

**A multidrug- resistance pattern of an *Escherichia coli* strain isolated from diarrheal stools at the China-Guinea Friendship Hospital of Kipé in Conakry**

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**1. Introduction**

*Escherichia coli* is a Gram-negative bacterium belonging to the family of *Enterobacteriaceae*. It is a bacterial species often associated with various infections in humans including diarrhea. *E. coli* is a commensal bacterium of the digestive tract in humans and animals. However, some strains are pathogens associated with diarrhea but also with many infections in humans particularly in developing countries [1-3].

**2. Method of work**

A sample of diarrheal stools from a 30-year-old female patient of a household profession was received on June 28, 2019 at the Biomedical Laboratory of the China-Guinea Friendship Hospital in Kipé/Conakry for coprological examinations.

**3. Results and discussion**

**Table 1 Susceptibility profile of the strain of *Escherichia coli* isolated from diarrheal stools**

Vitek 2 AST N233		Vitek 2 AST XN05	
Antibiotics	Susceptibility (MIC : µg/l)	Antibiotics	Susceptibility (MIC : µg/l)
Ampicillin	R≥32	Piperacillin	R>64
Amoxicillin/Clavulanic acid	R≥32	Cefuroxime	R >32
Ticarcillin	R ≥128	Cefuroxime axetil	R>32
Piperacillin/Tazobactam	R ≥ 128	Cefixime	R>2
Cephalothin	R ≥ 64	Ceftriaxone	R>32
Cefoxitin	R ≥ 64	Cefepime	R>32
Cefotaxime	R ≥ 64	Aztreonam	R>32
Ceftazidime	R ≥ 64	Meropenem	R>8
Ertapenem	S ≤ 0,25	Levofloxacin	R>4
Imipenem	S ≤ 0,25	Moxifloxacin	R>4
Amikacin	S ≤ 2	Minocycline	I=8
Gentamicin	R ≥16	Tetracycline	R>8
Tobramycin	R ≥ 16	Tigecycline	R>4
Nalidixic acid	R ≥32	Chloramphenicol	R>32
Ciprofloxacin	R ≥ 4	Trimethoprim	R>8
Ofloxacin	R ≥ 8		
Nitrofurantoin	S < 16		
Trimethoprim/Sulfamethoxazole	R≥320		

**4. Discussion**

The uncontrolled use of antibiotics is one of the main factors for the emergence and spread of antimicrobial resistance genes around the world, thus constituting a threat to global health [9]. The development of multi-resistance in *Escherichia coli* is a major concern worldwide. Multi-resistant *Escherichia coli* from diarrheal stools could be the cause of therapeutic failure with antibacterial molecules, reducing the possibilities of treatment with available molecules. This situation would be even more frequently dramatic in developing countries where the means of diagnosis are weak and the possibility of acquiring certain molecules such as carbapenems. The spread of bacterial multidrug-resistant strains in the environment can lead to many cases of

morbidity and mortality in humans and animals. Visitors to emerging economies stay in conditions with weak hygiene infrastructure. Their most common health problem is travelers' diarrhea [4]. In this study, the patient presented more than six episodes of diarrheal stool in daily. This is in line with the World Health Organization definition of diarrhea. Indeed, diarrhea was defined by the WHO criteria as passage of three or more loose or liquid stools per day, or more frequently than is normal for the individual [5]. Travellers' diarrhoea (TD) is the most frequent illness experienced by international travellers to lower-income countries with bacterial agents considered to account for 80–90% of cases [6]. Then, antibiotic resistance genes are subject to local, regional, national and international transmission. Indeed, multidrug-resistant bacteria are often carried around the world by international travelers.

**Bibliographie**

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