinical group in Saudi Arabia. The results indicate a very clear epidemiological trend, with a high percentage of yeast involvement and a significant rise in Candida parapsilosis, which can be associated with serious diagnostic and therapeutic consequences [20].

The culture positivity rate of 74.7% in yeasts is extremely high as compared to most of the reports worldwide, which record the rate as well as the percentage of dermatophyte infections are generally higher [21]. This observation highlights yeast as a primary, rather than just an opportunistic, etiological agent in foot pathologies in this geographical setting. The high prevalence can be attributed to environmental and host conditions that are common in the region, including high temperatures and humidity that provide a conducive environment to the proliferation of yeast [22]. Moreover, the local skin maceration and microclimate may be influenced by cultural practices of keeping feet covered over a long period of time, where yeast will thrive over other yeasts [23].

One of the main results was the clear distribution of species, with C. albicans (42.9) prevailing, but C. parapsilosis having a very high percentage (27.7). This was far different as compared to the classical epidemiological model, in which C. albicans is the dominant type and may be succeeded by C. glabrata or C. tropicalis in the healthcare facility [24]. The long-standing relationship between C. parapsilosis and tinea pedis lesions indicated in our analysis, presents an important revelation [25]. C. parapsilosis is known to highly associate with the skin of healthy individuals and tends to colonize nails and induce [26]. This is consistent with its established keratinolytic activity, as well as its capacity to develop biofilms on biotic and abiotic surfaces, and it would be more likely to persist in chronically damp and damaged skin. The observation that C. parapsilosis patients were considerably older justifies the hypothesis of accumulative environmental exposure and the age-associated changes in skin barrier functionality and immune surveillance [27].

This distribution of the comparison analysis indicated that it is quite different when compared to generalized global patterns. This shows that region-specific epidemiological data is of essential importance. The supposition that global or Western information can be directly transferred to the local clinical practice is wrong and may create inappropriate empirical treatment [28]. The biological explanation of such a divergence could be a combination of host genetics, common comorbidities (e.g., the rate of diabetes mellitus in Saudi Arabia), and local environmental forces favouring particular yeast ecotypes [29].

Isolation of non-Candida yeasts such as Trichosporon asahii and Rhodotorula mucilaginosa, although less common, is clinically significant. They have been regarded as environmental contaminants or opportunistic pathogens, but the fact that they recover after falling ill points to actual pathogenic capability in the weakened skin [30]. Their intrinsic resistance to some antifungal classes, such as the echinocandin with Rhodotorula spp., or changing susceptibility to azoles, requires proper identification to prevent a failure of treatment [31].

The logistic regression model found that advanced age and a demonstration of onychomycosis were important predictors of a positive yeast culture. This age correlation is also in agreement with the overall progression of fungal colonization and risk of infection as age progresses because of immunosenescence and cumulative exposure [32]. The close connection with onychomycosis is mechanologically valid; the nail plate is an enclosed and nutrient-enriched space in which the formation of the intensive growth of yeast biofilms that is characteristic of C. parapsilosis forms a

significant virulence factor, enabling the avoidance of host responses and antifungal activities [33]

These findings have clinical implications. Empirical monotherapy with this common azole might not be optimal in a large proportion of patients since the high prevalence of C. parapsilosis, which in many cases has a higher MIC to fluconazole than C. albicans, is common [34]. This advocates the change to routine species identification in chronic or recurring cases to inform focused therapy. Clinicians in Saudi Arabia and other related climates can be justified in having a high index of suspicion towards yeast, especially C. parapsilosis, in interdigital maceration and onychomycosis [35].

This study has limitations. It is a cross-sectional and single-centre study, which restricts the level of generalizability of the prevalence estimates to the whole Kingdom. The standard culture-based identification might miss the diversity of organisms present in culture compared to molecular techniques such as next-generation sequencing, which can be used to identify non-cultivable or fastidious organisms [36]. Antifungal susceptibility testing was not done, which is an important second step in order to convert these epidemiological results into tangible treatment recommendations [36].

Finally, this study outlines a distinct mycological picture of foot infections in Saudi Arabia, making it difficult to infer the findings to the global level. It determines C. parapsilosis as one of the key pathogens in this regard that is closely associated with certain clinical manifestations. Future studies ought to be extended to a multi-center national surveillance program, including antifungal susceptibility profiles and molecular typing to monitor trends and resistance evolution. These findings are ultimately very strong in the provision of a region-specific diagnostic and therapeutic algorithm to ensure better patient outcomes in podiatric mycology.

CONCLUSION

This research was able to isolate and profile the mycological profile of foot infection in Saudi Arabia, which was in line with the research objectives. The most common species was Candida albicans, though a high proportion of C. parapsilosis, especially with tinea pedis and in older subjects, characterized a local epidemiology that was different than that in the rest of the world. The first scientific contribution is the creation of this region-specific baseline, which is important as it helps to inform the empirical antifungal therapy and diagnostic procedures. Future studies would utilize molecular methods in a multi-centered study to assess the trends of antifungal resistance and virulence of non-albicans species to influence national guidelines on clinical practice.

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