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Molecular epidemiology and azole resistance mechanism study of Candida guilliermondii from a Chinese surveillance system

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Background: *Candida guilliermondii* has been reported to be an important pathogen causing a variety of deep-seated infections in immunocompromised patients, and it is of particular clinical importance as they have been shown to be more resistant to antifungal agents compared to other *Candida* species. Thus monitoring the epidemiological changes and studying the resistance mechanism of this organism is important for clinical therapy decision making and infection control strategies.

Material/methods: We studied the molecular epidemiology and mechanism of azole resistance of 164 *C. guilliermondii* isolates from a nationwide multi-center surveillance program in China. All the isolates were identified by ITS gene sequencing and the *in vitro* susceptibility to fluconazole and voriconazole was determined by Sensititre

YeastOne™ YO10 methodology. The 14-α-demethylase gene *ERG11* was amplified and sequenced, and the microsatellite analysis was performed to study the genetic relationship.

Results: Amongst 164 *C. guilliermondii* isolates, 12 isolates (7.3%), 3 isolates (1.8%), and 149 isolates (90.9%) were resistant, susceptible dose-dependent (SDD), and susceptible to fluconazole, respectively. A total of 16 sequence types (STs) were detected by comparing the amino acid sequence polymorphisms of the *ERG11* gene. Isolates with Y132F mutation were all resistant or SDD to fluconazole. A total of 40 different genotypes were identified by microsatellite analysis. The microsatellite genotypes were associated with drug resistance pattern but not so closely related with *ERG11* STs.

Conclusions: We found that the azole resistance patterns were closely related to *ERG11* sequence types, and microsatellite analysis may be a good typing tool to explore the clonal transmission and outbreak of *C. guilliermondii* isolates.