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TROPICAL MYCOSES (L MARTINEZ, SECTION EDITOR)

Epidemiological Attributes of *Candida* Species in Tropical Regions

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Abstract

Purpose of Review Global burden associated with the growing incidence of fungal infections poses as a serious threat especially in developing countries. Several local surveillance programs have already been established to follow the epidemiological characteristics of *Candida* infections; however, these programs often only focused on broadly researched regions, like Europe, North America, and certain Asian countries. Therefore, the need to evaluate epidemiological data is high in less studied regions, for example in the tropical climate zone countries, especially since the number of fungal infections is generally described to be higher in these locations.

Recent Findings *C. albicans* is still the most often isolated pathogenic species, in the *Candida* genus; however, the importance of other NAC (non-albicans Candida species) is increasing. Distributions of frequently isolated *Candida* species known to differ according to climate zones. For instance, Northern Europe and the USA generally report *C. glabrata* as the most prominent NAC species, while *C. tropicalis*-associated infections are more common in tropical regions.

Summary Current epidemiological data from tropic regions highlights the importance to study *Candida*-associated fungal infections in these locations, since besides the most common pathogens, emerging species like *C. auris* appearing to become more frequently isolated.

Keywords *Candida* · Candidaemia · Tropical · Climate zone · Infection · Species distribution

Introduction

The mortality rate associated with fungal infections is comparable with that of tuberculosis and malaria. An estimation made by Bongomin et al. suggests that about 1.6 million deaths are related to chronic or acute fungal infections annually [1]. Comparatively, according to a recent report by WHO (World Health Organization), approximately 400,000 and 1.5 million people die from malaria and tuberculosis, respectively, every year [2, 3], albeit these are single diseases. Besides the high mortality rates, global burden associated with fungal diseases takes major tolls both on the economy and healthcare of countries, especially in the developing world [4, 5].

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Candida species are the most prevalent invasive human pathogenic fungi globally [6]. The distribution of these species depends on several factors. These include the geographic location, age of the affected population, socioeconomic conditions, levels of urbanization, and application of antifungal drugs [1, 7, 8]. Irrespectively of age, predisposing factors, and geographical localization, in most cases, *C. albicans* is the most prevalent human pathogenic *Candida* species. However, there has been a substantial shift towards non-*albicans Candida* species (NAC) [9]. Isolation frequency of the most common NAC species, *C. parapsilosis*, *C. glabrata*, and *C. tropicalis*, even surpasses *C. albicans* in certain studies. [10–12].

Candida species are common commensals of the human skin, the genitourinary and gastrointestinal tract [13]. However, commensal to pathogenic shift can occur under certain predisposing conditions. The change of this commensal state leads to a broad number of infections. This can range from local mucosal and superficial infections to more severe manifestations like deep seated candidiasis and bloodstream infections (candidaemia) [14]. The emergence of invasive candidiasis cases can be linked with medical interventions that include the long-term use of central venous catheters, dialysis, parenteral nutrition, broad-spectrum antibiotic therapy,

hospitalization in intensive care units (ICUs), and therapeutic immunosuppression. All of these healthcare-associated factors increase the risk for infection [15]. Significantly, several diseases also directly or indirectly predispose patients to be at increased risk for fungal infections. These include AIDS, diabetes, neutropenia, premature birth, and primary immunodeficiencies [14, 16–18].

As noted above, the age of the patient population is another important aspect. Among neonates and extremely low birth weight neonates (< 1000 g), candidiasis is the most common mycoses [18]. While it is associated with high mortality (30–60%), among the survivors, it can also cause long-term neurodevelopmental impairment [19, 20]. A meta-analysis from 2014 found *C. parapsilosis* to be responsible for one third (33.47%) of all studied *Candida* infections in neonatal patients, making it one of the most significant pathogens in this age group [21]. On the other hand, among elderly patients, *C. glabrata* is the most frequently isolated NAC (non-albicans *Candida*) species [22, 23]. The dominance of *C. glabrata* and *C. parapsilosis* as NAC species in these two high-risk patient groups poses a therapeutic challenge, as significant percentages of isolates from both of these species are less susceptible to commonly applied therapeutic drugs, and these patients are commonly immunosuppressed. *C. parapsilosis* isolates are frequently less susceptible to echinocandins in vitro, and fluconazole-resistant isolates occur [24]. Interestingly, *C. glabrata* genome plasticity can be linked with acquired antifungal resistance, especially for fluconazole [25, 26]. *C. tropicalis* infections are particularly problematic in neutropenic and cancer patients, especially in nosocomial setting [27, 28]. Moreover, Ko et al. reported poor outcome of patients with candidiasis due to *C. tropicalis*, further increasing the importance of this species [29]. Another less common NAC species, *C. krusei*, also causes therapeutic challenge, since it is intrinsically resistant to fluconazole and can rapidly acquire resistance to other antifungals [30].

Despite some inconsistencies, several studies have described that distribution of the frequently isolated species and type of infection also differs according to the climate zones [4, 31, 32]. Close surveillance programs are in place to monitor *Candida* bloodstream infection (BSI) episodes in several regions worldwide. Scandinavian countries (Norway, Sweden, Finland, Denmark) and other countries in Europe and in Asia, the USA, and Canada have all collected comparable multicenter/multihospital or nationwide studies with epidemiological data of *Candida*-associated infections [33–37]. These data enable us to study changes in species and patient distributions, different predisposing factors, and frequency of antifungal resistance. In contrast, multicenter epidemiological studies are limited in tropical countries, and they generally concentrate only on one hospital unit or patient population. The studied patient population can be divided by age (neonates and elderly patients), infection site (vulvovaginal candidiasis (VVC), urinary infections, skin infections, bloodstream infections), and the associated predisposing conditions (oncologic, hematological malignancies) [38–45]. In 2005, a group of investigators in South and Central America formed a network, called Latin American Invasive Mycosis Network. Their surveillance data revealed different distribution of *Candida* species in Latin-American countries, compared with the Northern Hemisphere's countries [31]. This effort underscores the need for careful comprehensive studies in other tropical regions.

Candidaemia in Tropical Regions

In 2013, a report from the Latin American Invasive Mycosis Network concluded that the number of candida infections in tropical countries can be 3–10 times higher than cases reported from temperate zone countries [31]. Among the locations, the variance between the number of fatal cases is even greater than in incidence numbers, which is possibly due to the living standards of the regions where the study was taken [46–48].

Results from the comparison of tropical and temperate climate countries suggest that the rates of various clinical manifestations of *Candida* infections are also climate dependent. Fungal keratitis, superficial dermal infections, and vulvovaginal candidiasis (VVC) are relatively common in tropical climate countries, but less frequent in temperate and continental climate countries [40, 49, 50]. Despite not being directly lethal, VVC and fungal keratitis present a serious financial burden on countries with high rates of disease [49–52]. Furthermore, in severe cases, colonization of epithelial surfaces may also lead to deep seated infections and even bloodstream infections as well as invasive bacterial superinfections [53].

Inconsistencies in the preferred species identifying methods are problematic both in terms of generating comparable epidemiological data and in the selection of effective treatment methods. Identification techniques in epidemiological studies range from phenotype-based identification (microscopy, ChromAgar, germ tube formation for micro-, and macromorphology determination) to more accurate molecular identification techniques such as MALDI-TOF and ITS sequencing (Table 1) [7, 46, 64–66]. Data from studies where species discrimination is based on phenotypic traits is highly inaccurate, as they are subjective and identification could be isolate specific [67–69]. One of the possible dangers of these inaccuracies intensified in the last decades, as represented by the increasing number of antifungal resistant isolates of several species (especially *C. glabrata* and *C. parapsilosis*) and with the appearance and emergence of novel pathogens such as *C. auris*, as misidentification during

Table 1 Epidemiological studies evaluated in this review

Region	Type of study	Time period	Number of cases	Species distribution	Identification method	Admission rate	Reference
Brazil							
Southeast	Single center	2009–2016	352	43.7% *C. albicans* 21.3% *C. tropicalis* 16.5% *C. parapsilosis* 8.5% *C. glabrata*	VITEK 2 system	1.36 cases/1000 admission	[46]
Multiregion	Multicenter	2007–2010	137	34.3% *C. albicans* 24.1% *C. parapsilosis* 15.3% *C. tropicalis* 10.2% *C. glabrata*	MALDI-TOF	n.d	[54]
Southeast	Single center	2004–2016	113	35.6% *C. albicans* 30.0% *C. parapsilosis* 16.7% *C. tropicalis*	Microbiological classification	5.9 cases/1000 admission	[35]
Northeast	Single center	2011–2016	87	35.3% *C. albicans* 27.4% *C. tropicalis* 21.6% *C. parapsilosis*	VITEK 2 system (MALDI-TOF)	2.23 cases/1000 admission	[52]
Northeast	Multicenter	2011–2015	70	34.3% *C. albicans* 25.7% *C. tropicalis* 25.7% *C. parapsilosis*	MALDI-TOF	n.d	[55]
Southeast	Multicenter	1980–2015	78	33% *C. parapsilosis* 21% *C. tropicalis* 5% *C. albicans*	n.d	n.d	[38]
Southeast	Single center	1996–2016	331	37.5% *C. albicans* 28.1% *C. tropicalis* 18.4% *C. parapsilosis*	Microscopic morphology, VITEK 2 system	1.30 cases/1000 admission	[43]
South	Multicenter	2011–2016	149	52% *C. albicans* 15% *C. tropicalis* 15% *C. glabrata* 11% *C. parapsilosis*	VITEK 2 system, ITS sequencing	n.d	[56]
Southeast	Single center	2014–2015	79	44% *C. albicans* 19% *C. glabrata* 19% *C. tropicalis* 14% *C. parapsilosis*	VITEK 2 system, biochemical analysis	1.52 cases/1000 admission	[57]
India							
North India	Multicenter	2015–2018	228	67% *C. albicans* 16% *C. tropicalis* 5.5% *C. glabrata*	VITEK 2 system, MALDI-TOF	n.d	[58]
Delhi	Single center	2012–2017	114	39.4% *C. tropicalis* 17.5% *C. auris* 14% *C. albicans*	VITEK 2 system, MALDI-TOF	n.d	[51]
Delhi	Multicenter	2011–2015	91	22% *C. albicans* 22% *C. tropicalis* 20% *C. parapsilosis*	VITEK 2 system	n.d	[34]
Colombia							
	Multicenter	2010–2011	147	40.8% *C. albicans* 23.1% *C. parapsilosis* 17% *C. tropicalis*	MALDI-TOF	n.d	[59]
	Multicenter	2010–2013	2533	48.3% *C. albicans*		n.d	[60]

Table 1 (continued)

Region	Type of study	Time period	Number of cases	Species distribution	Identification method	Admission rate	Reference
				20% *C. tropicalis* 14.7% *C. parapsilosis*	Phenotype analysis, VITEK 2 system		
Ethiopia							
	Multicenter	2015–2016	210	58.6% *C. albicans* 17.2% *C. krusei*	VITEK 2 system	n.d	[48]
Gabon							
	Single center	2016–2017	249	82.73% *C. albicans* 4.02% *C. famata* 3.21% *C. rugosa*	Morphology analysis, ChromID	n.d	[36]
Reunion Island							
	Single center	2004–2015	171	54% *C. albicans* 17% *C. glabrata* 12% *C. tropicalis*	MALDI-TOF	7.6 cases/1000 admissions	[39]
Mexico							
	Multicenter	2005–2014	58	43.1% *C. albicans* 27.6% *C. parapsilosis* 12.1% *C. glabrata*	Phenotype analysis (ChromAgar, biochemical testing), VITEK 2 system	n.d	[61]
	Single center	2006–2015	89	52.8% *C. tropicalis* 30.4% C. albicans 10.1% *C. parapsilosis*	ITS sequencing	n.d	[61]
Peru							
	Multicenter	2013–2015	158	27.8% C. albicans 25.3% *C. parapsilosis* 24.7% *C. tropicalis*	Microbiological classification, VITEK 2, ITS sequencing	2.04 cases/1000 admission	[62]
Malaysia							
	Single center	2000–2013	1716	47.49% *C. tropicalis* 35.38% *C. parapsilosis* 26.86% *C. albicans* 11.08% *C. glabrata*	Phenotype analysis, ITS sequencing	n.d	[50]
Vietnam							
	Multicenter	2013–2015	93	50.54% *C. tropicalis* 19.35% *C. albicans/C. dubliniensis* 17.2% *C. parapsilosis*	RFLP analysis	n.d	[63]

n.d no available data

the diagnostic process could lead to insufficient treatment [70, 71].

Search Strategy

Review of the current literature was carried out using the PubMed database. The search was performed applying 'candida' and 'epidemiology' as key words and the search period was narrowed down to studies published between 2015 and 2020. Results were further narrowed down to tropical countries before the studies were evaluated in this review.

Distribution of *Candida* Species

As previously mentioned, the distribution of *Candida* species in tropical countries often differs from what is commonly observed in colder climates. For example, epidemiological studies from Northern Europe and the USA report more cases associated with *C. glabrata* infections, while this pathogen is less frequently identified in tropical regions [32].

Due to incomplete surveillance in tropical places, overarching estimates can only be deducted by analyzing data from more broadly researched locations, like those in Brazil, and

connect these findings to the limited number of studies from other tropical countries.

An extensive step was taken to study *Candida*-associated infections in these countries with limited data by the Latin American Invasive Mycosis Network [31]. The first report of this network included 672 cases of candidaemia from seven Latin-American countries, with the mean incidence of 1.31 per 1000 admissions. Overall *C. albicans* was the most commonly isolated pathogen (37.6%) followed by *C. parapsilosis* (26.5%) and *C. tropicalis* (17.6%). *C. guilliermondii* was the fourth (6.5%) while *C. glabrata* was the fifth most common species (6.3%). This contrasts with European and North American reports where *C. albicans* is dominant followed by *C. glabrata*, while *C. parapsilosis* and *C. tropicalis* cases are less common [32, 33].

Brazil

A recent study from Brazil identified 352 *Candida* isolates from blood cultures in a tertiary care university hospital, between 2009 and 2016 (Table 1). The identification process consisted of phenotypical methods (micromorphology analysis, Gram staining), which were confirmed later by VITEK 2 system. In this case, the incidence of *Candida*-related BSI was determined as 1.36 infections per 1000 admissions, with a mortality rate of 54.6%. From the 352 isolates, 43.7% were classified as *Candida albicans*, followed by *C. tropicalis* as the second most common species (21.3%) followed by *C. parapsilosis* sensu lato species (16.5%) and the *C. glabrata* complex (8.5%) [46].

The increased prevalence of NAC species is further highlighted by a multicenter study (16 participant hospitals). From the diagnosed 137 candidaemia cases, 34.3% were caused by *C. albicans*, 24.1% by *C. parapsilosis*, 15.3% by *C. tropicalis*, and 10.2% by *C. glabrata.* The crude mortality was remarkably high (72%) [54•].

Another retrospective cohort study from 2020 investigated candidaemia cases among pediatric oncology patients. In this case, the 12-year study (2004–2016) identified 113 candidaemia cases utilizing microbiological classification methods. In this setting, a relatively high incidence rate was defined (5.9 BSI case/1000 admissions). Pediatric oncology patients frequently receive chemotherapeutic treatments, which is a well-known predisposing factor for the development of candidiasis [72]. In the oncopediatric patient population, *C. albicans* was the most commonly isolated species (35.6%) followed closely by *C. parapsilosis* (30.0%) and then *C. tropicalis* (16.7%) [39].

To acquire information about candidaemia cases in the lowest income region of Brazil, a single-center study (January 2011 to December 2016) was performed, and the authors reported the registration of 87 bloodstream *Candida* infections. *Candida* species were identified by VITEK 2 system and, in some cases, MALDI-TOF. The annual incidence of candidaemia episodes was estimated to be 2.23/1000 admission, with an average mortality rate of 55.9% within 30 days after the diagnosis. The most prevalent species were *C. albicans* (35.3%), *C. tropicalis* (27.4%), and *C. parapsilosis* (21.6%) [66]. Another publication from a similar time period and location found similar species distribution in a multicenter setting. In the 70 diagnosed bloodstream infections, 34.3% were associated with *C. albicans*, while the *C. tropicalis* and *C. parapsilosis* complex species caused 25.7–25.7% of infections [55].

With a similar study period, another investigation was conducted in Northeast Brazil, between 2009 and 2016, focusing on mycoses. Vulvovaginal infections were the most frequent type of fungal disease (42.2%), while onychomycosis was diagnosed in 38.78% of cases followed by other less frequently affected sites, like feet (8%) and scalp (2%). Among the infections caused by yeasts (82.9%), *Candida* spp. were identified as causative agent in approximately 80% of cases. Species distribution within the *Candida* genus is not relevant in this case as the utilized methods were not suitable for the accurate identification of the isolates. As mentioned by the authors, this data further straightens the need for standardized diagnostical procedures to create comparable epidemiological data [73].

Dermatomycosis cases in Brazil were also studied between 1996 and 2011. According to the findings, 4815 of the 38,520 fungal infections were linked to the genus *Candida* (12.5%), which corresponds with previous studies observing high incidences of fungal dermal infections in warmer climate zones. This data further strengthens the importance of this genus, even among non-bloodstream mycoses [74].

A retrospective cohort study in five hospitals performed between 1980 and 2015 investigated fungal endocarditis cases. Of the 78 diagnosed patients, 66 (85%) were infected with *Candida* spp., making the genus the most prevalent pathogen in this setting. Regarding species distribution, *C. albicans* isolates were identified in only 5% of cases, whereas 20 cases (33%) were caused by *C. parapsilosis* followed by *C. tropicalis* (21%) [42].

Candidaemia cases in Rio de Janeiro were also monitored in a study that took place between 1996 and 2016. During this time period, 324 patients (331 cases) were diagnosed with *Candida*-related bloodstream infection, with the mean incidence of 1.30 episodes/1000 hospital admission annually. Bloodstream infection due to *C. albicans* was identified in 37.5% of cases, whereas *C. tropicalis* and *C. parapsilosis* were isolated in 28.1% and 18.4% of cases, respectively. Crude mortality rate was determined to be as high as 58.9%, higher than that of previous regional studies [47, 75, 76].

In Southern Brazil, a retrospective analysis identified 149 episodes of candidaemia between February 2011 and February 2016. *C. albicans* was the most prevalent (52%),

while candidaemia due to NAC species was less frequent (15% for both *C. tropicalis* and *C. glabrata*, 11% *C. parapsilosis*). As detailed above, the appearance of *C. glabrata* as a second/third most common isolate is alarming, since this species frequently develops antifungal resistance, decreasing therapy efficiency, and increasing medical costs [56]. The shift between *C. albicans* and non-*albicans Candida* species was further supported by Canela et al. in a single-center study conducted between June 2014 and November 2015 that identified 79 bloodstream *Candida* isolates via VITEK 2 system and biochemical characteristic analysis. The overall incidence of *Candida* infections was 1.52 cases/1000 admission. Infections due to *C. albicans* (44%) were followed by *C. glabrata* (19%), *C. tropicalis* (19%), and *C. parapsilosis* (14%) [57•].

In sum, according to recent epidemiological data, *C. albicans* is still the most prevalent Candida species in Brazil, followed by *C. tropicalis* as the most commonly isolated NAC species.

Colombia

Candidaemia cases in Medellín, Colombia, were examined in a single-center study, between August 2010 and November 2011. In the 15-month period, 147 patients were diagnosed with *Candida* bloodstream infections with *C. albicans* identified in 40.8%, 23.1% *C. parapsilosis* and 17% *C. tropicalis* [58]. Similar species distribution was reported in a broad multicenter study by Motoa et al. in 2016. This research group identified 2680 fungal isolates between 2010 and 2013 in several intensive care units. From the 2680 isolates, 2533 (94.5%) were members of the *Candida* genus and 1224 isolates (48.3%) were identified as *C. albicans*, followed by *C. tropicalis* as the second most common species (20%) and *C. parapsilosis* as the third (14.7%) [59]. Epidemiological data from the last 5 years revealed that species distribution is similar to the data observed in Brazil.

Interestingly, Armstrong et al. reported a multi-hospital outbreak of *C. auris*, which took place between 2015 and 2016. They identified 40 cases in 4 different hospitals, with a median patient age of 23 years. According to this study, 30% of the patients were infants, which is higher than what has been previously observed during other *C. auris* outbreaks. With an approximated crude mortality rate of 58%, *C. auris*-associated nosocomial infections are clearly a threat in certain tropical regions [48].

In Colombia, epidemiological data from the last 5 years revealed that species distribution is similar to the data observed in Brazil. The presence of *C. auris* was also registered in this country, with an alarmingly high incidence among infants during outbreaks.

India

Epidemiology studies on fungal infections have also been conducted in several locations in India. One study from the North Indian Haryana region reported the isolation of 228 *Candida* isolates in a 3-year time period (December 2015 and June 2018). As a result, *C. albicans* was identified in 153 cases (67%), followed by *C. tropicalis* (16%) and *C. glabrata* (5.5%). The work of Kumar et al. highlights the importance of utilizing methods like MALDI-TOF for identification, as 10 isolates of *C. auris* were proven to be previously misidentified as *C. haemulonii* by VITEK-2 [60]. Another study collecting epidemiology data of candidiasis in the semi-arid tropical region of India was performed at a trauma center in New Delhi where 114 patients were diagnosed with candidaemia. *C. tropicalis* was identified in 39.4% of all cases, highlighting its predominance. *C. auris* was the second most common (17.5%), while *C. albicans* was only the third most prevalent (14%) pathogen. The identification was performed by both VITEK 2 and MALDI-TOF analysis, and the results were compared. The comparison revealed that VITEK 2 system recognized *Candida* species correctly in only 65% of cases [65••]. Similarly, to the previous study by Kumar et al., misidentification was most common in case of *C. auris*, as these isolates were falsely referred to as *C. haemulonii* [60]. Taken together, since azole resistance is extremely common in *C. auris*, these results further highlight the need for mutual agreement on best practices for *Candida* species identification, since correct species identification is essential for the empiric selection of the antifungal therapy pending the determination of formal susceptibilities [69].

Another study was carried out in New Delhi, between July 2011 and February 2015, in the neonatal unit of a tertiary hospital. In this patient cohort, 91 of the 401 bloodstream isolates (22.7%) belonged to the genus *Candida*, with *C. albicans* and *C. tropicalis* being the most prevalent species with 20–20 cases, followed by *C. parapsilosis* (18 cases) [38].

Epidemiology data from India confirms the role of *C. tropicalis* as the most commonly isolated non-albicans *Candida* species and it even exceeds *C. albicans* in certain settings. The findings also highlight the need for universal and refined diagnostical methods indicated by the misidentification and growing significance of the novel pathogen *C. auris*.

Ethiopia

As previously mentioned, clinical manifestation of *Candida* infections might be location dependent. For example, vulvovaginal candidiasis (VVC) episodes are more prevalent in countries like Cameroon, Ethiopia, Ivory Coast, Senegal, and they are mostly associated with *C. albicans* infections [40].

A study from 2019, by Tufa et al., estimated the *Candida*-associated burden of fungal infections in Ethiopia. According to their data, about 6% of adult Ethiopian women are afflicted with recurrent vulvovaginal candidiasis, with the estimated number of 1,469,100 cases annually [77]. Species distribution from 210 VVC cases showed that the most prevalent species was *C. albicans*, as it was responsible for 58.6% of cases, followed by *C. krusei* (17.2%) [52].

Other Tropical Countries

The distribution of *Candida* species associated with VVC was also determined in Gabon, between January 2016 and December 2017. From the 249 cases, *C. albicans* was the etiological cause in 82.73%. The most prominent NAC isolates were atypical, as *C. famata* and *C. rugosa* were isolated from 10 (4.02%) and 8 (3.21%) patients [40].

Candidaemia cases in the ICU setting were analyzed in the French oversees department Reunion Island in the Indian Ocean between January 2004 and December 2015. During the 12-year period, 171 patients were diagnosed with *Candida*-associated bloodstream infections and 54% of the cases were caused by *C. albicans* with *C. glabrata* being the second most frequently isolated species (17%) and *C. tropicalis* the third (12%). The overall incidence of *Candida* infections was determined to be 7.6 episodes per 1000 admissions [43].

A retrospective review was conducted in a similar time period between 2005 and 2014 in Mexico City, Mexico. From the 58 isolates, identified by VITEK 2, 25 cases (43.1%) were caused by *C. albicans*, while 27.6% of the isolates was *C. parapsilosis* and 12.1% *C. glabrata* [61].

A multicenter study from Peru found that *C. albicans* was the predominant species in candidaemia cases with 27.8% (44/158 isolates) of all isolates followed by *C. parapsilosis* and *C. tropicalis* in 25.3% and 24.7% of the cases, respectively. The annual incidence was determined to be 2.04 episodes per 1000 admissions [62].

Ng et al. from Malaysia reported 34,392 *Candida* isolates between 2000 and 2013 that were obtain from clinical samples retrieved from various sites, including blood, oral cavity, respiratory tract, HVS (high vaginal swab), urine, and pus. Overall, 66.7% of the isolates was identified as *C. albicans*, followed by *C. glabrata* (11.71%), *C. parapsilosis* (10.74%), and *C. tropicalis* (9.19%). In the 1716 bloodstream samples, the prevalence of the NAC species was higher (73.14%) than observed in other isolation sites like oral cavity or urine. Of the bloodstream isolates, 47.49% were *C. tropicalis*, 35.38% were *C. parapsilosis*, and 11.08% were *C. glabrata* [64].

As mentioned previously, the incidence of certain NAC species in several studies in tropical countries was greater than that caused by *C. albicans*. A study evaluating *Candida* bloodstream isolates in two Vietnamese hospitals during the period between May 2013 and May 2015 identified 93 bloodstream isolates out of which 50.54% (47 cases) were identified as *C. tropicalis*, making it the most common species in this region [63]. A similar distribution was also found in Mexico in a study of isolates obtained between 2006 and 2015. In this case, from the 89 BSI cases, 52.8% were identified as *C. tropicalis*, while *C. albicans* was responsible for only 30.4% of all cases, followed by *C. parapsilosis* (10.1%) [78].

Conclusion

Candidaemia poses as a serious global threat, particularly in patients with predisposing factors in the hospital setting [79]. Epidemiological data from temperate climate countries is relatively broad, since it includes studies from intensively surveyed places including Europe and North America [33–36]. Despite the fact that there are some studies, particularly in Brazil and India, that provide well-curated data on the species distribution, surveillance studies are still needed from warmer countries to develop better estimates about invasive candidiasis cases.

By reviewing the available up-to-date epidemiological data from tropical climate countries, it can be concluded that the distribution of *Candida* species remained similar to what had been previously reported by the Latin American Invasive Mycosis Network in 2013. According to studies from Brazil, *C. albicans* is still the most commonly isolated species followed by *C. tropicalis* and *C. parapsilosis*.

An alarming observation in several studies is the high prevalence of *C. glabrata*, as antifungal resistance is commonly associated with these isolates [43, 56, 57•, 61, 64]. Studies from Ethiopia and Gabon highlight the high incidence of non-systemic candida infections, such as vulvovaginal candidiasis. While in both regions, most of these infections are caused by *C. albicans* (58.6% and 82.73%), less common species like *C. krusei* and *C. famata* are also responsible for VVC development [40, 77].

It is also noteworthy to point out the importance of correct species identification in these tropical regions, to avoid misidentification, such in the case of *C. auris*, as mentioned above [60]. Emergence of this novel, frequently azole-resistant pathogen could significantly increase the burden of fungal infections in these tropical climate countries. Overall, given the tremendous burden of disease due to *Candida* species, improved surveillance along with validated identification as well as susceptibility testing should be pursued within and across countries.

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Compliance with Ethical Standards

Conflict of Interest The authors declare that they have no conflict of interest.

Human and Animal Rights and Informed Consent This article does not contain any studies with human or animal subjects performed by any of the authors.

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Papers of particular interest, published recently, have been highlighted as:
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