Implication of genotypes for prognosis of *Candida glabrata* bloodstream infections

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**Background.** Genotyping a specific pathogen may demonstrate unique patterns of antimicrobial resistance and/or interaction between pathogen and host, which subsequently lead to miserable consequence. Herein, we conducted a retrospective single-center study to analyze the association between genotypes and clinical outcomes among *Candida glabrata* bloodstream infections (BSIs).

**Methods.** A standard case report form was used to collect the clinical data of hospitalized adults with *C. glabrata* BSIs in 2017. Antifungal susceptibility testing was performed by using the Sensititre YeastOne SYO-10 panel, and minimum inhibitory concentrations (MICs) were interpreted according to the Clinical and Laboratory Standard Institute. Genotyping was performed by using a multilocus sequence typing scheme, and further analyzed by the unweighted pair group method with arithmetic averages (UPGMA) method.

**Results.** Among 48 patients, clonal complex 7 (CC7, defined by UPGMA similarities >80%) was the most common CC (n=14, 29.2%). The rates of fluconazole and candid resistance were low (6.6% and 0%, respectively) without specific distributions among genotypes Charlson comorbidity index (adjusted odd ratio [aOR], 1.49; 95% CI, 1.05-3.11) was the only risk factor for CC7 *C. glabrata* BSIs. CC7 was independently associated with 28-day mortality (aOR, 5.88; 95% CI, 1.06-32.47) in addition to a APACHE II score of >18 (aOR, 5.84; 98% CI, 1.16-29.46). The Kaplan-Meier survival analysis also showed greater mortality in CC7 (Figure). Fluconazole resistance or candid therapy had no significant impact on mortality.

**Conclusion.** Our data shed light on the impact of genotypes on clinical outcomes in *C. glabrata* BSIs. Further virulence characterization of CC7 is warranted.

**Disclosures.** All Authors: No reported disclosures