JOURNAL OF CLINICAL MICROBIOLOGY, July 2003, p. 3450 Vol. 41, No. 7
0095-1137/03/$08.00+0 DOI: 10.1128/JCM.41.7.3450.2003

Inability to Decarboxylate Lysine as a Presumptive Marker To Identify Shiga Toxin-Producing *Escherichia coli* Strains of Serogroup O111

Shiga toxin (Stx)-producing *Escherichia coli* (STEC) strains are important agents of gastrointestinal disease in humans, particularly since such infections may result in a life-threatening complication such as the hemolytic-uremic syndrome (HUS) (10, 12). While numerous outbreaks have been related to *E. coli* serotype O157:H7, several other serotypes, including O111:NM (nonmotile) and O111:H8, are well-recognized causes of bloody diarrhea and HUS in different parts of the world (1, 3, 4). In Brazil, although human STEC infections are in general restricted to sporadic cases of nonbloody diarrhea, O111:NM and O111:H8 represent the most frequent serotypes so far identified (8; T. M. I. Vaz et al., submitted for publication).

Other important O111 serotypes, including O111:H2 and O111: NM, classified as enteropathogenic *E. coli* (EPEC) have been a leading cause of infantile diarrhea in our country for many years (7). Moreover, serotypes O111:H9 and O111:H12 were shown to belong to other diarrheagenic *E. coli* categories, i.e., atypical EPEC and enteroaggregative *E. coli* (EAEC), respectively (2).

Therefore, identification of O111 strains only by serogrouping, as performed in most laboratories, does not characterize properly the etiologic agent. Some biochemical characteristics have been proven useful for screening O157:H7 STEC strains (5), but the lack of a distinct phenotype in non-O157 STEC strains, except the production of Stx, can be considered a drawback in the isolation and identification of this group of bacteria in most clinical routine analyses.

In a previous study conducted in our laboratory (8), we interestingly observed that O111:NM STEC strains fail to decarboxylate lysine (6). Afterwards, this observation was confirmed in a large number of O111 STEC strains (Vaz et al., submitted). Thus, these results led us to examine our laboratory collection of O111 *E. coli* strains belonging to the different pathogenic categories for the ability to decarboxylate lysine. We observed that none of the O111 STEC strains decarboxylate this amino acid, whereas lysine decarboxylation was positive in 435 of the 438 (99.3%) *E. coli* O111 strains characterized as EPEC, atypical EPEC, or EAEC or as belonging to an as-yet-undefined pathogenic group (Table 1). Moreover, the inability to decarboxylate lysine seems to be a characteristic of O111 STEC strains that distinguishes it from other important STEC serotypes (Vaz et al., submitted).

The ability to metabolize β-phenylpropionic acid (PPA) has been demonstrated to be of significant value in detecting EPEC strains, particularly of serogroup O111, since O111 strains belonging to different pathogenic categories were PPA negative (9, 11). Thus, according to the results described in the present study, the use of lysine decarboxylation in association with PPA will permit the identification of STEC and EPEC strains, respectively, among *E. coli* strains of the O111 serogroup.

In conclusion, the lysine decarboxylation assay, which is a simple, routine biochemical assay, can be an important tool and can aid in the presumptive identification of O111 STEC strains, especially in clinical laboratories that usually do not include assays to detect Stx toxins or gene sequences.

TABLE 1. Lysine decarboxylation by *E. coli* O111 strains belonging to different diarrheagenic categories

Diarrheagenic category	No. of strains	Flagellar antigen (H)[a]	No. (%) of strains that decarboxylate lysine
STEC[b]	28	H8, NM	0
EPEC	382	H2, H6, H10, NM, NT	380 (99.5)
Atypical EPEC	14	H2, H9, H33, NM, NT	13 (92.8)
EAEC	10	H12	10 (100)
Unknown	32	H4, H9, H10, H12, H15, H28, H31, H45, NM, NT	32 (100)

[a] NM, nonmotile; NT, nontypeable.
[b] Except for 2 strains isolated from cattle all the others were of human origin.

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