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Role of wild birds in the dissemination of antibiotic
resistance

by Bálint József Nagy

Supervisor: Dr. Gábor Kardos, PhD



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By Bálint József Nagy, molecular biology MSc

Supervisor: Dr. Gábor Kardos, PhD

Doctoral School of Pharmaceutical Sciences, University
of Debrecen

Head of the **Defense Committee:**

Prof. Dr. Ildikó Bácskay Dr Kovácsné, PhD

Reviewers:

Dr. Renáta Knop, PhD

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Introduction

Bacteria of the Enterobacterales family are common causative agents of both nosocomial and community-acquired infections. These infections are often treated with 3rd generation cephalosporins but the efficacy of these drugs is compromised due to the rapid and worldwide dissemination of extended spectrum beta-lactamase (ESBL) -producing strains. Carbapenems are last resort antibiotics used to treat such infections, however the emergence of carbapenem resistant Enterobacterales (CRE) is of great concern. The One Health concept sets forth that the health of people, animals and the environment is interconnected and it applies to antibiotic resistance as well, as it was illustrated by the case of the emergence of *mcr* genes and the use of colistin. *Escherichia coli* is a characteristic One Health example as it is abundant member of human and animal gut microbiome and can persist in the environment for a long time. Human, animal and environmental strains can share mobile genetic elements (MGE) through horizontal gene transfer (HGT). Zoonotic or environmental reservoirs are important sources for newly emerging resistance genes,

such as *Kluyvera* ssp. for *bla*_{CTX-M} and *Shewanella* ssp. for *bla*_{OXA-48-like} genes. The huge amount of antibiotics used by human and veterinary medicine led to the contamination of the environment with antibiotics, resistance genes and resistant human or veterinary pathogenic strains. Omnivorous, carnivorous and philanthropic wild animals that live close proximity to landfills, agricultural fields and surface waters contaminated by wastewater are more likely to acquire resistant strains than those animals that live in remote areas. Once they acquire such, there is a possibility that these animals, especially the highly mobile species may disseminate the antibiotic resistance through the whole world, which can explain the presence of antibiotic resistance in remote areas with no human activity. Rooks and gulls are urbanised animals, their droppings pollute the urban areas and because of their migratory and vagrant behaviour these animals may act as reservoirs and long-distance vectors for the resistant strains and MGEs.

Aims

The main objective of our work was to examine the epidemiology of CRE and/or ESBL-producing *E. coli* in vagrant and migratory wild birds wintering in Hungary in line with the One Health concept and compared these isolates to local contemporary human-derived and/or environmental strains and we aimed:

To investigate the prevalence of ESBL-producing *E. coli* in rooks gathering at the Clinical Campus of the University of Debrecen and the asymptomatic carriage of ESBL-producing *E. coli* in humans.

To characterize and compare ESBL-producing *E. coli* isolates of rook, human fecal and clinical origin to reveal any possible epidemiological relations.

To investigate the prevalence of CRE in the Danube and black-headed gulls gathering at the docks of Budapest,

To characterize and compare the carbapenem resistant *E. coli* (CREc) isolates collected from gulls, Danube and the National Center for Public Health and Pharmacy (NPHPC).

To create a complex work which investigates the prevalence and the epidemiology of antibiotic resistant

bacteria carried by wild birds in Hungary and at the same time it compares the epidemiology of resistant strains of different origin in line with the One Health concept.

Materials and methods

Samples and bacterial strains

Between October 2016 and March 2017 a total of 112 and 2455 cloacal swabs and human stool samples were collected along with 42 invasive ESBL-producing *E. coli* isolates from clinical samples for comparison. Between January and March of 2019 and 2020, 122 and 105 samples were collected from black-headed gulls; 12 and 12 samples were gathered from Danube in 2019 and 2020, six from upstream and six from downstream of Budapest each year. To this collection we received 21 human clinical CREc isolates from the NPHPC for comparison. Sampling of both bird species was in accordance with institutional guidelines, carried out in accordance with local and national regulations in the least harmful and invasive way.

Human stool and bird samples were cultured on eosin-methylene blue media supplemented with 2 mg/l cefotaxime. Water samples were processed by Colilert-

18/Quanti-Tray test (IDEXX Laboratories, Westbrook, USA) supplemented with 10 mg/l cefotaxime. Identification of bacterial species was determined using matrix-associated laser desorption/ionization mass spectrometry (MALDI-TOF, Bruker, Bremen, Germany). All Gram-negative Enterobacterales were further characterized by disk-diffusion method using the guideline of the European Committee on Antimicrobial Susceptibility Testing (EUCAST) against the following antibiotics: ertapenem, meropenem, imipenem, cefotaxime, ceftazidime, cefepime, amoxicillin-clavulanic-acid, ceftazidime-avibactam, ciprofloxacin, amikacin, gentamicin, tobramycin, fosfomycin, tigecycline and co-trimoxazole. Colistin susceptibility was investigated using a broth microdilution method (MERLIN Diagnostika GmbH, Germany). ESBL-production was determined using double-disk synergy test, carbapenem resistance and the types by MASTDISCS Combi Carba Plus test (Mast Group Ltd, UK).

Resistance gene detection

Isolates showing ESBL phenotype were characterized by polymerase chain reactions (PCR) based on the work of

Pitout et al. for *bla*_{SHV} és *bla*_{CTX-M-1,-2,-8,-9} genes. Amplicons were purified by QIAquick Gel Extraction Kit (Qiagen, Hilden, Germany) and further characterized by sequencing (Macrogen Europe, Amsterdam, Netherlands). Sequences were analyzed by CLC Main Workbench (CLC Bio, Aarhus, Denmark). Carbapenem resistance genes were identified with multiplex PCRs developed by Poirel et al. for the following gene groups: *bla*_{NDM}, *bla*_{VIM}, *bla*_{IMP}, *bla*_{KPC} és *bla*_{OXA-48-like}. To investigate the presence of plasmid-mediated colistin resistance genes *mcr-1-mcr-5*, a multiplex PCR developed by Rebelo et al. was used.

Typing

The phylogroups of *E. coli* were determined using the multiplex PCR developed by Clermont et al. The presence of pandemic sequence type (ST) 131 clone and its clades was investigated by a multiplex PCR based on the work of Matsumura et al. The multiplex PCR assay by Persson et al. was performed to detect the presence of virulence factor genes characteristic for enterovirulent *E. coli* pathotypes.

Pulsed-field gel electrophoresis (PFGE)

The epidemiological relation between rook, human fecal and clinical isolates was determined by PFGE.

Macrorestriction was performed with XbaI (Fermentas, Vilnius, Lithuania) in 1% SeaKem Gold agarose (Lonza). Banding patterns were analyzed by Fingerprinting II software (Bio-Rad).

Whole genome sequencing (WGS)

Based on PFGE 20 isolates were selected for WGS to represent major pulsotypes carried by rooks and that contained both human and rook isolates. WGS was performed on all CRE isolates that carried acquired carbapenem resistance. Genomic DNA was extracted using DNeasy UltraClean Microbial Kit (Qiagen, Germany). WGS was performed using Nextera XT DNA Library Preparation Kit followed by 150 bp sequencing on Illumina platforms. FASTQ files were quality trimmed then assembled *de novo* using Velvet (v1.0.0.) Raw reads are available under BioProject ID PRJNA693168 and PRJNA807502 at the National Center for Biotechnology Information Database. Core genome multi locus sequence typing (cgMLST) was performed using SeqSphere + (Ridom, Münster, Germany) according to the “*E. coli* cgMLST” version 1.0 scheme. Resistance genes, plasmid replicons and virulence genes were identified using

ResFinder (v4.1), PlasmidFinder (v2.1) and VirulenceFinder (v2.0) databases available at the website of the Center for Genomic Epidemiology. Contigs containing carbapenem resistance genes were annotated by PROKKA (v1.13) and visualized using Clinker to identify the immediate genetic context of the carbapenemase genes.

Results

Occurrence and Characteristics of ESBL-Producing *E. coli* in Rooks

ESBL-producing *E. coli* was carried by 33% (37/112) of the sampled birds *bla*_{CTX-M-55} and *bla*_{CTX-M-27} being the dominant ESBL genes. Fluoroquinolone and sulfonamide resistance was frequent whereas all isolates were susceptible to aminoglycosides; 40% of the isolates including all *bla*_{CTX-M-15} producers were susceptible to all examined non-beta-lactam antibiotics. Two CTX-M-27-producing isolates belonged to ST131 C1-M27 subclade. In addition, 21% of the isolates carried the intimin-coding *eae* gene and all of these isolates were CTX-M-27-producers.

Fecal carriage rate and characteristics of ESBL-producing *E. coli* in humans.

The fecal carriage rate of ESBL-producing *E. coli* was 1.7% (42/2445). The dominant ESBL genotypes were *bla*_{CTX-M-15} followed by *bla*_{CTX-27}. Resistance to fluoroquinolones, sulfonamides, amikacin, gentamicin and to tobramycin was common and 24% of the isolates were resistant to all tested non-beta-lactam antibiotics

including eight CTX-M-15-producers. Two, one, one and ten isolates belonged to ST131 clade A, B, C2 and C1-M27.

Characteristics of ESBL-producing *E. coli* from inpatients.

The dominant ESBL genes were *bla*_{CTX-M-15} followed by *bla*_{CTX-M-27} and two isolates carried *bla*_{SHV-12}. Co-resistance rates were high, 60% of isolates were resistant to fluoroquinolones, sulfonamides and aminoglycosides, mostly the *bla*_{CTX-M-15} producers. Among ST131 isolates, one, nine and 16 belonged to clade B, subclade C2 and subclade C1-M27, respectively.

Comparing the characteristics of rook, human fecal and human clinical isolates.

In rooks, *bla*_{CTX-M-55} was the dominant ESBL gene while in humans it was *bla*_{CTX-M-15}; *bla*_{CTX-M-27} was the second most common ESBL gene in all three isolate collections. Rook-derived isolates showed lower co-resistance rates to non-beta-lactam antibiotics than human clinical isolates. Isolates resistant to aminoglycosides, fluoroquinolones and trimethoprim–sulfamethoxazole tend to produce enzymes of the CTX-M-1 group, particularly *bla*_{CTX-M-15},

except for rooks where *bla*_{CTX-M-15} carriers were susceptible; *bla*_{CTX-M-27} carriers were resistant to fluoroquinolones and to trimethoprim–sulfamethoxazole but not to aminoglycosides. The pandemic ST131 *E. coli* clonal lineage was present in isolates of rooks and humans with the dominance of C1-M27 subclade. All isolates were negative for plasmid-mediated colistin resistance genes tested.

Molecular epidemiology of the ESBL-producing *E. coli* isolates.

Clusters containing both rook and human isolates were identified. Out of these, a cluster of eight human fecal, ten human clinical and two rook isolates was the largest group; these isolates belonged to the ST131 clone. The two corvid ST131 isolates showed PFGE profiles indistinguishable from human clinical and human fecal isolates. A smaller cluster of three human clinical, one human fecal and one rook isolate was also detected, these belonged to ST744. Human ST744 isolates were closely related, while the rook isolate was distant from them. The two ST131 C1-M27 rook isolates were identical (0 allele difference) and in close connection with human strains (≤ 7

alleles). Both ST24 and ST162 rook isolates were highly uniform genetically, the distance based on allele presence was ≤ 1 . The rook ST744 isolate carried markedly more virulence genes compared to the human clinical and fecal ST744 isolates.

Prevalence and characteristics of CRE carried by gulls in 2019 and 2020

The overall prevalence of CRE carriage in 2019 was 7.4% (9/122); six *E. coli*, one *Escherichia fergusonii* and two *Enterobacter cloacae* complex were recovered; while in 2020, 6.7% (7/105) were positive for CRE yielding eight *E. coli*, one *Klebsiella pneumoniae*, one *Citrobacter braakii* and one *E. cloacae* complex; two birds carried multiple CRE isolates. All *Escherichia* isolates were metallo-beta-lactamase (MBL)-producers except for one *E. coli*, which carried *bla*_{OXA-181}. The most prevalent gene was *bla*_{NDM-1}; *bla*_{VIM-4} always occurred together with *bla*_{NDM-1}. Except for the OXA-181-producer, *Escherichia* isolates were co-resistant to all tested beta-lactams, fluoroquinolones, aminoglycosides and trimethoprim-sulfamethoxazole. More than half of the isolates carried 3rd generation cephalosporin resistance genes, mostly the

*bla*_{SHV-12}. Four *E. coli* were also resistant to fosfomycin and carried the *fosA3* or *fosL1* gene. One isolate had an amino acid substitution in the *pmrB* region (p.V161G); the MIC value for colistin was 2 mg/l. The *E. coli* isolates belonged to nine sequence types (ST); ST224 (2), ST226, ST372, ST744 (2), ST1437 (4), ST2772 ST8890, ST13079 and a novel ST. The ST1437 isolates recovered in 2019 shared the same resistome pattern and zero allelic differences were found in their cgMLST profile, while those collected in 2020 had similar resistance patterns with 22-24 allelic distances between them. ST744 isolates were not related based on their resistance and cgMLST profiles (allelic distance 124). ST224 strains were recovered from 2019 and 2020 with similar resistance patterns (24 allelic differences). Two *E. cloacae* complex isolates did not produce carbapenemases, the third belonged to ST1001 (*Enterobacter kobei*), carried *bla*_{VIM-1} and was resistant to colistin (MIC>64 mg/l) though we did not find any resistance genes (*mcr-1-10*) or known *PmrAB/PhoPQ* mutation associated with this phenotype. The *K. pneumoniae* was assigned to ST273 and was resistant to fosfomycin harbouring *fosA5*. The *C. braakii* belonged to

a new ST; it carried *mcr-9* but the MIC value for colistin was 1 mg/l. The *C. braakii* and the *K. pneumoniae* were *bla*_{NDM-1} carriers.

Prevalence and characteristics of CRE in River Danube

All samples from upstream and the 2019 downstream samples were negative for CRE. In 2020, five out of six downstream samples were positive and a total of seven *E. coli* and one *E. cloacae complex* were found. All *E. coli* harboured MBL-type carbapenemases; three *bla*_{NDM-1}, three *bla*_{NDM-1}+*bla*_{VIM-4} and one *bla*_{NDM-5} carriers were found. All isolates were also resistant to tested beta-lactams, fluoroquinolones and aminoglycosides. Two isolates were resistant to fosfomycin and harboured *fosA3* or *fosA4*. Each isolate belonged to a different ST (ST10, ST354, ST410, ST624, ST746, ST1303, ST1437). The *E. cloacae complex* was porin deficient.

Characteristics of CREc isolates from humans

MBL-producers were predominant and the following carbapenemases were found: *bla*_{NDM-1}, *bla*_{VIM-4}, *bla*_{OXA-48}, *bla*_{NDM-5}, *bla*_{KPC-3}, *bla*_{OXA-244}, *bla*_{NDM-7}, *bla*_{OXA-181}. Two isolates co-harboured *bla*_{VIM-4} and *bla*_{OXA-48}. Resistance to

fluoroquinolones, co-trimoxazole, amikacin, gentamicin and tobramycin was observed in 71%, 76%, 71%, 38% and 76% of the isolates, respectively. One isolate carried *mcr-9* yet the MIC of colistin was 0.125 mg/l. The isolates belonged to the following STs: ST38, ST69, ST73, ST88, ST131, ST405, ST410, ST448, ST617, ST648, ST1011. Isolates of the same STs (ST38, ST69, ST73, ST405) were highly uniform and related (allelic distances 15,8,1,1, respectively, except for ST131 isolates (allelic distance 122). The *bla*_{NDM-5} harbouring ST410 strains shared the same resistome and the allelic distances between them were 0 (Supplementary Table 1, Figure 1).

Comparing the CREc isolates from gulls, Danube and humans

The most prevalent gene in all isolate collections was *bla*_{NDM-1}; *bla*_{VIM-4} occurred only with *bla*_{NDM-1} in gull and water isolates, while it was co-harboured with *bla*_{OXA-48} or found alone in human isolates. Overall ESBL/AmpC genes were frequently found; the dominant gene was *bla*_{CTX-M-15} in human isolates while it was *bla*_{SHV-12} in gull and river isolates. Fosfomycin resistant isolates were present only in river and gull isolates, *fosA3* being the most

frequent resistance gene. The 42 *E. coli* isolates belonged to 25 different STs; in general, different STs were found in human, river and gull isolates. ST1437 was present in a Danube sample and in gulls from both periods; gull isolates collected in 2019 were highly similar (allelic distance 0) while those collected in 2020 and the river isolate differed by 22-24 alleles with minor differences in their resistome. NDM-5-producing ST410 isolates were recovered from humans and the Danube; the river isolate showed an allelic distance of 46 compared to the human isolates and similar resistance patterns. *bla*_{NDM} genes were localized within the same immediate genetic context (*dsbD-trpF-bleMBL-bla*_{NDM1/5/7} or *bla*_{NDM1}-*ISAba125-aph(3')*-*VIa*). Consistent co-carriage of resistance genes found on the same contig was demonstrated in case of *bla*_{NDM-1} and *aph(3')*-*VI* in river and gull isolates, in case of *bla*_{OXA-181} and *qnrS1* (on a IncX3 replicon) in human and gull isolates and in case of *bla*_{VIM-4} and *aac(6')*-*Ib-cr* in all *bla*_{VIM-4} carriers.

Discussion

In the present work, *bla*_{CTX-M-55} and *bla*_{CTX-M-27} were predominant in rooks; *bla*_{CTX-M-55} is rarely reported in Europe from humans but it is highly prevalent in Southeast Asia. It has been suggested that *bla*_{CTX-M-55} in humans in Asia arose from food animal sources highlighting the importance of One Health in the dissemination of antibiotic resistance. As *bla*_{CTX-M-55} is dominant in livestock in Asia and manure is often used to fertilize crop fields and may contain ESBL-producing *E. coli*, rooks foraging in these may acquire *bla*_{CTX-M-55} producers. Previously, *bla*_{CTX-M-14} and to a lesser extent, *bla*_{CTX-M-15} were dominant ESBL genes in Asia; recently, *bla*_{CTX-M-55} emerged as the most common ESBL gene in human and animal isolates, while *bla*_{CTX-M-27} started to outcompete *bla*_{CTX-M-14}. In our work *bla*_{CTX-M-55} have been associated with IncN replicon type, which often harbors various ESBL genes but rarely *bla*_{CTX-M-55}. This association of *bla*_{CTX-M-55} with IncN plasmids carried by ST162 may open a new way for the dissemination of *bla*_{CTX-M-55} within Asia and from Asia towards Europe by bird migration or vagrancy.

This shift in the epidemiology of ESBL genes in Asia may be the cause of the alteration of ESBL genes in rooks as compared to earlier studies where *bla*_{CTX-M-15} and *bla*_{CTX-M-1} were the dominant ESBL genes.

All ST24 isolates were CTX-M-27-producers and carried the *eae* gene, which encodes a major virulence factor of enteropathogenic *E. coli* (EPEC); the lack of the *bfp* gene indicates that these isolates are atypical EPEC strains, which are reported to have potential to cause diarrhea in humans. ESBL-producing ST162 strains have previously been identified in rooks wintering in Europe though their prevalence were much lower compared to our results and they did not carry *bla*_{CTX-M-55}. Based on the virulence factors our rook ST744 isolate is probably an avian pathogenic *E. coli* (APEC) strain, which is the main cause of avian colibacillosis worldwide. Therefore, wild birds carrying APEC strains might pose a potential economic risk towards poultry especially that this strain was resistant to beta-lactams and fluoroquinolones. The *bla*_{CTX-M-15} remained the dominant ESBL gene in the human isolates and *bla*_{CTX-M-27} became the second most common ESBL gene in our work and this change also occurred in other

hospitals in Hungary. The prevalence of ST131-CTX-M-15 *E. coli* decreased and the prevalence of C1-M27 clones increased compared to earlier findings suggesting a slow replacement of C2 subclade carrying *bla*_{CTX-M-15} by the C1-M27 subclade.

CRE have been previously reported from the Danube in Serbia and Romania in 2013 but not in Hungary and later in Austria in 2016, though the species distribution and carbapenemases differed from our results. In previous European studies *bla*_{NDM-1} was rare, while *bla*_{VIM-4} and its combinations, prevalent in our study, were not reported to our knowledge. These genes also dominated among the human CREc isolates but the co-carriage of *bla*_{NDM-1} and *bla*_{VIM-4} was not observed. The prevalence of CRE found in black-headed gulls in this work was similar to that found in other European studies conducted on different gull species in countries with higher CRE prevalence in humans. ST224 and ST744 are high-risk extraintestinal pathogenic *E. coli* (ExPEC) lineages capable of causing several infections in animals and humans and are usually associated with ESBL and/or carbapenemase carriage. ST372 is an international ExPEC clone causing mainly

urinary tract infections in dogs, but is also associated with human infections. As dog faeces is a common contaminant of the urban environment and gulls consume fecal material, presence of ST372 in gulls suggests a One Health link between wild and companion animals as well as humans. ST1437 isolates shared by the Danube and by gulls in different years were related, suggesting that *E. coli* ST1437 is maintained in the gull population or is a frequent and recent acquisition from a common source visited by gulls. ST1437 *E. coli* is a rarely reported commensal strain probably of porcine origin based on literature data. Thus, arable land fertilised by manure may be its source in the gulls creating a parallel dissemination route to the spread of *bla*_{CTX-M-55} from livestock to wildlife through agricultural fields.

Close similarity of carbapenemases and their combinations between human, gull and water isolates but diversity of carrier STs indicate that epidemiology of CRE in this setting is shaped predominantly by horizontal gene transfer (HGT). Aquatic environments are excellent sites for HGT; resistance genes may accumulate in the sediment and wild animals in proximity to water bodies can acquire

those resistant strains from hospital waste reaching the surface waters. In Hungary, *K. pneumoniae* is the dominant CRE which was previously carried *bla*_{VIM-4} but in recent years the carried carbapenemase genes diversified and *bla*_{OXA-48-like}, *bla*_{KPC} és *bla*_{NDM} genes appeared, which is in accordance with our finding in our CREc isolates. Considering the high prevalence of *bla*_{NDM-1} among the clinical *E. coli* isolates and the high similarities of the immediate genetic context of *bla*_{NDM-1} it seems probable that a proportion of carbapenemases found in the Danube are of hospital origin (samples taken upstream of Budapest were negative). Because of their omnivorous, urbanised, vagrant and migratory behaviour these gulls and rooks are important reservoirs, local and long-range vectors for the resistant strains, MGEs and resistance genes linking different geographical areas into a complex dissemination network of antibiotic resistance and highlighting the role of wild birds and the importance of One Health in the dissemination of antibiotic resistance.

Summary

The One Health concept sets forth that the health of the animals, humans and the environment is interconnected and it also applies to antibiotic resistance. Thus, we examined the role of wild birds in the dissemination of antibiotic resistance. Between October 2016 and March 2017 the prevalence of ESBL-producing *E. coli* in rooks was 33% while the asymptomatic carriage was 1.7% in human stool samples. ESBL genes were sequenced; rook isolates carried mostly *bla*_{CTX-M-55} or *bla*_{CTX-M-27} genes while *bla*_{CTX-M-15} and *bla*_{CTX-M-27} dominated in human stool and clinical isolates. Based on PFGE clinical and stool isolates clustered separately from rook isolates with minor exceptions. ST131 clone was present in rooks, stool and clinical samples C1-M27 being the dominant subclade. A large PFGE cluster contained rook, stool and clinical isolates belonging to ST131 C1-M27 subclade, which were in close connection based on WGS and cgMLST results. Rooks carried ST24 atypical EPEC strains, *bla*_{CTX-M-55} harbouring ST162 strains and APEC strains. Overall 7.4% and 6.7% of sampled gulls in 2019 and 2020 carried CRE, respectively. CRE was found in

the Danube only in samples taken in 2020 downstream of Budapest. *E. coli* was the dominant species and these CREc isolates were compared to human clinical strains. Based on WGS the predominant carbapenemase was *bla*_{NDM-1} located within the same immediate genetic context in all isolate collections. In gull and river isolates *bla*_{VIM-4} occurred only in *bla*_{NDM-1} carriers while it was carried alone or with *bla*_{OXA-48} in human isolates. Generally human river and gull isolates belonged to different STs but important high-risk clones were also found in gulls and Danube (ST224, ST372, ST744 and ST10, ST354, ST410, respectively). Direct link was not found between gull and human isolates. Human and river ST410 isolates were connected. Gull ST1437 isolates found in 2019 were identical while those collected in 2020 from gulls and Danube had 22-24 allelic distances between them. Because of their omnivorous, urbanised, vagrant and migratory behaviour these gulls and rooks are serious reservoirs, local and long-range vectors for the resistant strains, MGEs and resistance genes highlighting the role of wild birds and the importance of One Health in the dissemination of antibiotic resistance.



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List of publications related to the dissertation

1. **Nagy, J. B.**, Koleszár, B., Khayer, B., Róka, E., Laczkó, L., Ungvári, E., Kaszab, E., Bali, K., Bányai, K., Vargha, M., Lovas-Kiss, Á., Tóth, Á., Kardos, G.: Carbapenem-resistant *Escherichia coli* in Black-headed gulls, the Danube, and human clinical samples: a One Health comparison of contemporary isolates.
Journal of Global Antimicrobial Resistance. 35, 257-261, 2023.
DOI: <http://dx.doi.org/10.1016/j.jgar.2023.10.002>
IF: 4.6 (2022)
2. **Nagy, J. B.**, Balázs, B., Benmazouz, I., Gyüre, P., Kóvér, L., Kaszab, E., Bali, K., Lovas-Kiss, Á., Damjanova, I., Majoros, L., Tóth, Á., Bányai, K., Kardos, G.: Comparison of Extended-Spectrum Beta-Lactamase-Producing *Escherichia coli* Isolates From Rooks (*Corvus frugilegus*) and Contemporary Human-Derived Strains: A One Health Perspective.
Front. Microbiol. 12, 1-9, 2022.
DOI: <http://dx.doi.org/10.3389/fmicb.2021.785411>
IF: 5.2

List of other publications

3. Balázs, B., Tóth, Z., **Nagy, J. B.**, Majoros, L., Tóth, Á., Kardos, G.: Faecal Carriage of Carbapenem-Resistant *Acinetobacter baumannii*: comparison to Clinical Isolates from the Same Period (2017-2019).
Pathogens. 11 (9), 1-9, 2022.
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IF: 3.7





4. Tóth, H., Buchholz, G., Fésüs, A., Balázs, B., **Nagy, J. B.**, Majoros, L., Szarka, K., Kardos, G.:
Evolution of the Gram-Negative Antibiotic Resistance Spiral over Time: a Time-Series
Analysis.
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DOI: <http://dx.doi.org/10.3390/antibiotics10060734>
IF: 5.222
5. Balázs, B., **Nagy, J. B.**, Tóth, Z., Nagy, F., Károlyi, S., Turcsányi, I., Bistyák, A., Kálmán, A.,
Sárközi, R., Kardos, G.: Occurrence of *Escherichia coli* producing extended spectrum [beta]-
lactamases in food-producing animals.
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DOI: <http://dx.doi.org/10.1556/004.2021.00036>
IF: 0.959
6. Balázs, B., Tóth, Z., Nagy, F., Kovács, R. L., Tóth, H., **Nagy, J. B.**, Tóth, Á., Szarka, K., Majoros,
L., Kardos, G.: The Role of Uniform Meropenem Usage in *Acinetobacter baumannii* Clone
Replacement.
Antibiotics. 10 (2), 1-12, 2021.
DOI: <http://dx.doi.org/10.3390/antibiotics10020127>
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