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ORIGINAL ARTICLE/ARTICLE ORIGINAL

The identification of *Meyerozyma guilliermondii* from blood cultures and surveillance samples in a university hospital in Northeast Turkey: A ten-year survey

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Summary *Meyerozyma (Pichia) guilliermondii* exists in human skin and mucosal surface microflora. It can cause severe fungal infections like candidemia, which is an opportunistic pathogen. One hundred and forty-one *M. Guilliermondii* isolates, consisting of 122 blood culture isolates, belonging to 126 patients; 13 total parenteral nutrition solution isolates; and two rectal swab isolates were identified according to carbohydrate assimilation reactions in a university hospital in Turkey between January 2006 and December 2015. Following *Candida albicans* (34.0%) and *C. Parapsilosis* (21.2%), the third yeast species most commonly isolated from blood cultures in the Farabi Hospital was *M. guilliermondii* (20.6%). The patients were hospitalised in 27 different departments. A total of 50% of the patients were in pediatric departments, 49.2% were in intensive care units, and 17.2% were in haematology-oncology departments. Molecular identification of the isolates was performed using DNA sequence analysis of ribosomal ITS gene regions and IGS amplification-*Alu*I fingerprinting (IGSAF). With molecular identification, 140 isolates were identified as *M. guilliermondii* and one isolate was identified as *Candida membranifaciens*. It was observed that the ITS1 region specifically helps in identifying these species. It was demonstrated that biochemical and molecular methods were 99.3% consistent in identifying *M. guilliermondii*. The Wild-Type (WT) Minimum Inhibitory Concentrations (MICs) distribution of fluconazole, voriconazole, itraconazole, and flucytosine were determined using

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the Sensititre YeastOne YO2V system after 24 h of incubation. One *M. guilliermondii* strain was determined to be non-WT for fluconazole, voriconazole, itraconazole and flucytosine. In total, three *M. guilliermondii* strains, for fluconazole, were determined to be non-WT in this study.

Introduction

Isolates identified as *Candida guilliermondii* (teleomorph *Pichia guilliermondii*) were included in the new *Meyerozyma* genus by Kurtzman and Suzuki in 2010 [1]. The *M. guilliermondii* complex is a genetically heterogeneous complex comprising several phenotypically indistinguishable taxa, including *M. guilliermondii*, *Candida fermentati*, *Candida carpophila*, and *Candida xestobii* [2—5]. However, the species *Candida famata* (teleomorph *Debaryomyces hansenii*) and *M. guilliermondii* are extremely difficult to differentiate phenotypically. They have a phylogenetically close relationship [6,7].

M. guilliermondii is widely distributed in nature and is a common constituent of the normal human microflora [8] and is reported to be responsible for severe fungal infections such as candidemia, a human opportunistic pathogen. *M. guilliermondii* is defined as a newly emerging, rare pathogen that is responsible for a small percentage of all candidemia. Moreover, in the past 20 years, it was observed that this pathogen was responsible for 1—11.7% of all candidemia, with increasing incidence [9—11]. This species is a more common cause of candidemia in cancer patients than it is in general hospital populations [11—14]. *M. guilliermondii* fungemia may occur in children with underlying conditions other than cancer [15,16]. Besides sporadic candidemia cases, candidemia outbreaks (real or pseudo) caused by the species were seen [17—19]. Candidemias are infections with high mortality [20]. Furthermore, this species is especially notable for its greater propensity to express multidrug resistance than other organisms of the genus *Candida* [21]. Nevertheless, antimycotic sensitivities of this fungus have not been clarified.

In the Farabi Hospital, the *M. guilliermondii* has been the third yeast species most frequently isolated from blood cultures in the past 10 years. The objective of the present study was to assess whether the biochemical identification was correct using nucleotide sequencing and Restriction Fragment Length Polymorphism Analysis of PCR-Amplified Fragments (PCR-RFLP) and to determine in vitro sensitivity of *M. guilliermondii* to fluconazole, voriconazole, itraconazole and flucytosine.

Materials and Methods

Yeast strains

This retrospective study evaluates a ten-year-period between January 2006 and December 2015 at Farabi Hospital, which is a university hospital in Trabzon, Turkey. The *M. guilliermondii* isolate, which was first isolated from the blood cultures of each patient, was included in the study. *M. guilliermondii* strains isolated at intervals of ≥ 4 weeks, from successive specimens of the same patient, were considered as different candidemia episodes. One isolate representing each episode was included in the study. One hundred and forty-one *M. guilliermondii* isolates were identified from blood cultures (126 isolates) of 122 patients. Surveillance specimens consisted of total parenteral nutrition (TPN) solutions (13 isolates) and rectal swabs (two isolates). Most of the isolates (87.23%) belong to times of outbreak (Fig. 1).

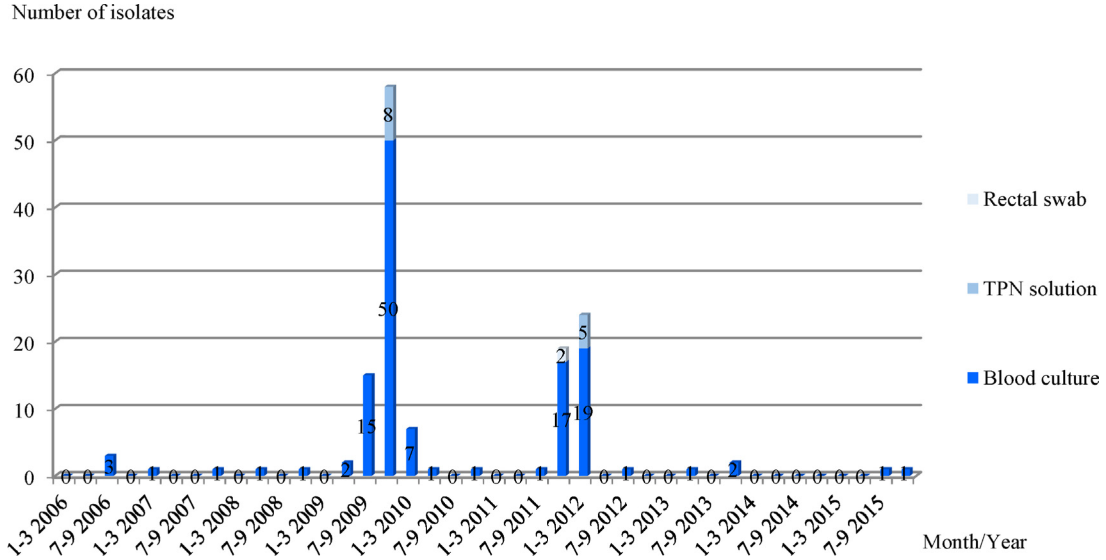

Figure 1 Distribution of *M. guilliermondii* isolates isolated from blood cultures and surveillance specimens in the university hospital in Northeast Turkey.