**ABSTRACT**

Candida species are the most common cause of invasive fungal infections, with fks1 mutations on high sensitivity hotspots (HS1) of 1,3-β-D-glucan synthase. We previously described mutation patterns on other HSs of Candida spp. isolates for fks2. Reduced echinocandin susceptibility has primarily been reported in C. glabrata (S645P) among 34 isolates (2.9%), and 2 isolates of C. tropicalis (S644T) of 12 strains evaluated (16.7%).

Materials and Methods: To obtain C. albicans, C. krusei, and C. glabrata strains from worldwide surveillance collections: the SENTRY Antimicrobial Surveillance Program and ARTEMIS. For determining the fks1 mutation patterns, we performed sequencing. For determining fks2 mutation patterns, we performed sequence alignments. The results were analyzed using the Lasergene software package (DNASTAR, Madison, WI). Sequences were compared to published sequences (GenBank). Sequences were compared to published sequences (GenBank).

**RESULTS**

- **Materials and Methods**: A total of 134 C. albicans isolates were sequenced. Sixteen FKS MIC values were selected from worldwide surveillance collections: the SENTRY Antimicrobial Surveillance Program and ARTEMIS.

- **Materials and Methods**: For determining the fks1 mutation patterns, we performed sequencing. For determining fks2 mutation patterns, we performed sequence alignments. The results were analyzed using the Lasergene software package (DNASTAR, Madison, WI). Sequences were compared to published sequences (GenBank).

- **RESULTS**: Isolates were collected from medical centers located in North America (41.0% of the strains), Europe (23.5%), Asia (29.6%), and Latin America (5.9%). FS2 strains had a high MIC range that was not tested. One isolate was further tested. One isolate was further tested. One isolate was further tested. One isolate was further tested.

- **RESULTS**: Among 7 C. glabrata strains tested for mutations of HS2 and HS1, and 2 isolates displayed mutations in the hotspots (CASP; [ECH class surrogate] and [CTRO] [ECH class surrogate] were selected for this study. Antimycotics and activities are defined as defined in the Informational Supplement. JMI Laboratories.

- **RESULTS**: All strains showed the fks1 mutations demonstrated elevated caspofungin MIC results (Table 2). However, two strains displayed non-susceptible MIC values for all echinocandin compounds. The remaining strain had lower MIC values for these echinocandin compounds. The remaining strain had lower MIC values for these echinocandin compounds. The remaining strain had lower MIC values for these echinocandin compounds.

- **RESULTS**: C. albicans strains harboring the fks1 mutations demonstrated no cross-resistance with other echinocandin compounds. The results were analyzed using the Lasergene software package (DNASTAR, Madison, WI). Sequences were compared to published sequences (GenBank).

- **RESULTS**: Mutations in fks1 were detected in C. glabrata, however one of the strains showed very low MIC values for echinocandin values on white blood cells.

- **RESULTS**: C. albicans strains showing caspofungin MIC values corresponding to WT distribution did not have the fks1 mutations. In C. glabrata, mutations displayed anidulafungin and/or micafungin MIC values within the WT population, suggesting that caspofungin could be the most sensitive agent for detection of these resistance mutations.

- **RESULTS**: C. albicans isolates showing clonal echinocandin MIC values were selected from worldwide collections and tested for the presence of a fks1 mutations. Results indicate that these mutations of this region appear to be uncommon.

**CONCLUSIONS**

- **CONCLUSIONS**: In C. glabrata, the fks1 mutations were found in 2.9% of the strains tested, and 16.7% of the strains tested. The results were analyzed using the Lasergene software package (DNASTAR, Madison, WI). Sequences were compared to published sequences (GenBank).

**REFERENCES**

