



## Anthropogenic environmental drivers of antimicrobial resistance in wildlife



Benjamin M.C. Swift <sup>a,1</sup>, Malcolm Bennett <sup>a</sup>, Katie Waller <sup>a</sup>, Christine Dodd <sup>b</sup>, Annie Murray <sup>c</sup>, Rachel L. Gomes <sup>d</sup>, Bethan Humphreys <sup>e</sup>, Jon L. Hobman <sup>b</sup>, Michael A. Jones <sup>a</sup>, Sophia E. Whitlock <sup>c</sup>, Lucy J. Mitchell <sup>c</sup>, Rosie J. Lennon <sup>c</sup>, Kathryn E. Arnold <sup>c,\*</sup>

<sup>a</sup> School of Veterinary Medicine and Science, University of Nottingham, UK

<sup>b</sup> School of Bioscience, University of Nottingham, UK

<sup>c</sup> Department of Environment and Geography, University of York, UK

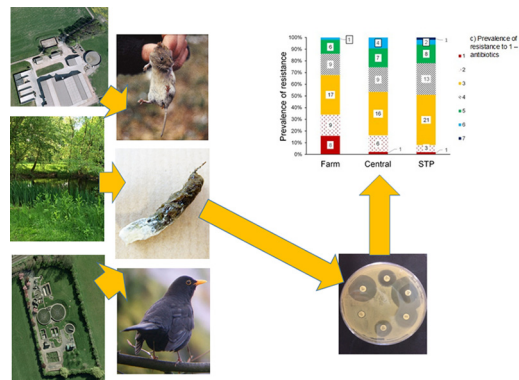
<sup>d</sup> Food, Water, Waste Research Group, Faculty of Engineering, University of Nottingham, UK

<sup>e</sup> School of Life Sciences, University of Nottingham, UK

### HIGHLIGHTS

- Does AMR in wildlife reflect exposure to human or livestock wastes?
- AMR patterns in *E. coli* from birds and mammals varied with site, season and host.
- Colistin resistance and ESBL/AmpC activity high in wildlife exposed to human waste.
- Our data question the use of wildlife as sentinels of anthropogenic environmental AMR.

### GRAPHICAL ABSTRACT



### ARTICLE INFO

#### Article history:

Received 1 July 2018

Received in revised form 13 August 2018

Accepted 14 August 2018

Available online 16 August 2018

Editor: D. Barcelo

#### Keywords:

*E. coli*

Antimicrobial resistance

Wildlife

### ABSTRACT

The isolation of antimicrobial resistant bacteria (ARB) from wildlife living adjacent to humans has led to the suggestion that such antimicrobial resistance (AMR) is anthropogenically driven by exposure to antimicrobials and ARB. However, ARB have also been detected in wildlife living in areas without interaction with humans. Here, we investigated patterns of resistance in *Escherichia coli* isolated from 408 wild bird and mammal faecal samples. AMR and multi-drug resistance (MDR) prevalence in wildlife samples differed significantly between a Sewage Treatment Plant (STP; wastes of antibiotic-treated humans) and a Farm site (antibiotic-treated livestock wastes) and Central site (no sources of wastes containing anthropogenic AMR or antimicrobials), but patterns of resistance also varied significantly over time and between mammals and birds. Over 30% of AMR isolates were resistant to colistin, a last-resort antibiotic, but resistance was not due to the *mcr-1* gene. ESBL and AmpC activity were common in isolates from mammals. Wildlife were, therefore, harbouring resistance of clinical relevance. AMR *E. coli*, including MDR, were found in diverse wildlife species, and the patterns and prevalence of resistance

\* Corresponding author: Department of Environment and Geography, University of York, YO10 5NG, UK.

E-mail addresses: [bswift@rvc.ac.uk](mailto:bswift@rvc.ac.uk) (B.M.C. Swift), [m.bennett@nottingham.ac.uk](mailto:m.bennett@nottingham.ac.uk) (M. Bennett), [svyklw@nottingham.ac.uk](mailto:svyklw@nottingham.ac.uk) (K. Waller), [Christine.Dodd@nottingham.ac.uk](mailto:Christine.Dodd@nottingham.ac.uk) (C. Dodd), [am1400@york.ac.uk](mailto:am1400@york.ac.uk) (A. Murray), [rachel.gomes@nottingham.ac.uk](mailto:rachel.gomes@nottingham.ac.uk) (R.L. Gomes), [mbybmh@nottingham.ac.uk](mailto:mbybmh@nottingham.ac.uk) (B. Humphreys), [Jon.Hobman@nottingham.ac.uk](mailto:Jon.Hobman@nottingham.ac.uk) (J.L. Hobman), [michael.a.jones@nottingham.ac.uk](mailto:michael.a.jones@nottingham.ac.uk) (M.A. Jones), [sew553@york.ac.uk](mailto:sew553@york.ac.uk) (S.E. Whitlock), [ljr540@york.ac.uk](mailto:ljr540@york.ac.uk) (L.J. Mitchell), [rjl529@york.ac.uk](mailto:rjl529@york.ac.uk) (R.J. Lennon), [kathryn.arnold@york.ac.uk](mailto:kathryn.arnold@york.ac.uk) (K.E. Arnold).

<sup>1</sup> Current address: Pathobiology and Population Sciences, Royal Veterinary College, UK.

were not consistently associated with site and therefore different exposure risks. We conclude that AMR in commensal bacteria of wildlife is not driven simply by anthropogenic factors, and, in practical terms, this may limit the utility of wildlife as sentinels of spatial variation in the transmission of environmental AMR.

© 2018 Published by Elsevier B.V.

## 1. Introduction

Antimicrobial resistance (AMR) has existed for millions of years, and is an inevitable evolutionary consequence of microbial competition in the environment (D'Costa et al., 2011; Davies and Davies, 2010; Martinez, 2009). While the increasing prevalence of AMR in clinically important and commensal bacteria in both humans and livestock can be attributed largely to selection through the use of antimicrobials (Ibrahim et al., 2016; Karesh et al., 2012), AMR has also been reported in the commensal bacteria of wildlife (Arnold et al., 2016). Commensal bacteria have the potential to act as reservoirs of resistance genes, contributing to the development of AMR in pathogens by horizontal transmission (Arnold et al., 2016; Taylor et al., 2011; von Wintersdorff et al., 2016). AMR is a problem in human and veterinary medicine worldwide, inhibiting the treatment of bacterial infections and estimated to be responsible for 25,000 preventable human deaths in Europe annually (Marston et al., 2016) and an estimated global economic cost of 100 trillion USD by 2050 if not addressed (O'Neill, 2016). Thus, there is increasing interest in the environment, including wildlife, as both a source of clinically relevant AMR and in order to better understand the effects of anthropogenically-derived antimicrobial pollution and resistance in ecosystems (Arnold et al., 2016; Carroll et al., 2015; Huijbers et al., 2015).

It is often assumed that antimicrobial-resistant bacteria (ARB) in wildlife result from contact with anthropogenic sources such as farms and human waste that pollute the environment with AMR bacteria and/or with antimicrobials (Allen et al., 2010; Clarke and Smith, 2011; Radhouani et al., 2011). Farms on which manure and slurry can be contaminated with ARB, antibiotics (or their metabolites) and other selective drivers of AMR are important habitats for many small mammals and birds, as are sewage treatment plants (STPs) where some birds and mammals feed directly from the bioprocessers (reviewed in Arnold et al., 2016). Run-off from farms, slurry tanks and manure-fertilised fields, along with sewage effluent, can result in antimicrobial drug and ARB contamination of local water courses and land (Fahrenfeld et al., 2013). Consequently, it is unsurprising that ARB have been found in wild animals in close contact with humans (Allen et al., 2011; Bondo et al., 2016; Furness et al., 2017; Gilliver et al., 1999).

Assigning the source and directionality of AMR dissemination is challenging. Even within wildlife populations living in close contact with humans or livestock, or at least their wastes, there is little evidence directly linking an anthropogenic source of AMR with specific patterns of AMR and/or resistance genes. For example, few overlaps in resistance patterns and AMR genes were found between *E. coli* isolated from wildlife living on or near dairy farms and dairy cattle in England (Arnold et al., 2016; Wu et al., 2018). Whereas wild rodents nearer to a river receiving sewage effluent excreted more resistant *E. coli* than inland animals (Furness et al., 2017), this was an association lacking evidence of a clear transmission pathway. Other highly mobile taxa such as birds also carry ARB that have not been attributed to any particular anthropogenic source (Guenther et al., 2017; Schaufler et al., 2016). Moreover, AMR has been detected in wildlife living in remote and isolated locations with no obvious contact with the wastes of antimicrobial-treated humans or livestock (Cristobal-Azkarate et al., 2014). Thus, although transmission of AMR from humans or livestock to wildlife via direct contact with sewage, slurry or faeces, has been suggested, the empirical evidence is lacking or contradictory. Species or ecological guilds with different dispersal patterns, resource requirements and foraging

behaviours are likely to have different roles in the evolution and dispersal of AMR (Arnold et al., 2016). We argue that the efficacy of wildlife species as sentinels of environmental transmission of AMR will vary depending on the spatial and temporal scales of interest.

In this study, three nearby communities of small wild rodents and birds were investigated for evidence of AMR in faeces. The antimicrobials used to screen for resistance were chosen as they represent a range of antibiotic classes of medical and veterinary interest. For example, cefpodoxime resistance is seen as an indicator of extended spectrum beta-lactamase (ESBL) or AmpC beta-lactamase producing bacteria which cause significant problems in human medicine especially with urinary tract infections (Rawat and Nair, 2010). Colistin resistance is also of relevance due to colistin being an antibiotic of last resort. The sites for sampling were chosen to represent different exposures to wastes and thus potentially different selection pressures for AMR: a dairy farm with antimicrobial-treated livestock, a STP containing waste from humans treated by antimicrobials and an area of parkland and neighbouring arable field edge with no obvious sources of waste containing antimicrobials or ARB. We sampled wildlife species typical for small woodlands, farmland and hedgerow habitats in the UK; small rodents including wood mice *Apodemus sylvaticus*, bank voles *Myodes glareolus* and a number of bird species.

The overall aim of this study was to investigate the role of environmental contamination in the patterns of AMR found in wildlife. We addressed whether the spatial location where wild birds and mammals were sampled, including proximity to human and livestock wastes, explained variation in: 1) prevalence and genomic diversity of AMR *E. coli* in birds and mammals; 2) patterns of AMR and MDR prevalence in *E. coli* isolates; and 3) prevalence of phenotypic resistance to medically important antimicrobials and the resistance genes responsible.

## 2. Material and methods

### 2.1. Study sites

Three nearby study sites in the East Midlands of England, on a 1200 m transect, were selected (Fig. S1), based on their differing potential exposure to human and livestock sources of AMR and antimicrobial drugs. The 'Farm site' was a small woodland and hedgerows immediately adjacent to a dairy farm that received run-off from farm buildings and livestock faeces potentially contaminated with AMR bacteria and antimicrobials. The 'Central site', around 600 m from the Farm site, comprised an arboretum and neighbouring hedgerow edging an arable field. It was not adjacent to known sources of human or livestock waste. The 'STP site' was a small sewage treatment plant around 450–600 m from the Central-site, comprising the land and hedgerows surrounding all the tanks and trickling filters making up the STP and hedgerows adjacent to the pipe where treated water outflowed into a local stream. All the sites were close enough to share common environmental traits and weather. Conversely, the three sites were far enough apart, with physical barriers to dispersal (roads and a railway line), such that most of the species sampled would not regularly move between the sites.

### 2.2. Sampling wildlife

All sampling took place between July and August ('Summer'), and October and November ('Autumn') 2016 and was subject to full ethical

Download English Version:

<https://daneshyari.com/en/article/10138356>

Download Persian Version:

<https://daneshyari.com/article/10138356>

[Daneshyari.com](https://daneshyari.com)