Invasive fungal infections have always been a life-threatening disease for immunocompromised patients. Traditionally, the microbiology laboratory often offers little help in the diagnosis and treatment of these patients. However, with the advent of molecular and chemical diagnostic methods, and the standardization of susceptibility testing, more insights can now be shed. Molecular techniques generally detect the presence of the highly conserved region of the fungal organisms. Its success has been variable, and standardization of methods has been slow in progress. Chemical detection methods such as mannan, galactomannan has received renewed interest. The application of beta-D-glucan detection in the clinical settings has raised further enthusiasm not only in its high sensitivity, but also potentially as a monitoring marker for disease progress and treatment response. Disc diffusion susceptibility testing has allowed certain azole agents to be readily tested in the laboratory. Although the susceptibility of most Candida species can be predicted from its speciation, the availability of susceptibility surveillance programmes allows monitoring of resistance pattern. The advent of echinocandins further improves the clinical outcomes. Its selective toxicity is a much needed contribute in the treatment of these fatal diseases. With further clinical trials and animal models, understanding of this class of anti-fungal agent should widen its clinical application.

Fungal Infections — Insights from the bench-side

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Genotype distribution of Candida albicans in China

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Candida albicans is the most common opportunistic fungal pathogen of humans. It causes from benign infections such as oral and vaginal candidiasis to fatal, systemic infections in immunocompromised or critically ill patients. The genotype distributions of C. albicans strains with different sources were investigated using single-strand conformation polymorphism and GeneScan analyses of a microsatellite locus called CAI. The C. albicans strains from various extragenital sites, those from vagnas of asymptomatic women, and those causing vulvovaginal candidiasis (VVC) of women and balanoposthitis of men, were employed. Genetic similarity of representative strains with the same and different CAI genotypes were examined by sequence analysis of housekeeping genes CaADP1, CaSly1 and CaVPS13. The CAI genotypes of independent C. albicans strains from extragenital sites were mostly of individual specificity. In contrast, strains associated with VVC were mainly concentrated to a few dominant genotypes, with two CAI genotypes being the most common. The enrichment trend of the dominant genotypes of C. albicans strains correlated positively with the severity of VVC. A similar biased genotype distribution pattern of C. albicans strains associated with balanoposthitis was also revealed. The genetic similarity of strains with the dominant genotypes associated with both VVC and balanoposthitis was confirmed by sequence analysis of the three genes. The results suggest the existence of vaginopathic C. albicans strains with enhanced virulence and tropism for the vagina, and the high possibility of sexual transmission of genital C. albicans infection. Identification of specific genotypes that correlate with severity of VVC is certainly of diagnostic and therapeutic significance.

Non-culture diagnosis of fungal infection

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In recent years, as the growing number of immunocompromised hosts, there is an obviously increasing of opportunistic fungal infections. Candida infection is the commonest one especially Candidemia could lead to a high mortality. Other non-Candida yeasts infections are emerging, such as Trichosporon spp. infection. In BMT patients and other immunocompromised patients, invasive aspergillosis has been one of the major causes of death. How to improve the early and specific diagnosis level of fungal infection, especially the invasive fungal infection, is a big challenge.

Invasive fungal infections in Asia-Pacific region

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Invasive fungal infection has emerged as an important nosocomial infection, especially in critically ill patients. An increasing incidence of candidemia became apparent from the 1980 to the end of the 1990’s followed by relative stability. The incidence of candidemia in intensive care units (ICUs) is 5 to 10-fold that in overall hospitals, and more than 100-fold greater than in the general population in Asia-Pacific region. The crude mortality rate of patients with candidemia is in the range of 35–60%, however, ICU patients with candidemia had a higher mortality rate than non-ICU patients. The crude mortality with invasive aspergillosis is more than 60%, particularly in patients with hematological malignancy and transplant patients. Candida albicans remains the predominant cause of invasive candidiasis in more than 50% of all cases. C. tropicalis, C. glabrata and C. parapsilosis are the three most common non-albicans Candida species causing invasive candidiasis. The above four Candida species account for more than 90% of invasive candidiasis. Overall, invasive non-albicans Candida isolates remained highly susceptible to fluconazole (>90% susceptible) over the past two decades. However, the susceptible rate of C. glabrata to fluconazole varied widely from 22 to 72% and the resistant rate ranged from 2 to 16% in Asian countries. Analysis of the fluconazole susceptibilities of 204 bloodstream C. glabrata isolates revealed a rapid shift from susceptible (64% in 1999 to 2001 to 19% in 2007) to susceptible-dose dependent (27% in 1999 to 2001 and 75% in 2007) in Taiwan. Periodic surveillance is needed to monitor antifungal resistance because reduced fluconazole susceptibility in non-albicans Candida is not an uncommon trend. Echinocandins continue to exhibit excellent in vitro fungicidal activities against all Candida isolates and are promising agents for the treatment of patients with invasive candidiasis, particularly in ICU patients.