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Letter to the Editor

Autochthonous case of mobile colistin resistance gene *mcr-1* from a uropathogenic *Escherichia coli* isolate in Sétif Hospital, Algeria

Sir,

Urinary tract infections (UTIs) are considered one of the most common bacterial infections occurring both in community and hospital settings [1]. *Escherichia coli* is the most prevalent pathogen known to cause UTIs [1]. As with any other species of Enterobacteriaceae, *E. coli* has become more resistant to the action of antibiotics such as third-generation cephalosporins and carbapenems [1]. The re-introduction of colistin in some clinical situations to treat carbapenem-resistant Enterobacteriaceae was quickly followed by the emergence of resistance to this antibiotic [2]. Currently, nine mobile colistin resistance genes (*mcr-1* to *mcr-9*) have been described [3]. The aim of this study was to screen for uropathogenic colistin-resistant *E. coli* strains at Sétif Hospital in Northeastern Algeria and to investigate the molecular mechanisms conferring colistin resistance.

A total of 237 non-duplicate uropathogenic *E. coli* isolates were obtained between January 2015 and October 2017 from urine samples received at the microbiology laboratory of CHU de Sétif (Sétif, Algeria). Isolates were identified by matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry (MALDI-TOF/MS). Real-time and standard PCR were performed for all 237 isolates to screen for *mcr-1*, *mcr-2*, *mcr*-3, *mcr-4*, *mcr-5* and *mcr-8* plasmid-mediated colistin resistance genes. Positive standard PCR products were purified and were sequenced using a 3500xL Genetic Analyzer (Applied Biosystems/Hitachi, Foster City, CA, USA). The nucleotide sequences obtained were assembled using CodonCode Aligner software and were analysed using the ARG-ANNOT database.

Molecular analysis revealed that one isolate (*E. coli* strain 115) harboured the *mcr-1* gene. This isolate was recovered from a urine sample of a 69-year-old man with a urinary catheter hospitalised at Sétif Hospital. This patient had not received colistin during his hospital stay and had no history of travel abroad. Broth microdilution revealed that *E. coli* 115 had a colistin minimum inhibitory concentration (MIC) of 4 mg/L and was also resistant to amoxicillin, amoxicillin/clavulanic acid, cefalotin, doxycycline, trimethoprim/sulfamethoxazole and ciprofloxacin, but remained susceptible to ceftriaxone, cefepime, piperacillin/tazobactam, imipenem, ertapenem, gentamicin, amikacin, nitrofurantoin and fosfomycin. A conjugation experiment conducted in triplicate was unsuccessful, suggesting that the *mcr-1* gene was located on a non-transferable plasmid or on the chromosome, as previously reported [4–6].

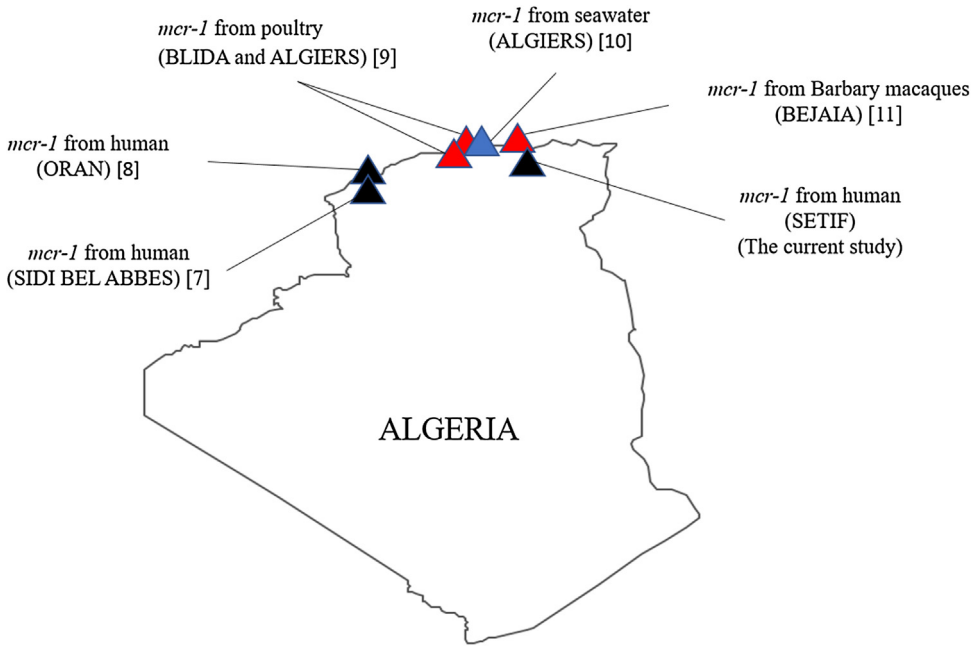

Fig. 1. Geographic distribution of the plasmid-mediated colistin resistance gene *mcr*-1 isolated from humans, animals and the environment in Algeria.

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Real-time PCR assay targeting the *mcr-2* to *mcr-8* genes was negative for all 237 isolates tested. Other molecular analyses performed for the 237 isolates are summarised in Supplementary Table S1.

To the best of our knowledge, here we report the first autochthonous case of a phosphoethanolamine transferase *mcr-1* gene isolated from a uropathogenic *E. coli* isolate in Sétif Hospital (Northeast Algeria). To date, *mcr-1* is the only plasmid-mediated colistin resistance mechanism reported in Algeria (Fig. 1). This gene was described previously from two clinical isolates from the west of Algeria, one in Sidi Bel Abbes [7] and the second in Oran [8] (Fig. 1). In the current study, the origin of the uropathogenic *E. coli* strain harbouring the *mcr-1* gene and its relationship with a possible animal reservoir remain unknown. Use of colistin in some livestock in Algeria suggests that these farms may be the main source of transmission of colistin resistance to humans. As shown on Fig. 1, reported *mcr*-1 cases from humans and the environment in Algeria has been highlighted [9,10,11].

Screening for *mcr-1* and other colistin resistance genes in further clinical isolates and samples should be immediately investigated in order to estimate their prevalence and to understand the mechanisms of dissemination of these genes in the clinical setting.

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Competing interests

None declared.

Ethical approval

Not required.

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Appendix A. Supplementary data

Supplementary material related to this article can be found, in the online version, at doi:https://doi.org/10.1016/j.jgar.2019.10.006.

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