of *C. glabrata*, accounting for less than 15% of isolates from blood cultures. However, if *Candida* spp are isolated from blood cultures, *C. parapsilosis* and *C. tropicalis* were detected up to ten fold more often in comparison to other sources of isolation. This difference in local epidemiology should be taken into account for treatment decisions of candidemia.

doi:10.1016/j.ijid.2008.05.773

45.032

Differential Expression Study of a Potentially Novel Gene in *Candida albicans* Morphology Switching

C.S.Y. Lim1,∗, W.F. Wong2, C.H. Tung1, R. Rosli1, H.F. Seow1, P.P. Chong1

1 University Putra Malaysia, Serdang, Malaysia
2 Tohoku University, Sendai, Japan

Candidiasis and systemic candidiasis are on the rise in recent years, especially in immunologically challenged persons. Morphology switching in *Candida albicans*, the most virulent human fungal pathogen, has been identified as one important factor of virulence. Nevertheless, the exact mechanism of this phenomenon has not been fully understood. This has prompted intensive research into the genetic aspects of *Candida albicans* pathogenicity, albeit the elusive gene(s) causing morphology switching has not been uncovered. In our study, an uncharacterized gene fragment of interest was previously found via differential display reverse transcription-PCR. A1–1 was identified as upregulated in the *Candida albicans* hyphal forms at 1, 3 and 6 hours after hyphal induction compared to the yeast form. The differential expression of A1–1 in yeast-hyphae switching was then studied in further detail. *Candida albicans* yeast forms were grown at 25 °C in Winge medium. Half of this culture was incubated in hyphal-induction conditions in RPMI-1640 added with penicillin-streptomycin and fetal bovine serum at 37 °C with 5% CO2. RNA from the yeast form and hyphal forms at 1, 3, 6, 12 and 24 hour time-points were extracted. All RNA were reverse transcribed into cDNA. A1–1 sequence-specific primers were designed, with beta-actin as the housekeeping gene. The Pfaffl mathematical method of relative quantitative real-time PCR using SYBR Green was used to validate the differential expression. A1–1 was found to be upregulated in the hyphal forms of *Candida albicans*. This gene fragment has presented itself as an interesting target for ongoing further studies to elucidate the function of this potentially novel gene in *Candida albicans* yeast-hyphae morphology switching.

doi:10.1016/j.ijid.2008.05.774

45.033

Prevalence of *Trichophyton rubrum* in Tehran, Isolated from Different Levels of Society and Study of Its Probable Organ Orientation

F. Asghari Paskiabi∗, A.A. Khaksar, S. Basiri, G. Sadeghi, A. Najafi

Pasteur Institute of Iran, Tehran, Iran (Islamic Republic of)

**Background:** *Trichophyton rubrum* is the most common dermatophyte species and the most frequent cause of fungal skin infections in humans worldwide. It’s a major concern because feet and nail infections caused by this organism is extremely difficult to cure.

**Methods:** A total of 3942 patients referred to Mycology Department of Pasteur Institute of Iran, were examined for fungal infection during 20 March 2006 to 20 March 2007. Samples were gathered by scalping the suspected area, and then were inspected by microscope and also were cultured. Two different media (Sabouro-Dextrose-Agar with Chloromphenicol and Sabouro-Dextrose-Agar with Chloromphenicol and Cyclohexamid) were used for all samples to specify the name of fungus in positive ones and also to confirm lack of them in negative samples.

**Results:** The proportion of male and female in number of people who were examined for fungal infections was equal. % 5.63 of whole (222 people) suffered from *Trichophyton rubrum* infection that %63.5 of them were men. People between 41 to 50 years old were the most infected by this fungus, followed by age groups of 31-40, 21-30, 51-60 and 10-20 years old respectively. There were just a few people in 61-70 and 71-80 years old groups infected and only one child under 10 years old was infected by *Trichophyton rubrum*. Totally sole was the most involved organ followed by groin, toe webs and sole together, toe nail, toe webs singly and foot. However *Trichophyton rubrum* trended to infect men’s groins slightly more than their soles.

**Conclusion:** There should be more care about hygienic issues especially for people who are in their active age and are unavoidably involved in social activities. It is recommended not to use common wears especially shoes and slippers in order to decline the rate of *Trichophyton rubrum* infection.

doi:10.1016/j.ijid.2008.05.775

45.034

Molecular Differentiation and Antifungal Susceptibility of *Candida parapsilosis* Isolated from Patients with Fungemia

S.T. Tay∗, K.P. Ng, S.L. Na, J. Chong

University of Malaya, Kuala Lumpur, Malaysia

The genetic heterogeneity and antifungal susceptibility patterns of *Candida parapsilosis* isolated from blood cultures of our patients were examined in this study. Polymerase chain reaction of yeast DNA with a single primer generated four unique fingerprints for the 45 blood isolates investigated in this study. Based on the fingerprints, the isolates were identified as genotype P1 (32 isolates), P2 (10 isolates), P3 (2 isolates) and P4 (1 isolate). Sequence analysis