26th ECCMID
Amsterdam, Netherlands
9 – 12 April 2016
ESCMID

Prevalence of ESBL and/or carbapenemase-producing *Escherichia coli* isolated from yellow–legged gulls from Barcelona, Spain

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Background

In the last decade, the number of bacterial pathogens presenting multidrug resistance to antibacterial agents has increased dramatically, becoming an emergent global disease and a major public health problem. The main cause behind the increasing rates of resistance can ultimately be found in the abuse and misuse of antibacterial agents, whether used in patients and livestock or released into the environment. Once antimicrobial resistant bacteria emerge, they can spread locally or globally. The main factors contributing to their spread at a global level comprise migrant birds, globalization of commercial food and international traveling. The objective of this study was to investigate the prevalence of ESBL and/or carbapenemase-producing *Enterobacteriaceae* from faecal swabs obtained from a group of yellow–legged gulls in Barcelona, Spain.

Matherial/Methods

One hundred and thirty-two faecal swabs from yellow–legged gulls (Photo 1) were obtained during a one-month period. The samples were plated on ESBL chromogenic agar. Identification of ESBL-producing enterobacteria was carried out by mass spectrometry (MALDI-TOF). Antimicrobial susceptibility was tested by disk diffusion. Characterization of ESBL and carbapenemases genes was performed by PCR followed by sequencing (ESBL: bla_{TEM}, bla_{SHV}, bla_{CTX-M}; carbapenemases: bla_{KPC}, bla_{OXA-48}, bla_{VIM}, bla_{IMP} and bla_{NDM}; cephamycinases: bla_{CMY}, bla_{DHA}, bla_{FOX}, bla_{ACC}, bla_{EBC}, bla_{MOX}). To evaluate the genetic relationship among the strains, REP-PCR was performed. Agglutination with antiserum O25 was used to know if those CTXM-15-carrying isolates belong to the high risk clone O:25b-ST131.

Photo 1. A yellow–legged gull on a pile of garbage.

Results

Seventy two (54%) out of 132 faecal samples were positive for ESBL, carbapenemases or cephamycinases producing *Escherichia coli* (Table 1). Forty-five strains (62.5%) were resistant to quinolones, 22 (30.6%) to gentamicin and 9 (12.5%) to amikacin. Rep-PCR showed a high genetic heterogeneity among the strains (Figure 1). Those strains with CTXM-15 did not show agglutination with antiserum O25. The two isolates carrying the KPC and VIM carbapenemases were not genetically related and belonged to the ST1011 (phylogroup E) and ST354 (phylogroup F), which have been previously found in humans.

Figure 1. Example of REP-PCR results from 14 different strains.

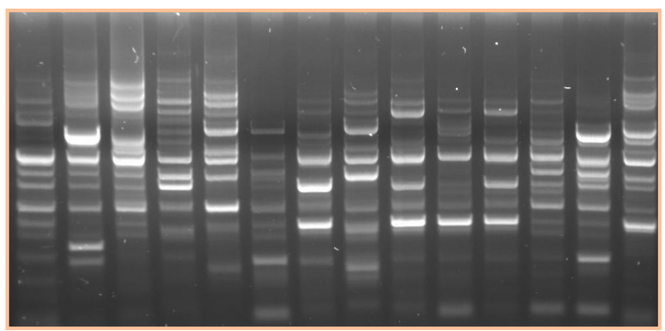

Table 1. Distribution of the β-lactamases found among the *E. coli* isolated.

β-lactamase	Nº strains	%
SHV Group	**38**	**52.8**
SHV-12	24	33.3
SHV-12 + TEM-1	13	18
SHV-2	1	1.4
CTX-M group	**30**	**41.6**
CTX-M-15	11	15.3
CTX-M-15 + TEM-1	2	2.8
CTX-M-1	1	1.4
CTX-M-1 + TEM-1	5	6.9
CTX-M-1 + TEM-84	1	1.4
CTX-M-14	4	5.5
CTX-M-14 + TEM-1	6	8.3
VIM-1 + KPC-2	**2**	**2.8**
CMY-2	**2**	**2.8**
TOTAL	**72**	100

Conclusions

The yellow-legged gulls screened in the present study presented a high prevalence of ESBL-producing *E. coli*. The isolation of two carbapenemase-producing *E. coli* strains is a matter of concern. These results reinforce the knowledge that the feeding and migratory habits of these birds play an important role in the dissemination of antibiotic-resistant bacteria between geographically distant ecosystems.

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