Presence of extended-spectrum beta-lactamase-producing *Enterobacteriaceae* (ESBL-E) in the fecal flora of patients from general practice
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Cécile Meex[1], Pierrette Melin[1], Jean Denis Docquier[2], Tukumbane Kabasele[1], Pascale Huynen[1], Paul M. Tulkens[3], Patrick De Mol[1]

[1] Microbiologie médicale, Centre hospitalier universitaire de Liège, Liege, Belgique
[2] Centre d'ingénierie des protéines, Université de Liège, Belgique et université de Sienne, Italie
[3] Unité de Pharmacologie cellulaire et moléculaire et Centre de Pharmacie clinique, Université catholique de Louvain, Bruxelles, Belgique

Objectives
The aim of this study was to determine the ESBL-E carriage in community patients' fecal flora and to characterize the detected ESBLs.

Methods
This study was performed at the University Hospital of Liège (Belgium). From March 2007 to June 2007, a total of 284 fecal specimens were collected from 284 patients who consulted their general practitioner. Each sample was homogenized in 1 ml of sterile saline and aliquots were inoculated on three different selective culture media: ChromID ESBL agar (bioMérieux) and MacConkey agar + ceftazidime (2mg/L) and Drigalski agar + cefotaxime (1.5 mg/L). All the *Enterobacteriaceae* growing on these media were identified and tested for susceptibility by the Vitek2 (bioMerieux). The detection of ESBL production was performed by combined double disks (ceftazidime, cefotaxime and cefepime disks alone and a disk containing clavulanic acid). Characterisation of these ESBLs was performed by PCR assays targetting bla_{TEM}, bla_{SHV}, $bla_{CTX\text{-}M}$, the most frequent ESBL genes, followed by amplicon sequencing.

Results
Overall, 53 *Enterobacteriaceae* were recovered on the selective media from 284 samples (18.7%). Among these, 25 were identified as ESBL producers: 20 *Escherichia coli,* 3 *Proteus mirabilis*, 1 *Serratia fonticola* and 1 *Enterobacter aerogenes.* These 25 ESBLE originated from 20 patients (7.04%). Among the ESBL-*E.coli*, the following ESBLs were found: TEM-19 (n=1), TEM-52 (n=4), CTX-M-1 (n=5) and CTX-M-15/28 (n=2); 2 amplicons of TEM genes were not correctly sequenced. The ESBL from the *E. aerogenes* was TEM-52 and those from the 3 *P. mirabilis* were TEM-24. For 6 isolates, 5 *E.coli* and 1 *S.fonticola,* PCR did not demonstrate any ESBL gene of type TEM, SHV or CTX-M.

Conclusion
1) Of the screened community patients, 7% were found to be colonized in their fecal flora with ESBL-E strains. 2) *E.coli* accounted for the majority of ESBL-E isolates, while *P.mirabilis* and *E.aerogenes* were found in a minor proportion. No ESBL-*Klebsiella sp.* was recovered. 3) Various ESBL genes were identified. 4) TEM- and CTX-M-derived enzymes were the most frequently encountered ESBLs. No SHV-derived enzyme was found.

Key words: ESBL, community, prevalence