



**One Health EJP Thematic
Report on AMR**
**WP5 Science to policy
translation**

Responsible Partner: BfR, SSI

Contributing partners: PMT members, JRP
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ONE HEALTH EJP THEMATIC REPORT ON AMR

The main focus of the One Health European Joint Programme (One Health EJP) is to reinforce international collaboration between institutes by enhancing transdisciplinary cooperation and integration of activities by means of Joint Research Projects, Joint Integrative Project and through education and training in the fields of Foodborne Zoonoses, Antimicrobial Resistance (AMR) and Emerging Threats. Of the 29 [One Health EJP projects](#), seven are in the domain of AMR, and several others also include the topic in their work.

In this Thematic Report we provide an overview of the key outcomes and publications produced by the One Health EJP projects in the field of AMR by end of August 2020. The work is ongoing, and updates can be found on the webpages of the [projects](#) as well as in the [One Health EJP Outcome Inventory](#). Publications are listed on the [publication page](#).

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One Health EJP projects in the domain of AMR



[ARDIG](#) - Antibiotic Resistance Dynamics: the influence of geographic origin and management systems on resistance gene flows within humans, animals and the environment

Project Leader: [Muna Anjum](#) (APHA)

The [ARDIG](#) project examines the dynamics of AMR in the human, animal, food and environment epidemiological unit from six European countries (UK, Norway, France, Netherlands, Germany, Spain), which represent significant difference in their usage of antimicrobial agents and AMR prevalence, as well as different climate and management systems, and the potential for transmission of resistance.

Results:

- Project members are comparing AMR and antibiotic sales/usage (AMU) data collected through existing national surveillance and research programs and assessing risk factors.
- A description of surveillance and monitoring systems for AMU and AMR in the human and livestock sectors, as well as national surveillance and monitoring systems for AMR in food of six European countries, is available in [Mesa et al., 2020](#).
- Work is ongoing to match Whole Genome Sequencing data, in particular AMR genotypes, with the corresponding phenotypes.



[IMPART](#)- Improving phenotypic Antimicrobial Resistance Testing by development of sensitive screening assays for emerging resistances, and setting missing ECOFFs

Project Leader: [Kees Veldman](#) (WUR)

The [IMPART](#) project deals with harmonization of cost-effective phenotypic methods for detection of AMR. Actions are in line with the [Commission's Action Plan Against the rising threats from Antimicrobial Resistance: Road Map](#) (updated on November 2016), supporting surveillance in animal pathogens and determining the risk of transmission of resistance from animals to humans via food. IMPART included ring trials between different institutions to ensure optimal harmonisation.

Results:

- Harmonisation of isolation and characterisation of AMR was carried out on 17 different species of bacteria important in human, animal and environmental health (incl. colistin-resistant Enterobacteriaceae and carbapenemase-producing Enterobacteriaceae).
- Of 3000 isolates, 1300 minimal inhibitory concentration (MIC) distributions consisting 47,640 MIC values of 34 different antimicrobials were determined (data will be uploaded in the EUCAST database in August 2020). Epidemiological Cut Off (ECOFFs) values for a number of drug/microorganism combinations are being calculated.
- A strain collection of 525 *Clostridium difficile* strains has been assembled and inhibition zone diameter distributions have been determined for eight antimicrobials. ECOFF values will be proposed.



RaDAR - Risk and Disease burden of Antimicrobial Resistance

Project Leader: [Eelco Franz](#) (RIVM)

The [RaDAR](#) project has developed a number of datasets and computational methods aimed at addressing the contribution of animal and environmental sources to the public health burden of AMR. The approaches included linking data on AMU on AMR in animal husbandry, modelling the spread of resistance determinants in microbial communities, the environment and along the food chain, and quantifying human exposure and disease burden.

Results:

- The project developed the [COMPASS](#) database, that collects AMR plasmid sequences compiling 12,084 complete plasmids with associated metadata from 1571 distinct species isolated worldwide over more than 100 years ([Douarre et al., 2020](#)). The database is associated with a plasmid identification pipeline aiming at identifying plasmids from sequencing data.
- An inventory of exposure risk assessment models (i.e. machine learning methods for risk profiling, methods for testing model -validity, -sensitivity and -robustness), as well as an inventory of exposure assessment models (i.e. methods to model the change of prevalence and concentration of bacteria with phenotypic resistance or specific resistance determinants along the food chain for exposure assessments) have been developed.
- Computational methods have been developed to model the relationship between the use of antibiotics and the development of resistance, including modelling on-farm transmission, assessment of intervention measures, and modelling transmission between livestock and human populations and through the food chain (for example, [Mughini-Gras et al., 2020](#)).
- The models developed are briefly described in the [One Health EJP Outcome Inventory](#)

One Health EJP Projects involving work on AMR



[NOVA](#) - Novel approaches for design and evaluation of cost-effective surveillance across the food chain

Project leader: [Jenny Frössling](#) (SVA)

The [NOVA](#) project strives to develop new surveillance tools and methods, and to optimise the use of existing surveillance system data. Although not focused on AMR, the project inevitably touches upon the topic.

Results:

- A number of computational models have been developed, including a model simulating spread of AMR in large animal populations based on metagenomic data, which informs how the use of metagenomics in surveillance can be optimised using different sampling strategies.



ORION - One health surveillance Initiative on harmonization of data collection and interpretation

Project Leader: [Matthias Filter](#) (BfR)

As in integrative project, ORION deals with the semantic and technical interoperability between the sectors, in particular regarding surveillance information. All of its solutions are currently tested in national pilot studies; some of them also with ECDC and EFSA..

Results:

- [OHS Codex](#) provides users with guidance and resources that improve collaboration, mutual understanding, knowledge exchange and better data integration between the different One Health surveillance sectors. The OHS Codex is aligned to and supports the [Tripartite Guide](#). Detailed information are available [here](#). A pilot study is testing resources of the OHS Codex on the topic of One Health AMR Surveillance.
- [OH-CRAC](#): the Consensus Report Annotation Checklist is a checklist for surveillance reports aiming at harmonization across sectors. It allows existing One Health surveillance metadata to be mapped to one concurrent metadata schema. The OH-CRAC was recently applied to existing AMR surveillance data reports provided by the One Health EJP project [ARDIG](#) and the [German One Health Initiative](#). The OH-CRAC resource is available as web-based interactive annotating [tool](#) for functional meta-information extraction in reports/documents uploaded as pdf files.
- [OHEJP Glossary](#) (in collaboration with the One Health EJP projects [COHESIVE](#) and [NOVA](#)) includes core terminology relevant for the three domains: Animal Health, Food and Public Health. A text processing [web service](#) allows to find matches between a document provided by the user and the OHEJP Glossary. Coverage and quality of AMR and AMU related terms was recently improved in collaboration with the One Health EJP project [ARDIG](#) and the [German One Health Initiative](#).
- [OHS Knowledge Hub](#): a cross-domain inventory of currently available data sources, methods / algorithms / tools, that support One Health surveillance data generation, data analysis, modelling and decision support.

New projects in the domain of AMR and including AMR

In January 2020, four new One Health Joint Research Projects focusing on AMR started – [FARMED](#), [FED-AMR](#), [FULL-FORCE](#) and [WORLDCOM](#). In addition, other projects not strictly in the domain of AMR, for example the Joint Integrative project [OH-HARMONY-CAP](#), include AMR in their plans.



PhD projects in the domain of AMR



ECO-HEN – Dynamics of *Escherichia coli* in laying hens

PhD Student: [Irene Aldea Ramos](#) (UCM); Main Supervisor: [Miguel A. Moreno](#) (UCM)
Start Date: February 2019; duration: 3 years

The ECO-HEN project aims to fill the gap on the transmission dynamics of AMR *E. coli* in commercial laying hen production and to determine to what extent this animal production poses a public health risks via food and/or environment contamination.

Results to Date:

- A review of the bioinformatic analysis of WGS data already available has been completed, along with reviewing the existing data on the collection of bacterial isolates from a laying hens farm.
- Bioinformatics analysis was performed along with new searches on the WGS of AMR isolates.
- Work is ongoing to reconstruct the plasmids responsible for dissemination of AMR genes across isolates from different sources, and to follow the dynamics of AMR.



LIN-RES - Investigation of the molecular basis, origin, transferability and risk factors associated with linezolid-resistance emergence in Gram-positive bacteria of human and animal origin

PhD Student: [Michaël Timmermans](#) (Sciensano); Main Supervisor: [Cécile Boland](#) (Sciensano)
Start Date: January 2019; Duration: 3 years

The LIN-RES project investigates the molecular basis, origin, transferability and risk factors associated with linezolid-resistance emergence in Gram-positive bacteria of both human and animal origin such as staphylococci and enterococci.

Results to Date:

- Over 1000 faecal/caecal samples from cattle, pigs and poultry and almost 150 pools of nasal swab pig samples were collected and screened for linezolid resistance.
- Work is ongoing to complete the strain-typing and associated host specificity, resistance profiling, and transferability markers analysis of the strains collected.
- The results will be presented at the World One Health Congress 2020.



METAPRO – Metagenomics and genomic approaches for the prevention of the spread of plazomicin resistance in humans, animals and the environment

PhD Student: [Bosco Rodriguez Matamoros](#) (UCM); Main Supervisor: [Bruno Gonzalez-Zorn](#) (UCM)
Start Date: March 2020; duration: 3 years

The METAPRO project is focused on the antibiotic plazomicin, which is a novel semisynthetic aminoglycoside approved in June 2018 by the FDA to be used as a last resort antibiotic in complicated urinary tract infections caused by multidrug resistant Gram-negative bacteria in humans. Approval by the EMA is foreseen in the upcoming months. However, the acquired 16S rRNA methyltransferase genes result in high level of resistance to plazomicin. The objective of this Doctoral project is to apply a combination of metagenomics and classical genomic techniques to assess the prevalence of 16S methyltransferases in eight different ecological niches in the UK and Spain using metagenomic analysis; to elucidate the bacterial and ecological reservoirs of plazomicin resistance prior to its clinical use in Europe; to describe the clones and genetic platforms that entail a major risk for plazomicin application



and finally, to develop a guideline for early detection of 16S rRNA methylases in the relevant ecological niche to preserve plazomicin for human clinical use.

Results to Date:

- The PhD student was recruited in March 2020. Shortly after the coronavirus emerged, the lab joined the network to diagnose COVID-19 in elderly homes in Madrid. As the PhD student was actively involved in this task, the project start was delayed until June 2020.
- Ongoing work includes producing a Spanish sampling design and executing this design.



KENTUCKY – Exploring the evolutionary success of the antibiotic resistant *Salmonella Kentucky* ST198

PhD Student: [Alaa Albasiony](#) (Sciensano); Main Supervisor: [Pieter-Jan Ceysens](#) (Sciensano)

Start Date: January 2020; duration: 3 years

The KENTUCKY project investigates *Salmonella Kentucky* (*S. Kentucky*) which is one of most notorious *Salmonella* serotypes, as it is strongly associated with AMR. The ECDC launched an Urgent Inquiry (UI-464) on a CIPR *S. Kentucky* ST198 strain carrying a chromosomally integrated gene encoding for cephalosporin resistance. To date, this clone is only reported in humans, as opposed to the CIPS *S. Kentucky* ST152 clone widely found in poultry in the USA but rarely reported in humans.

The KENTUCKY project will investigate what explains the evolutionary success of the multidrug resistant *S. Kentucky* ST198 clone, what the mechanisms of the integration and potential further transfer of the ESBL gene in its chromosome and determine whether there are there genetic determinants of different human-animal host ranges in epidemic *S. Kentucky* ST198 and ST152.

Results to Date:

- This project started in Jan 2020, and during the first nine months of the project, *S. Kentucky* strains were selected for full genome sequencing using hybrid assemblies of short and long sequence reads. The isolates selected were either *S. Kentucky* ST198::*bla*_{CTX-M-14b} (i.e. chromosome-encoded), CIP^R, CTX^R or Kentucky ST198 *pbla*_{CTX-M14-b} (i.e. plasmid-encoded). These sequenced strains will form the basis for detailed investigation of these mobile genetic elements.



WILBR – Contribution of wild birds to AMR in the environment and on farms

PhD Student: [Olivia Turner](#) (APHA); Main Supervisor: [Muna Anjum](#) (APHA)

Start Date: February 2020; duration: 3 years

The WILBR project aims to understand the contribution of factors such as wild birds to dissemination of AMR in the environment in general, and on livestock farms in particular to help provide an assessment of the environmental risk posed by AMR and identify management options with clear indicators of effectiveness.

Migratory birds (represent ~40% of total birds in the world) can fly many thousands of kilometres and add another level of complexity to identify and control the routes for dissemination of AMR, as they often overwinter in countries or areas where there may be paucity of information of resistance trends due to limited surveillance and diagnostic capacity, with the burden of AMR unknown.

Results to Date:

- A literature review is currently being undertaken on the role of wild birds in dissemination and persistence of antimicrobial resistance (AMR) in the farm environment



VIMOGUT – In vitro and in vivo analyses and modulation of the chicken gut microbiome to combat AMR

PhD Student: [Ingrid Cardenas Rey](#) (WUR); Main Supervisor: [Michael Brouwer](#) (WUR)
Start Date: August 2019; duration: 4 years

The VIMO-GUT project studies the chicken microbiome development of chickens on farms to determine if the reported microbial progression is reproducible between different production rounds and farms. By screening these samples for the presence of extended-spectrum beta-lactamase (ESBL) *E. coli*, the significance of the reduced diversity of early colonised chickens will be determined. The *in vitro* chicken gut model will be set up for use at WBVR to test strategies for the reduction of ESBL *E. coli* and compare these with published data from *in vivo* studies. When the model can efficiently reproduce these *in vivo* studies, it can be used for further study of new ESBL *E. coli* colonisation prevention strategies.

Results to Date:

- 16S sequence analysis of samples collected and isolated was performed successfully.
- Work is ongoing with further data analysis to understand the relationship of the chicken gut microbiota and colonisation of the gut by ESBL *E.coli*.
- Work has started to prepare an *in vitro* chicken gut model.



UDoFRiC – Understanding the development of fluoroquinolone (FQ) resistance in *Campylobacter* present in broilers and the risks of FQ resistance persisting through the food-chain to cause disease in people

PhD Student: [Taylor Hanford](#) (APHA); Main Supervisor: [John Rodgers](#) (APHA)
Start Date: March 2020; duration: 3 years

The UDoFRiC project aims to exploit the archives of *Campylobacter* and associated information (phenotypic, genomic, epidemiological meta-data) from surveillance and research across the food-chain to investigate temporal trends in the development and diversity of FQ resistance (FQR) in UK and French broiler flocks. The study will examine the relationship between FQ use in poultry and development of resistance, assess fitness costs/benefits of acquired resistance and determine if any specific FQ resistance variants found in poultry are likely to persist and cause disease in people. The project would provide data to feed into the risk assessment for ongoing use of FQ in poultry and consequent risks of FQ resistance in clinical cases.

Results to Date:

- A review of available datasets from *Campylobacter* research and national surveillance in broilers at APHA was undertaken. The datasets consisted of a collection of *Campylobacter* isolates from broiler chicken sources, and various accompanying meta-data, e.g antimicrobial resistance phenotype, genotypic data (including AMR), and farm and production data. Work is being carried out on the data from this period to characterise and to identify trends or sources of FQR amongst *Campylobacter*.



HME-AMR – Investigating the role of heavy metals in the environment as a selective pressure for the dissemination of antimicrobial resistance

PhD Student: [Mariel Stefhanie Aybar Espinoza](#) (TEAGASC); Main Supervisor: [Kaye Burgess](#) (TEAGASC)
Start Date: October 2020; duration: 3 years

The HME-AMR project is driven by the clear need for more data on the impact of heavy metal concentrations in the natural environment and their potential impact on the co-selection and



dissemination of AMR in the environment and the food chain. Very limited information is currently available regarding the impact of selective pressures such as heavy metals which may be present in the environment on the mobilisation of antimicrobial resistance and its potential transfer into the food chain.

Results to Date:

- The COVID-19 pandemic has resulted in the delayed recruitment of a PhD student. The PhD student has now been recruited and will commence in October 2020.



[Codes4strains](#) – Tracking bacterial pathogens through sources, geography and time using stable phylogenetically informative genome codes

PhD Student: [Mélanie Hennart](#) (Institut Pasteur); Main Supervisor: [Sylvain Brisse](#) (Institut Pasteur)

Start Date: October 2019; duration: 3 years

The [Codes4strains](#) project focuses on the implementation of genome sequencing in public health microbiology, which has allowed the natural variation exhibited by pathogenic bacteria to be leveraged for infectious disease surveillance and outbreak detection. To track strains globally, and as they spread between the environment, food, animals and humans, universal strain nomenclatures are necessary. The current SNP address or multi-level cgMLST classifications have limitations which leads to an unstable approach. This gap slows down communication and action against the transmission of pathogens across sectors, world regions and over long periods of time.

Currently, there is no genomic nomenclature system of bacterial pathogens which combines complete stability of identifiers, high standardization and reproducibility and high resolution. This PhD project will address this critical gap.

Results to Date:

- A pilot genome dataset has been defined for *Klebsiella pneumoniae*, which represents the non-redundant diversity and population structure of *Klebsiella pneumoniae*, including the different phylogroups and some strain sets derived from outbreaks. Work is ongoing to repeat this process with *Escherichia coli*.
- Re-evaluation of the cg-MLST schema with the pilot genome set for *Klebsiella pneumoniae*. Work is ongoing to repeat this process with *Escherichia coli*.
- The pilot genome dataset was used to develop a LIN coding software tool, which defines a LIN code scheme (*LIN code = Life Identification Number code*)



Publications in the domain of AMR

Stepwise evolution and convergent recombination underlie the global dissemination of carbapenemase-producing *Escherichia coli*.

Patiño-Navarrete et al. (2020), *Genome Medicine*, DOI: <https://doi.org/10.1186/s13073-019-0699-6>, Project: [ARDIG](#)

Keywords:

Carbapenems, Bacterial evolution, Lateral gene transfers, Multidrug resistance, Porin, Penicillin-binding Proteins

Carbapenem-resistant *Enterobacteriaceae* are considered by WHO as ‘critical priority pathogens’ for which novel antibiotics are urgently needed. Based on whole genome sequencing data, the authors reconstructed the phylogeny of carbapenemase-producing *E. coli* corresponding to a total of 2026 non-redundant isolates. The authors determined the association between specific mutations and the acquisition of

a carbapenemase gene and the most probable order of events, and concluded that the selection of carbapenemase-producing *E. coli* lineages is a multistep process involving mutations, recombination, acquisition of antibiotic resistance genes, and selection by β -lactams from diverse families.

Monitoring Antimicrobial Resistance and Drug Usage in the Human and Livestock Sector and Foodborne Antimicrobial Resistance in Six European Countries.

Mesa Varona et al. (2020), *Dovepress*, DOI: <https://doi.org/10.2147/IDR.S237038>, Project: [ARDIG](#)

Keywords:

AMR, AMU, food-producing animals, harmonization, monitoring, surveillance

Differences in the surveillance and monitoring systems between countries and sectors make comparisons of AMU and AMR challenging. In this paper, the authors described all surveillance and monitoring systems for AMU and AMR in the human and livestock sectors, as well as national surveillance and monitoring systems for AMR in food, in six European

countries (Spain, Germany, France, the Netherlands, the United Kingdom and Norway) and analysed comparability between data from the different sectors and countries. This study points out the need for standardisation and harmonisation between countries and sectors.

Analysis of COMPASS, a New Comprehensive Plasmid Database Revealed Prevalence of Multireplicon and Extensive Diversity of IncF Plasmids.

Douarre et al (2020), *Frontiers in Microbiology*, DOI: <https://doi.org/10.3389/fmicb.2020.00483>, Project: [RaDAR](#)

Keywords:

plasmid database, host range, replicon typing, MOB typing, plasmid mobility, multireplicon, IncF plasmid

Conjugative plasmids are predominantly responsible for the global dissemination of antimicrobial resistance, representing an important threat to global health. The authors describe COMPASS, a database compiling 12,084 complete plasmids with associated metadata from 1571 distinct species isolated worldwide over more than 100 years. Thanks to the database it was possible to identify identical plasmids across different

bacteria revealing mainly intraspecies dissemination and rare cases of horizontal transmission. The results highlight the crucial role of IncF alleles in plasmid’s replication and propagation.

Attributable sources of community-acquired carriage of *Escherichia coli* containing β -lactam antibiotic resistance genes: a population-based modelling study.

Mughini-Gras et al. (2019), *Lancet Planetary Health*, DOI: [10.1016/S2542-5196\(19\)30130-5](https://doi.org/10.1016/S2542-5196(19)30130-5), Project: [RaDAR](#)



Keywords:
ESBL, AMR from animals to humans, Modelling

In this population-based modelling study, authors collected data of Extended-spectrum β -lactamase-producing *E. coli* (ESBL-EC) and plasmid-mediated AmpC-producing *E. coli* (pAmpC-EC) in the Netherlands population for 2005-17 from different sources. They applied an established source attribution model to assess the sources of community-acquired ESBL-EC and pAmpC-EC intestinal carriage. The authors concluded that although humans are the main source of community-acquired ESBL-EC and pAmpC-EC carriage, intracommunity ESBL-EC and pAmpC-EC spread alone is unlikely to be self-maintaining without transmission to and from non-human sources.

Identifying emerging trends in antimicrobial resistance using *Salmonella* surveillance data in poultry in Spain.

Alvarez et al. (2019), *Transboundary and Emerging Diseases*, DOI: <https://doi.org/10.1111/tbed.13346>, Project: [NOVA](#)

Keywords:
Antimicrobial resistance, foodborne, monitoring, Non-typhoidal *Salmonella*, poultry, serotype Kentucky

Infection with non-typhoidal *Salmonella* (NTS) remains one of the major causes of foodborne disease worldwide, and poultry is considered one of the major sources of NTS. The authors investigated the information from the monitoring programme for AMR in *Salmonella* from poultry in Spain in 2011–2017 to assess the diversity in phenotypic resistance and to evaluate the programme's ability to detect multi-resistance patterns and emerging strains in the animal reservoir. The authors analysed the association of phenotypic resistance and serotype within certain hosts. Moreover the widespread presence of certain serotype-resistotype combinations in certain hosts/years suggested the possible expansion of multi-drug resistant strains in the animal reservoir.

Salmonella Surveillance Systems in Swine and Humans in Spain: A Review.

Martínez-Avilés et al. (2019), *Veterinary Sciences*, DOI: [10.3390/vetsci6010020](https://doi.org/10.3390/vetsci6010020), Project: [NOVA](#)

Keywords:
Zoonoses, foodborne, disease control, public health, domestic livestock; pig, one health

Non-typhoid salmonellosis is a common and problematic foodborne zoonotic disease in which pork and pork products can be an important source of infection. The authors reviewed *Salmonella* surveillance systems in swine and humans in Spain, identified gaps and opportunities for improvement, and discussed potential ways of integration under a “One-Health” approach.

Broad-Spectrum Cephalosporin-Resistant *Klebsiella* spp. Isolated from Diseased Horses in Austria.

Loncaric et al. (2020), *Animals*, DOI: <https://doi.org/10.3390/ani10020332>, Project: [MedVetKlebs](#)

Keywords:
AmpC, ESBL, *Klebsiella pneumoniae*, antibiotic-resistance, β -lactamases, horses

Broad-spectrum cephalosporin-resistant *Klebsiella pneumoniae* is considered as a serious problem for public human health. In this cross sectional study the authors sampled 1541 horses and found 51 specimens positive for *Klebsiella* spp, 7 of which multidrug-resistant, the majority of antibiotic resistance genes being encoded on plasmids. The

study stresses the risk of acquiring multidrug-resistant *Klebsiella* spp. from horses, and ultimately underlines the need to prioritise the monitoring of domestic animals for the presence of broad-spectrum cephalosporin-resistant *Klebsiella*.

***Klebsiella pneumoniae* carriage in low-income countries: antimicrobial resistance, genomic diversity and risk factors.**



Huynh et al. (2020), *Gut Microbes*, DOI: <https://doi.org/10.1080/19490976.2020.1748257>, Project: [MedVetKlebs](#)

Keywords:
Klebsiella pneumoniae, carriage, antibiotic resistance, genomic diversity, community, low-income countries

In this cross-sectional study the authors investigated prevalence and microbiological characteristics of *Klebsiella pneumoniae* in asymptomatic human carriage, and attached risk factors. The authors screened 911 pregnant women from communities in Madagascar, Cambodia, and Senegal for gut colonization and investigated associated risk factors. One third of *Klebsiella pneumoniae* isolates had acquired AMR genes,

although with variation between countries. Environmental exposure factors associated with AMR and hypervirulence were identified, the risk factors being country-specific and *Klebsiella pneumoniae* subpopulation-specific.

The ZKIR Assay, a Real-Time PCR Method for the Detection of *Klebsiella pneumoniae* and Closely Related Species in Environmental Samples.

Barbier et al. (2020), *Applied and Environmental Microbiology*, DOI: <https://doi.org/10.1128/AEM.02711-19>, Project: [MedVetKlebs](#)

Keywords:
Klebsiella, phylogroup, soil, detection, screening, ZKIR qPCR, culture method, environment

The current lack of screening methods to detect *Klebsiella pneumoniae* in complex matrices limits research on its ecology. The authors used a novel real-time PCR method, the ZKIR (*zur-khe* intergenic region) assay, to detect *Klebsiella pneumoniae* in 96 environmental samples. The authors compared the ZKIR assay with traditional methods and found that the ZKIR assay is an accurate, specific, and sensitive

novel method to detect the presence of *Klebsiella pneumoniae* in complex matrices. In addition, based on genomic sequencing, the authors show that strains from environmental samples differ from clinical isolates in AMR and virulence gene content.

Antimicrobial Resistance in the Food Chain in the European Union.

Florez-Cuadrado et al. (2018), *Advances in Food and Nutrition Research*, DOI: [10.1016/bs.afnr.2018.04.004](https://doi.org/10.1016/bs.afnr.2018.04.004), Project: [MoMIR-PPC](#)

Keywords:
Safety food, AMR, Antimicrobials, Surveillance, European Union

The authors give an outlook of mechanisms of AMR and AMR transmission in bacteria, and describe the surveillance programmes of AMR of zoonotic bacteria according to the European legislation.