Abstract 2.5

Species Identification and Susceptibility Patterns of Trichosporon Clinical Isolates

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Background: There is limited data on Trichosporon species clinical isolate in Thailand. Then, DNA sequence and MADI-TOF mass spectrometry technique should support this information, including antifungal drug susceptibility patterns.

Methods: We examined 86 Trichosporon clinical isolates from 84 patients during December 2011-August 2014. They were from 73 urine, 6 blood, 2 sputum, 1 tissue biopsy, 1 pus and 3 others. They were investigated into species by sequencing of the IGS 1 region and MADI-TOF mass spectrometry, and broth microdilution antifungal drug susceptibility.

Results: Six isolates from blood were 3 T. mycotoxinivorans, 2 T. asahii and 1 T. facale. Trichosporon asahii was identified from 75/86 (87.2%) isolates by sequencing. The other species were 1 T. debeumanianum and 1 T. montevideens, 2 T. inkin, 2 T. asteroids. MADI-TOF technique could not identify 33/75 T. asahii, 1 T. asteroids, 1 T. debeumanianum, 1 T. mycotoxinivorans, 1 T. facale and 1 T. inkin. For T. asahii, amphotericin B MICs ranged at 0.12-8 mg/liter, (MIC at which 90% of isolates were inhibited [MIC90], 4 mg/liter). Theazole MICs were low such as MIC90s at 8 mg/liter for fluconazole, 0.5 mg/liter for itraconazole, 0.25 mg/liter for voriconazole, and 0.5 mg/liter for posaconazole. The echinocandins, caspofungin and anidulafungin demonstrated no against activity with high MIC > 8 mg/liter.

Conclusion: T. asahii was the most common recovered isolates from clinical specimens. Molecular analysis was required for species identification. According to high MIC to antifungal drugs, in vitro drug susceptibility testing was necessary.