Carbohydrate assimilation profiles of the first Italian *Candida dubliniensis* clinical isolates recovered from an HIV-infected individual

Giovanni M. Giammanco*, Sarina Pignatob, Santa Salvob, Giuseppe Giammancob

aDipartimento di Igiene e Microbiologia, Università di Palermo, via del Vespro 133, I-90127 Palermo, Italy
bIstituto di Igiene e Medicina Preventiva, Università di Catania, via Biblioteca 4, I-95100 Catania, Italy

Received 25 January 2000; accepted 5 July 2000

**Abstract** – A total of six *Candida dubliniensis* isolates were obtained during 1 year of monitoring by monthly swabs from the oral cavity of an asymptomatic human immunodeficiency virus-infected individual in Catania, Italy. To the authors’ knowledge, this constitutes the first recovery of *C. dubliniensis* from a human in Italy. Our identification procedure was based on colony color on CHROMagar *Candida* and carbohydrate assimilation profiles obtained by two commercial systems: API ID 32C and API 20C AUX. Karyotyping by pulsed-field gel electrophoresis confirmed the phenotypic identification. The biocodes obtained with API 20C AUX and with API ID 32C were 6172134 and 7142140015, respectively, for all six isolates. Both biocodes corresponded to those described in the literature as being produced by most *C. dubliniensis* isolates with each of the two identification systems. Our results confirm that both API 20C AUX and API ID 32C are able to rapidly and accurately differentiate *C. dubliniensis* from *C. albicans*. © 2000 Éditions scientifiques et médicales Elsevier SAS

*Candida dubliniensis* / Italy / first isolates / assimilation profiles / AIDS / HIV

*Candida dubliniensis* is a newly described species, closely related phylogenetically to *C. albicans*, that is commonly associated with oral candidiasis in human immunodeficiency virus-positive patients [2, 9, 10] and can develop resistance to fluconazole [4–6], a common antifungal drug used for the treatment of mycoses in AIDS patients. During a study of oral *Candida* carriage in asymptomatic human immunodeficiency virus-infected individuals from Catania, Italy, we repeatedly isolated *C. dubliniensis* from a single subject. A total of six isolates were obtained from monthly swabs of the oral cavity during 1 year of monitoring. This constitutes, to the authors’ knowledge, the first recovery of *C. dubliniensis* from a human in Italy.

Our identification procedure was based on colony color on CHROMagar *Candida* (CHROMagar, Paris, France) and carbohydrate assimilation profiles. The absence of intracellular β-glucosidase activity [1] and growth at 42 °C [9] were used to differentiate *C. dubliniensis* from *C. albicans*. The karyotype of our *C. dubliniensis* isolates was also studied by pulsed-field gel electrophoresis and all of the six isolates showed the number and size of chromosomes typical for *C. dubliniensis*, thus confirming the phenotypic identification [9].

Both API ID 32C and API 20C AUX (bioMérieux Vitek, Marcy-l’Etoile, France), were used to study the carbohydrate assimilation profile of the isolates. According to previous reports [3, 7, 8], after 48 h of incubation, our *C. dubliniensis* isolates could not assimilate α-methyl-D-glucoside (MDG), xylose (XYL) or D-trehalose (TRE), among the substrates common to both systems. In addition, glycerol (GLY) was assimilated in the API 20C AUX, while DL-lactate (LAT) was not in the API ID 32C. For all six isolates, the resulting biocodes were
6172134 for API 20C AUX and 7142140015 for API ID 32C (Table I). Both biocodes have been recently published for C. dubliniensis [7]. The one we found with API 20C AUX was the code most frequently detected by Pincus et al. [7] after 48 h incubation (64% of the strains tested) and resulted in an excellent identification level with the 3.0 release of the identification database. Also, the biocode we found with API ID 32C perfectly corresponded to one of four published biocodes produced by the majority of C. dubliniensis isolates (61%) and resulted in a very good identification level with the 2.0 version of the ID 32C system database [7].

To gain a better understanding of the role of C. dubliniensis in clinical infections, it is essential that microbiology laboratories be able to identify this species rapidly and accurately in clinical specimens. Primary CHROMagar screening followed by carbohydrate assimilation tests with commercial yeast identification systems could be the most straightforward identification procedure. The recovery of a larger number of C. dubliniensis isolates by means of this identification procedure would confirm its effectiveness.

### References


**Table I.** Main phenotypic and genotypic characters of the six clinical isolates compared to those reported in literature [7] for C. albicans and C. dubliniensis.

<table>
<thead>
<tr>
<th>Clinical isolates</th>
<th>C. dubliniensis</th>
<th>C. albicans</th>
</tr>
</thead>
<tbody>
<tr>
<td>Growth at 42 °C</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Intracellular β-glucosidase</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Glycerol (GLY) assimilation*</td>
<td>+</td>
<td>96*, 88*</td>
</tr>
<tr>
<td>DL-lactate (LAT) assimilation*</td>
<td>–</td>
<td>10*, 0*</td>
</tr>
<tr>
<td>D-trehalose (TRE) assimilation*</td>
<td>–</td>
<td>0*,b, 15*, 30d</td>
</tr>
<tr>
<td>α-methyl-D-glucoside (MDG) assimilation*</td>
<td>–</td>
<td>0*,a,b,c,d</td>
</tr>
<tr>
<td>Xylose (XYL) assimilation*</td>
<td>–</td>
<td>0*,a,b,c,d</td>
</tr>
<tr>
<td>Biocodes API 20C AUX*</td>
<td>6172134</td>
<td>2172134 see identification</td>
</tr>
<tr>
<td>Biocodes API ID 32C*</td>
<td>7142140015</td>
<td>7042100011 see identification</td>
</tr>
</tbody>
</table>

**EK (bands of < 1 Mb)**

* After 48-h incubation; a % positive according to API 20C AUX database version 3.0; b % positive according to API ID 32C system database version 2.0; c % positive with API 20C AUX in [7]; d % positive with API ID 32C in [7]; EK = electrophoretic karyotype in pulsed-field gel electrophoresis. EK = electrophoretic karyotype in pulsed-field gel electrophoresis.


