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ePoster Viewing

Highlights from molecular mycology

MULTI LOCUS SEQUENCE TYPING OF INVASIVE AND COLONIZING CANDIDA ALBICANS ISOLATES

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Objectives

With the exception of *Candida parapsilosis* infections invasive candidiasis has been considered an endogenous infection originating from *Candida* isolates colonizing the orointestinal tract. To proof this concept we investigated whether invasive and colonizing *Candida albicans* isolates belong to same or different MLST profiles.

Methods

Twenty *Candida albicans* isolates colonizing the oral cavity of healthy adults and 22 blood culture *Candida albicans* isolates as well as 2 orally colonizing *Candida albicans* isolates of candidemic patients were investigated by multilocus sequence typing (MLST) to determine relatedness of colonizing and invading *Candida* isolates. MLST profiles were examined by comparison of 7 DNA sites that encode housekeeping genes: AAT1a, ACC1, ADP1, PMI1b, SYA1, VPS13, and ZWF1b. UPGMA and eBURST analysis was used for phylogenetic assignment.

Results

Three isolates did not provide adequate PCR results and were excluded from analysis leading to comparison of 21 orally colonizing isolates and 22 invasive isolates obtained from blood cultures. There was no difference in distribution of invasive and commensal isolates in different clades as determined by UPGMA ($p > 0.05$ for all distributions to different clades) and eBURST analysis. The neighbor joining tree is presented as a figure; green circles=orally colonizing *Candida albicans* isolates, red circles=orally colonizing *Candida albicans* isolates from candidemic patients, red dots=invasive *Candida albicans* isolates from blood cultures

Conclusion

We could not find a certain MLST profile indicative for invasive *Candida albicans* isolates. Our investigation shows that colonizing and invasive *Candida albicans* were distributed to various genotypes.





