

Multi Locus Sequence Typing (MLST) of invasive and colonizing *Candida albicans* isolates



Medical University of Graz

K. Heidrich¹, W. Buzina¹, M. Hönigl², R. Krause².

¹ Medical University of Graz, Institute of Hygiene, Microbiology and Environmental Medicine, Graz, Austria.

² Medical University of Graz, Department of Internal Medicine, Section of Infectious Diseases and Tropical Medicine, Graz, Austria.

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Objectives

Except for *Candida parapsilosis* infections, invasive candidiasis has been considered an endogenous infection originating from *Candida* species colonizing the orointestinal tract [1]. To proof this concept we investigated whether invasive and colonizing *Candida albicans* isolates belong to same or different clades by means of multilocus sequence typing (MLST), currently the most suitable method for populational studies in *C. albicans* [1].

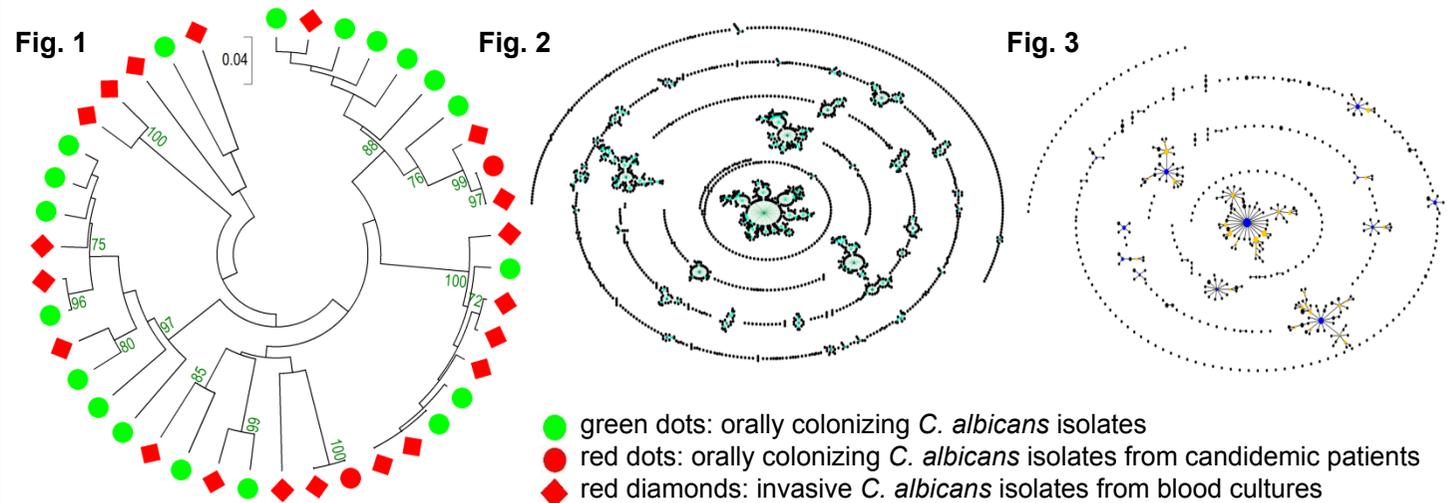
Materials and Methods

Twenty *C. albicans* isolates colonizing the oral cavity of healthy adults, 22 blood culture *C. albicans* isolates, and 2 orally colonizing *C. albicans* isolates obtained from candidemic patients were investigated by MLST to determine relatedness of colonizing and invading *Candida* isolates. MLST profiles were examined by comparison of 7 DNA sites that encode fragments of 7 housekeeping genes: *AAT1a*, *ACC1*, *ADP1*, *PMI1b*, *SYA1*, *VPS13*, and *ZWF1b* [2]. UPGMA analysis was used for phylogenetic assignment of our isolates [3]. Additionally, the phylogenetic relationships of all strain types from the *C. albicans* database (calbicans.mlst.net) were plotted by means of eBURST [4].

Results

Three isolates did not provide adequate PCR results and were excluded from analysis leading to comparison of 21 orally colonizing isolates (including 2 from candidemic patients) and 20 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 UPGMA analysis is presented in fig. 1. The scale shows the cut-off value for the clade assignment $p = 0.04$ [5].

Fig. 2 shows the eBURST analysis of all isolates within the database and fig. 3 only the isolates obtained from blood cultures. The affiliated clusters show the *C. albicans* clades, while isolated dots represent singletons – strains that do not cluster within a clade. The cluster in the center represents clade 1, the largest *C. albicans* clade.



Conclusion

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

References

- [1] Saghrouni F, Ben Abdeljelil J, Boukadida J, Ben Said M. Molecular methods for strain typing of *Candida albicans*: a review. J Appl Microbiol 2013; 114: 1559-1574.
- [2] Bournoux ME, Tavanti A, Bouchier C, et al. Collaborative consensus for optimized multilocus sequence typing of *Candida albicans*. J Clin Microbiol 2003 Nov;41:5265-5266.
- [3] Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Mol Biol Evol 2013; 30: 2725-2729
- [4] Feil EJ, Li BC, Aanensen DM, Hanage WP, Spratt BG. eBURST: inferring patterns of evolutionary descent among clusters of related bacterial genotypes from multilocus sequence typing data. J Bacteriol 2004; 186: 1518-1530.
- [5] Odds FC, Bournoux ME, Shaw DJ, Bain JM, Davidson AD, Diogo D, et al. Molecular phylogenetics of *Candida albicans*. Eukaryot Cell 2007; 6: 1041-1052.