

First enteric *Escherichia fergusonii* from Italy

Primo isolamento enterico di *Escherichia fergusonii* in Italia

Vincenzo Savini, Chiara Catavitello, Azaira Bianco, Gioviana Masciarelli, Daniela Astolfi, Andrea Balbinot, Domenico D'Antonio

Clinical Microbiology and Virology Unit, Department of Transfusion Medicine, 'Spirito Santo' Hospital, Pescara, Italy

Dear Editor,

Escherichia fergusonii is a Gram-negative rod which belongs to the family *Enterobacteriaceae*. Though known to behave as a commensal organism in the gut of warm-blooded animals, knowledge regarding its natural habitat mostly remains unclear. *E. fergusonii* is very rarely recovered from clinical specimens and it has recently emerged as the causative agent of wound, biliary and urinary tract infections, as well as bacteraemias, enteritis and pleuritis. This organism appears closely related to *Escherichia coli*, and forms typical lactose non-fermenting *Salmonella*-like colonies on MacConkey agar [1-4].

Only one *E. fergusonii* strain was isolated from 2007 to date. It was collected from faeces of a hospitalized leukaemic male patient without signs of enteric infection. Strain identification was provided by bioMérieux Vitek2 and confirmed by 16S rRNA sequencing, whereas incorrect identification as *Escherichia coli* was obtained by the bioMérieux miniAPI. Susceptibilities were provided by Vitek2 (see Table 1) and confirmed by a CLSI disc diffusion test (discs by Liofilchem, Italy) [5]. Also, Vitek2 MIC for tigecycline was confirmed by performing an Etest (AB BIODISK), which documented an MIC of 0.19 mg/l.

Lack of derepressed or inducible AmpC production, as well as ESBL (*extended-spectrum beta-lactamase*) expression, was documented by performing a disk approximation test (D-test), and an Etest ESBL screen (AB BIODISK ceftazidime-ceftazidime/clavulanate and cefotaxime-cefotaxime/clavulanate commercial strips), respec-

tively, so that the isolate was finally labelled a *non-AmpC/non-ESBL* phenotype [6, 7].

While ESBLs have never been found in *E. fergusonii*, cephalosporinases have been occasionally reported, with AmpCs being first described in 2002. Also, gentamicin is known to be poorly effective against members of this species, whilst reduced ciprofloxacin-susceptibility has been reported elsewhere.

Cotrimoxazole resistance was largely described in 1999; further, lack of ampicillin and tetracycline sensitivity was reported by Farmer in 1985. Finally, piperacillin-moderately susceptible and amoxicillin/clavulanate-resistant strains first appeared in 1993, while resistance to carbapenems, tigecycline and nitrofurantoin

Table 1 - *E. fergusonii* susceptibilities (S, susceptible - R, resistant).

Antimicrobial	MIC (mg/L)
Ampicillin	≤2 (S)
Piperacillin	≤4 (S)
Cefoxitin	≤4 (S)
Imipenem	≤1 (S)
Meropenem	≤0.25 (S)
Ciprofloxacin	≤0.25 (S)
Gentamicin	2 (S)
Cotrimoxazole	≤0.20 (S)
Tetracycline	≥16 (R)
Nitrofurantoin	≤0.25 (S)
Tigecycline	≤0.5 (S) [Etest: 0.19]

has not been observed to date [8, 9]. Although the *E. fergusonii* natural habitat remains largely unknown, our brief communication may contribute to define it by presenting the first recovery of this organism as part of bacterial commensal flora in the human enteric tract. According to published works from countries other than Italy, we confirm the paucity of *E. fergusonii* strains from Italian hospitals, given that the isolate we studied was the only strain we collected during a two-year period and represented the second from Italy [10]. However, we suppose that the eventual failure of automatic instruments in biochemically identifying this species may explain the very rare isolation of this species from human specimens. We would then suggest confirming identification by using rRNA analysis when *Salmonella*-like colonies are grown, as this could contribute to distinguish non-fermenting *E. coli* strains, true *Salmonella* isolates, and *E. fergusonii*, and to provide reliable epidemiological and clinical data about this uncommon organism.

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