Distinctive Carbohydrate Assimilation Profiles Used To Identify the First Clinical Isolates of *Candida dubliniensis* Recovered in the United States

The conventional identification (assimilation profiles in the API 20C [bioMérieux Vitek, Inc., Hazelwood, Mo.] identification system, colony color on CHROMagar *Candida* [CHROMagar, Paris, France], and morphology on cornmeal-Tween 80 agar) of 32 atypical isolates of *Candida albicans* recovered during a study of oropharyngeal candidiasis in human immunodeficiency virus-infected individuals could not be confirmed by genetic fingerprinting (1, 3). Comparative studies of the nucleotide divergence in the 5' end of the 26S ribosomal DNA gene conducted at the National Center for Agricultural Utilization Research, Peoria, Ill., revealed that 10 of these 32 isolates were *Candida dubliniensis* and the remaining 22 were atypical *C. albicans* isolates (2). This constitutes, to the authors' knowledge, the first recovery of *C. dubliniensis* in association with human infections in the United States (4).

When the 10 *C. dubliniensis* isolates were reexamined with the API 20C identification system, none were found to assimilate α -methyl-D-glucoside (MDG). Similar results were reported by Sullivan et al. in their initial description of the organism's phenotypic characteristics (4, 5). However, MDG cannot be utilized as the sole carbon source by many isolates of *C. albicans* (1). It became clear upon closer examination of the API 20C carbohydrate assimilation profiles that none of the 10 *C. dubliniensis* isolates assimilated xylose (XYL) and MDG (API 20C biocodes of 2172170 or 6172170). In contrast, all 22 *C. albicans* isolates utilized one or both of these carbon sources (API 20C biocodes of 2542170, 2552170, 2556170, 2572170, or 2576170).

In summary, we have recovered the first clinical isolates of *C. dubliniensis* in the United States and found that all could be differentiated from *C. albicans* by their inability to assimilate XYL and MDG in the API 20C identification system. The absence of simple, reproducible tests for phenotypic characteristics of use in diagnostic microbiology laboratories to differentiate *C. albicans* from *C. dubliniensis* has greatly curtailed our clinical and epidemiological understanding of *C. dubliniensis*. Furthermore, the finding of distinct API 20C assimilation profiles associated with *C. dubliniensis* may stimulate clinical laboratories to evaluate our results and, if our results are substantiated, to initiate the use of assimilation profiles in their definitive identification of presumptive *C. albicans* isolates recovered from clinical specimens. The authors are currently investigating this and other phenotypic characteristics with

larger experimental populations in an effort to provide additional simple and effective methods for the differentiation of *C*. *dubliniensis* from *C. albicans*.

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