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Molecular biology, including diagnostics: Molecular mycology

The molecular identification of non-albicans *Candida* species

M. Golas[1], K. Piskorska[1], M. Sikora[2], I. Netsvyetayeva[1], E. Swoboda-Kopec[2]

[1]Medical Microbiology, Warsaw Medical University, Warsaw, Poland ; [2]Dental Microbiology, Warsaw Medical University, Warsaw, Poland

Objectives:
In the last decade, *Candida* spp were considered the fourth most common etiological factor of nosocomial infections. *Candida albicans* is the most frequently isolated species, but the increase in the proportion of non-*albicans Candida* spp in such infections were reported each year. The most clinically relevant species belonging to this group are: *C. glabrata* and *C. parapsilosis.* Within the 'old' species of *C. parapsilosis* two new species were identified: *C. orthopsilosis* and *C. metapsilosis* while within the *C. glabrata*: *C. nivariensis* and *C. bracarensis*. At the current stage of mycological diagnostics, there is the lack of routine mycological methods for the identification of these pathogens only by phenotypic methods in the standard equipped microbiology laboratory. The aim of the study was analysis of the collection of clinical strains belonging to the 'old' species C. glabrata and C. parapsilosis based on the molecular methods.
Methods:
The isolation and identification of strains belonging to the complexes of *C. glabrata* and *C. parapsilosis* were performed by standard diagnostic methods. The detailed analyzes of the following features were performed: colony phenotype produced by the strain on Sabouraud agar and chromogenic medium and the assimilation of nutrient substrates in the test ID32C. Within *C. glabrata* complex the species identification was confirmed with the use standard PCR method. The D1-D2 region of the 26S rRNA gene were sequenced for strains without PCR product for *C. glabrata* and next analysed by BLAST search for best matches. Within *C. parapsilosis* complex by PCR-RFLP of SADH gene.
Results:
A total number of 313 strains were initially identified as *C. glabrata*. In the result of molecular biology tests, 39 strains with the lack of CGL1 gene specific for *C. glabrata*, were detected. All of this strains were characterized by the production of white colonies on the chromogenic agar plates and assimilated two sugars: trehaloze and glucose in API 32C test. The sequences analyzed in BLAST showed 98% of homology with *C. nivarensis* reference strain.
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