LETTER TO THE EDITOR

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Antimicrobial resistance (AMR) has increased dramatically over the past few years and has now reached a level that places future of humanity in real danger [1-3]. We have read the article "*In vitro* antimicrobial resistance of urinary *Escherichia coli* isolates from outpatients collected in a laboratory" by Ciontea *et al.* [4] with great interest. The authors have evaluated the AMR profiles of *E. coli* isolates/strains from the urine specimens of outpatients between 2015 and 2017 in Romania. One hundred fifty eight from five hundred forty three isolates/strains described as multidrug resistant (resistance to more than two classes of antibiotics) and more than 13 % of investigated isolates were extended-spectrum β-lactamase (ESBL)-positive [4].

AMR spreading in hospitals is explained by the interplay of microorganisms, patients and the hospital-environment [5]. Generally, hospital borne AMR [6, 7], food chain related AMR [8] and AMR transmission through vectors [9] are the main sources for AMR spreading in the environment. Our studies in Armenia revealed a gradual increase in the frequency of antibiotic resistance among human commensal *E. coli* strains isolated from healthy and diseased cohorts [10]. Multidrug resistance increased six-fold in commensal *E. coli* strains in the Armenian general population in the period 2002-2005, and this trend continued, according to 2010 and future data [11]. Multidrug resistance *Enterobacteriaceae* strains were isolated from the water reservoirs of lake Sevan basin rivers [12], from the gut and gill microbiota of rainbow trout from lake Sevan [13], from the midgut microbiota of *Anopheles* mosquitoes [14] as well as from the dairy milk [15] and grape species from the Ararat Valley [16]. However, these investigations like the investigations of Ciontea *et al.* [4] are pilot investigations only and there is a need for systematic investigations of AMR dissemination in Armenia and Romania.

These might not only include investigations on AMR profiles of *E. coli* strains and urine specimen, but also data collection for nosocomial carbapenem-resistant *Enterobacteriaceae* (CRE) infection prevalence and risk-factors investigation, investigation of the CRE isolates for the presence of class A KPC, class B metallo-β-lactamases (VIM, IMP, NDM), MOX/CMY (class C), and OXA48 (class D) and Genomic sequencing and MLST of CRE-positive strains.

Conflict of interests: None to declare.

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