



RESISTANCE ELEMENTS — DAY 6

Antimicrobial Resistance : from phenotypes to genotypes

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03.06.2024

Intended Learning Objectives

Specific objectives of this session:

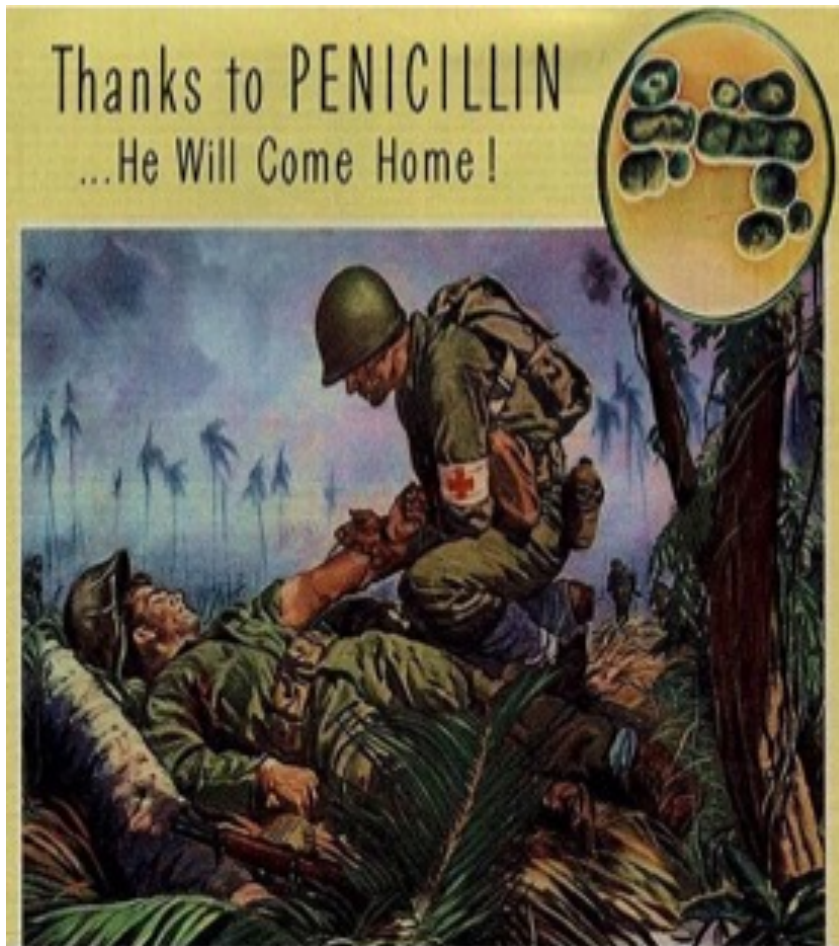
1. Understand antimicrobial resistance (AMR) and the diversity AMR genes and their associated mechanisms
2. Background on the current epidemiology of AMR in the main foodborne pathogens (*Salmonella*, *Shigella*/*E. coli*, *Campylobacter*, *Listeria*)
3. Gain knowledge on AMR genes databases and tools for *in silico* genotyping
4. Current situation and perspectives of AMR prediction phenotype from the genotype

Outline

This session consists of the following elements

1. Antimicrobial resistance (AMR) – overview
2. AMR genes and their associated mechanisms
3. From farm to fork: epidemiology of AMR in the main foodborne pathogens (*Salmonella*, *Campylobacter*, *Shigella*, *Listeria*)
4. AMR genes databases and tools for *in silico* genotyping
5. Group exercises integrating phenotype and genotype detection of AMR

Antibiotics Revolutionized Medicine

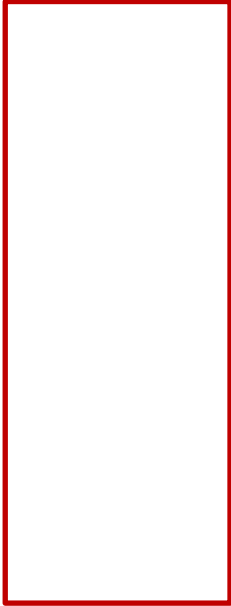


After just over 75 years of penicillin's clinical use, the world can see that its impact was immediate and profound. In 1928, a chance event in Alexander Fleming's London laboratory changed the course of medicine. However, the purification and first clinical use of penicillin would take more than a decade. Unprecedented United States/Great Britain cooperation to produce penicillin was incredibly successful by 1943. This success overshadowed efforts to produce penicillin during World War II in Europe, particularly in the Netherlands. Information about these efforts, available only in the last 10–15 years, provides new insights into the story of the first antibiotic. Researchers in the Netherlands produced penicillin using their own production methods and marketed it in 1946, which eventually increased the penicillin supply and decreased the price. The unusual serendipity involved in the discovery of penicillin demonstrates the difficulties in finding new antibiotics and should remind health professionals to expertly manage these extraordinary medicines.

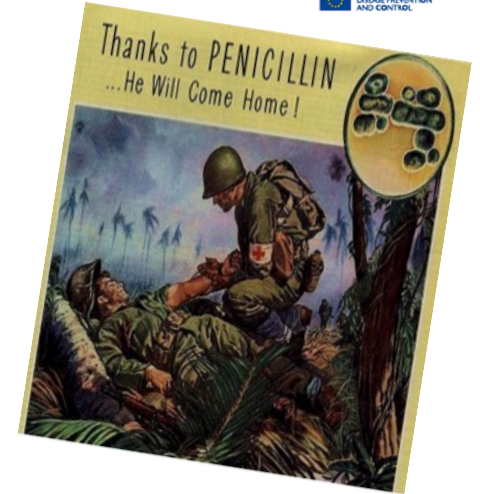
Gaines, EID 2017

Antimicrobial Resistance (AMR) – a silent pandemic

Global Deaths in 2019



FIGURES



A Woman Was Killed by a Superbug Resistant to All 26 American Antibiotics

She won't be the last.

SARAH ZHANG | JAN 13, 2017 | HEALTH



Back to the pre antibiotic era !!

AMR and One Health

DEFINITION

Antimicrobial Resistance – Main settings

> 50% in animals
- Therapy
- Prophylaxis
- Growth promotion (banned in
EU in 2005*)

FIGURES

Different AB policies according to the country
Absence of regulation and control on AB use in most areas of the world
Cumulative effects - e.g. 7000 tones / 12 years / Netherlands

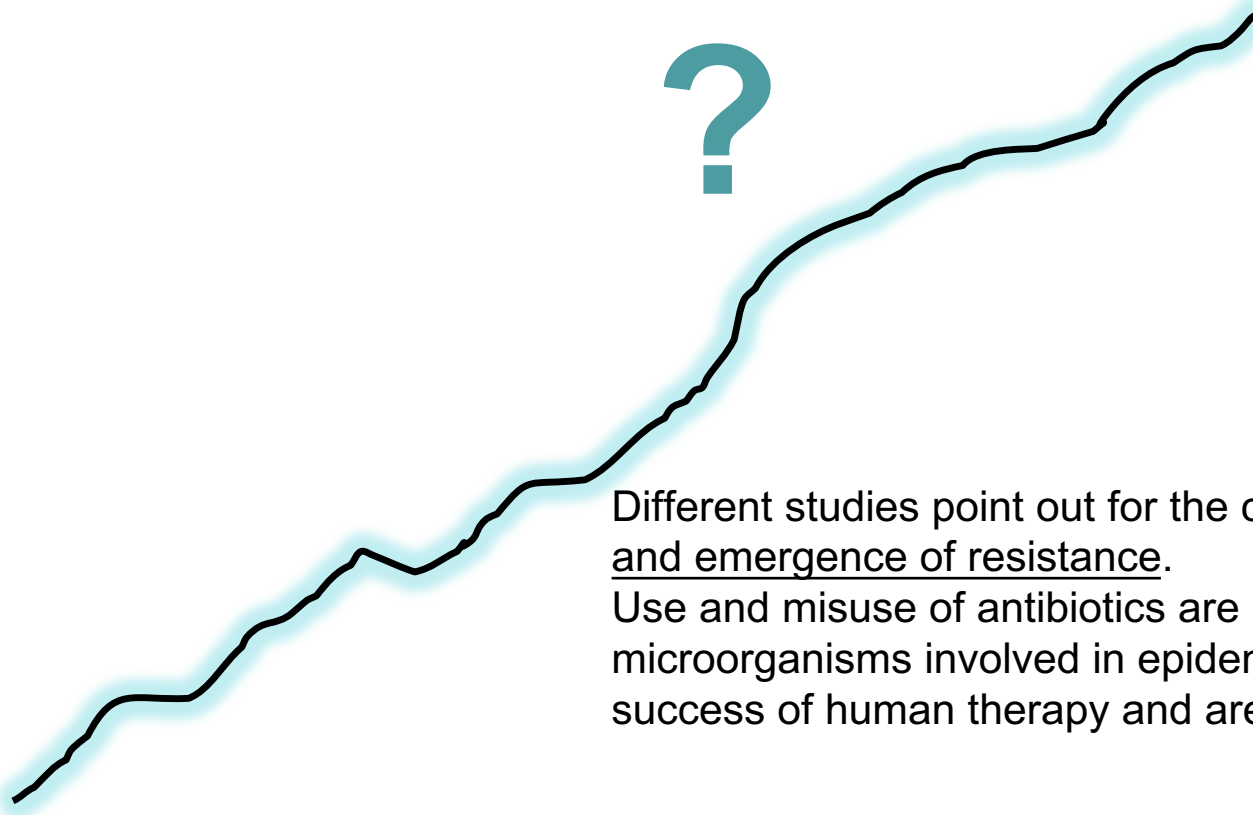
*This prohibition was extended by a EU Regulation which entered into force on 28 January 2022: Article 118 of Regulation (EU) 2019/6 on veterinary medicinal products requires **that products imported into the EU come from animals which have not been treated with growth-promoting antibiotics**

Antimicrobial Resistance – Main settings

But the contribution of animal setting to this burden has been a matter of debate for too long...

ANTIBIOTIC RESISTANCE

MRSA, VRE
GN-ESBL/Carba



Different studies point out for the correlation between antibiotic use in humans and emergence of resistance.

Use and misuse of antibiotics are involved in the emergence of resistant microorganisms involved in epidemic and endemic situations that menace the success of human therapy and are associated with higher rates of mortality.

Most antibiotics used both in humans and animals

FIGURES

Antibiotics commonly used in animals are **identical or belong to the same classes of important human antibiotics**

Extended spectrum cephalosporins, macrolides and fluroquinolones

Few molecules with new activities in the last years!!

Black colour- antibiotics or similar molecules not used in animals for food production

Medically Important Antimicrobials – WHO - 2024

[Home](#) / [Documents](#) / WHO List of Medically Important Antimicrobials

WHO List of Medically Important Antimicrobials



**DOWNLOAD
DOCUMENT**

There is a global need to preserve the efficacy of antimicrobial agents and minimize the risk of antimicrobial resistance (AMR). Because AMR develops and transfers within and among all sectors, minimizing the risk of emergence and transmission of AMR calls for a One Health approach (1). To improve the responsible and prudent use of antimicrobial agents – and in particular medically important antimicrobial agents – it is thus essential to decrease their inappropriate use across sectors.

13 Feb 2024

Update of the 2019 version

References

FIGURES

FIGURES

AMR main characters ?

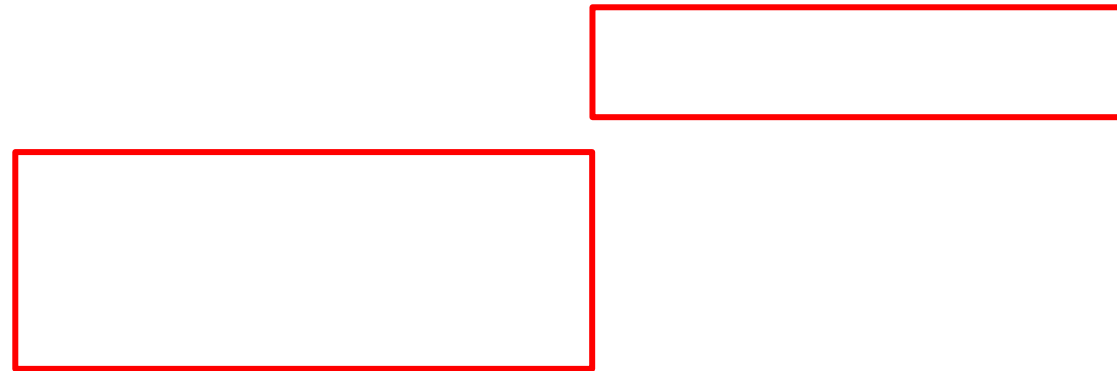
FIGURES



AMR main characters ?



FIGURES



Main mechanism of AMR



E.g. AcrAB; OqxAB, Tet,
Porin mutations

FIGURES

E.g. QRDR, MgrB, PmrB, Qnr;
16S rRNA methylases; Mcr,
PBPs

E.g. β -lactamases; AMEs

Main mechanisms of AMR



E.g. AcrAB; OqxAB, Tet,
Porin mutations

1. **Mutations in chromosomal genes** leading to increased expression of intrinsic R mechanisms (antibiotic-inactivating enzymes or efflux pumps), alterations in permeability due to loss of EM porins, or changes in the target (QRDR)

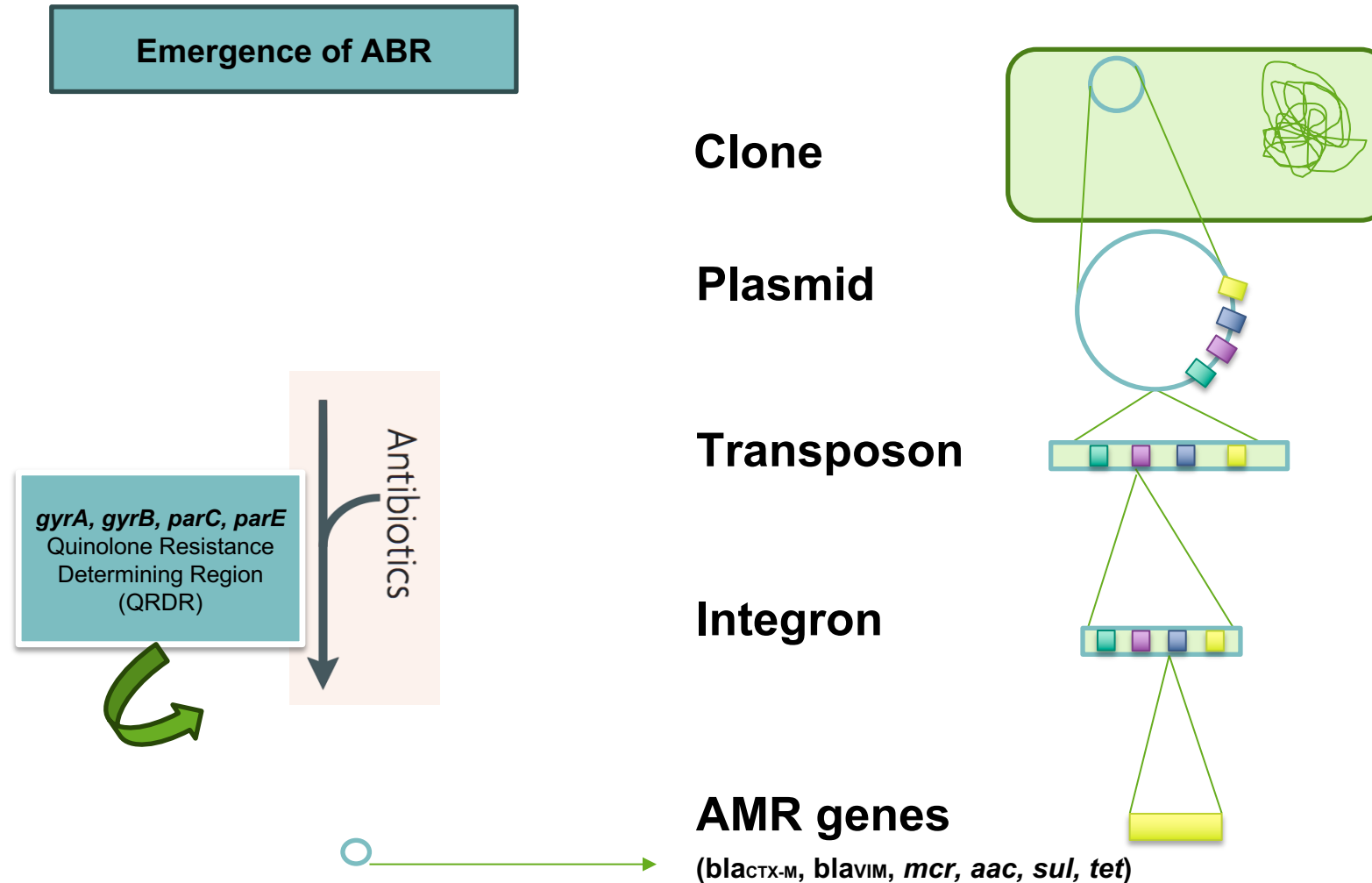
2. **Horizontal transfers of mobile genetic elements** carrying β -lactamase genes; aminoglycoside-modifying enzymes (AMEs), Mcr - or non-enzymatic mechanisms (Qnr).

FIGURES

E.g. GyrA, ParC, MgrB, PmrB ,
Qnr; 16S rRNA methylases;
Mcr, PBPs

E.g. β -lactamases; AMEs

Main mechanisms of AMR



The accumulation of genes in different mobile genetic elements/strains
↑ co-selection events

Resistance to beta-lactams

FIGURES

Resistance to other critical antimicrobials

Aminoglycosides

Aminoglycoside-modifying enzymes (AMEs)

AAC (aminoglycoside N-acetyltransferase)
ANT (aminoglycoside O-adenyltransferase)
APH (aminoglycoside O-phosphotransferase)

16S rRNA methylases (16S-RMTase)

ArmA
Rmt

(high R levels)

Fluoroquinolones

Plasmid-mediated quinolone resistance (PMQRs)

Qnr (A,B,C,D,S,VC)
QepA
OqxAB
AAC(6')-IB-cr *

(low R levels)

*aminoglycoside and quinolone inactivating acetyl-transferase

Polymyxins

Mobilizable colistin resistance genes

Mcr

(variable R levels)

Macrolides

23S rRNA methylases

Erm
Mef
MsrA
MphA
(high R levels)

DNA gyrase (GyrA) and topoisomerase IV (ParC) mutations (QNDRs)

Mutations in genes involved in outer membrane polarity

PmrAB-PhoPQ
MgrB

Point mutations in 23S rRNA

MGE

CROMOSOMAL
High R levels

Epidemiology of AMR in non-typhoid *Salmonella*



FIGURES

Higher resistance rates to older drugs such as ampicillin – sulfamethoxazole - tetracycline

R to ciprofloxacin arising specially in food-producing animals, low R to 3GC

Antibiotics are usually not recommended for mild cases. However, in severe cases or for high-risk groups (infants, elderly, immunocompromised), 1st line antibiotics are **ciprofloxacin, ceftriaxone or azithromycin**.

Epidemiology of AMR in non-typhoid *Salmonella*

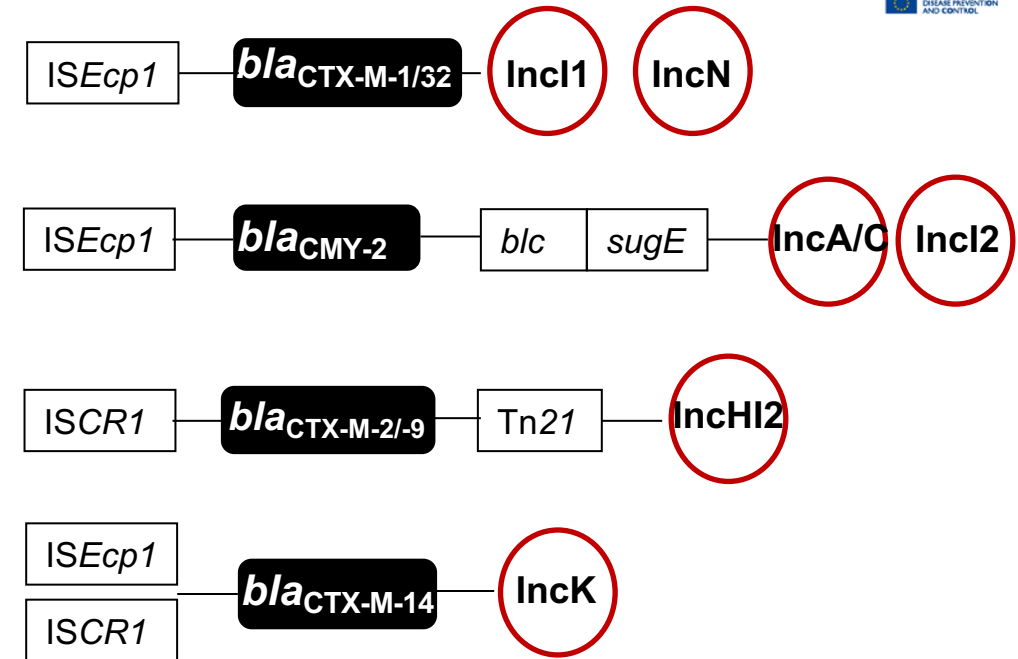


FIGURES

Trends in resistance to ampicillin, ciprofloxacin/pefloxacin/nalidixic acid, cefotaxime and tetracycline in *Salmonella* spp. from humans in 27 reporting countries and EU MSs group, 2013–2021

Epidemiology of AMR in non-typhoid *Salmonella*

FIGURES



Quinolone/fluoroquinolone R:

- Mainly due to point mutations within the DNA gyrase (*gyrA* and *gyrB*) and topoisomerase IV (*parC* and *parE*) genes (QRDRs).
- Plasmid-mediated quinolone resistance (PMQR) mechanisms have also been recognised: efflux pumps (*qepA* and *oqxAB* genes), enzymatic modifications (*aac(60)Ib-cr* gene) and protection of the DNA gyrase (*qnr*)

Epidemiology of AMR in non-typhoid *Salmonella*



FIGURES

Epidemiology of AMR in *Campylobacter*



FIGURES

In both species - High R levels to **ciprofloxacin** (point mutations on the *gyrA* gene) and **tetracycline**
R to macrolides arising levels to **macrolides** (*ermB*)

Epidemiology of AMR in *Campylobacter*

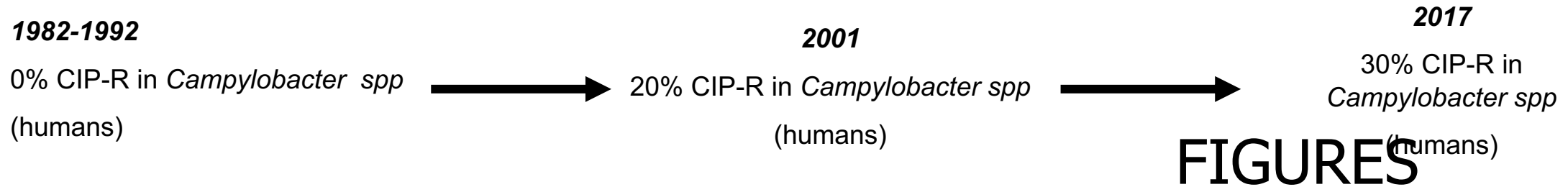


FIGURES

Epidemiology of AMR in *Campylobacter*

AMR acquisition in zoonotic bacteria: First Evidences

Fluorquinolones introduction (animals), USA in the 90's



Epidemiology of AMR in *Campylobacter*

Campylobacter jejuni

Campylobacter coli



FIGURES

Usually campylobacterioses are mild, self-limiting

Due to the high levels of CIP-R, **macrolides** are now the first-line treatment of human campylobacteriosis

Epidemiology of AMR in *Campylobacter*



FIGURES

Epidemiology of AMR in *Shigella*



FIGURES

Moderate to severe infection is typically treated with antibiotics (CIP, 3CG or AZM) => growing incidence of MDR and XDR *Shigella* globally – limited treatment options

Epidemiology of AMR in *Shigella*



FIGURES

AMR genes databases and tools for *in silico* genotyping

NCBI - NDARO

CARD

ResFinder

PathogenWatch

Bandage

AMR genes databases and tools for *in silico* genotyping

<https://www.ncbi.nlm.nih.gov/pathogens/antimicrobial-resistance/>

[Health](#) > [Pathogen Detection](#) > National Database of Antibiotic Resistant Organisms (NDARO)

Search page ^ v

National Database of Antibiotic Resistant Organisms (NDARO)

Welcome to the NCBI National Database of Antibiotic Resistant Organisms (NDARO), a collaborative, cross-agency, centralized hub for researchers to access AMR data to facilitate real-time surveillance of pathogenic organisms.

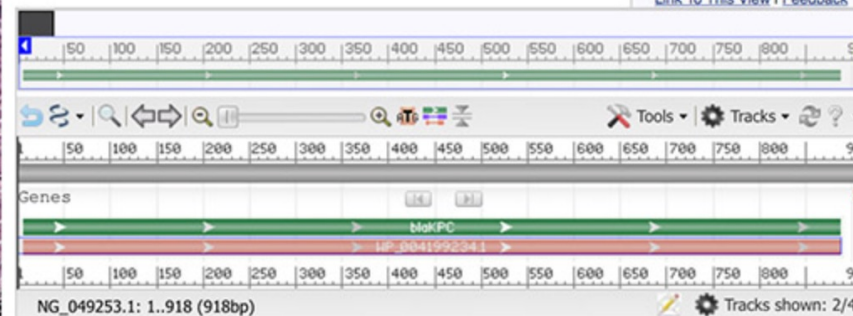


Klebsiella pneumoniae blaKPC gene for carbapenem-hydrolyzing class A beta-lactamase KPC-2, complete CDS

NCBI Reference Sequence: NG_049253.1

[GenBank](#) [FASTA](#)

[Link To This View | Feedback](#)



From left to right: Multi-drug resistant *Salmonella enterica*, kpc2 carbapenem resistance gene

FIGURES

NDARO – Reference Gene Catalog

<https://www.ncbi.nlm.nih.gov/pathogens/refgene/#>



National Library of Medicine
National Center for Biotechnology Information

Log in

Health > Pathogen Detection > Reference Gene Catalog

Help

Search

ctx-m-1

x

You can now download the sequences directly from this reference gene catalog. Please see [Help](#) for details.

db version: 2024-05-02.2 [Changelog](#)

Bacterial Antimicrobial Resistance Reference Gene Database

Filters

Page 1 of 1

Records per Page 20

Choose columns

Download

Displaying 1 - 1 of 1

#	Allele	Gene fa...	Product name	Scope	Type	Subtype	Class	Subclass	RefSeq ...	RefSeq ...	GenBan...	GenBan...	Curated...	Links
1	blaCTX-...	blaCTX-M	extended-spectrum class A beta-lactamase CTX-M-1	core	AMR	AMR	BETA-L...	CEPHAL...	WP_013...	NG_048...	CAA632...	X92506.1	No	PubChem

Search

AMR_genotypes:blaCTX-M*

x

Share

Save

Saved Searches

Watched Isolates

Filters

Matched Clusters

count:16,190

#	Organism groups	SNP cluster	Matched isolates	Matched clinical isolates	Matched environmental isolates	Total isolates	Minimal min-diff	Minimal min-same	Latest up
1	Salmonella enterica	PDS000171305....	6864	2499	4107	14100	0	0	2024-06-
2	E.coli and Shigella	PDS000117091....	2347	1697	97	2435	0	0	2024-05-
3	Klebsiella pneumoniae	PDS000182303....	1822	1656	4	2368	0	0	2024-05-
4	E.coli and Shigella	PDS000150675....	1691	1600	2	1983	0	0	2024-06-
5	E.coli and Shigella	PDS000111134....	1271	1012	44	1417	0	0	2024-05-
6	E.coli and Shigella	PDS000181516....	871	669	3	5407	0	0	2024-06-
7	Salmonella enterica	PDS000002867....	862	635	6	9029	0	0	2024-06-

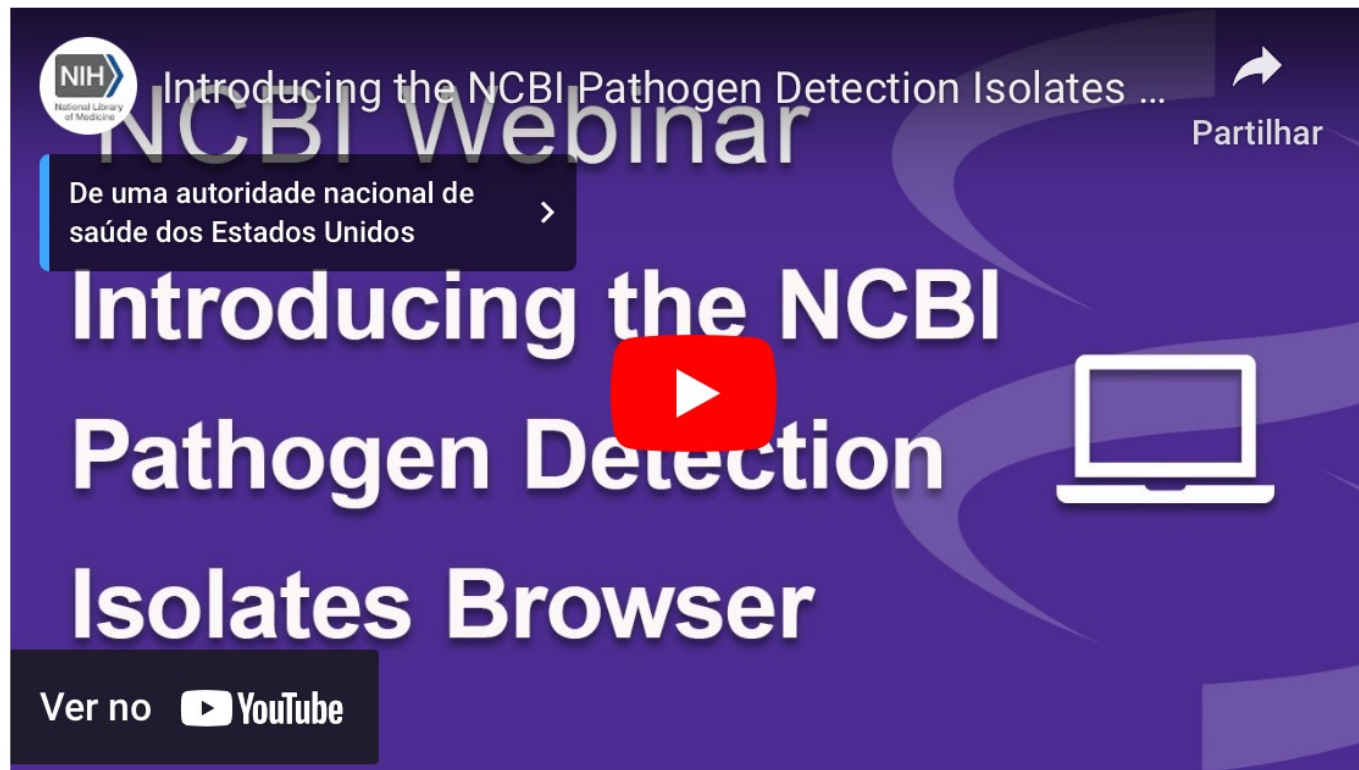


NDARO – Reference Gene Catalog

<https://youtu.be/T8HluuzOb5c>

Learn more

Watch our short video on NCBI Pathogen Detection and how to use some of our tools and resources. [Contact Us](#)



The Comprehensive Antibiotic Resistance Database (CARD)



<https://card.mcmaster.ca>

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The Comprehensive Antibiotic Resistance Database

A bioinformatic database of resistance genes, their products and associated phenotypes.

6504 Ontology Terms, 4970 Reference Sequences, 1922 SNPs, 2913 Publications, 5016 AMR Detection Models

Resistome predictions: 263 pathogens, 16719 chromosomes, 2675 genomic islands, 33860 plasmids, 136704 WGS assemblies, 285146 alleles

[CARD Bait Capture Platform 1.0.0](#) | [State of the CARD 2021 Presentations & Demonstrations](#)

Browse

The CARD is a rigorously curated collection of characterized, peer-reviewed resistance determinants and associated antibiotics, organized by the Antibiotic Resistance Ontology (ARO) and AMR gene detection models.

Analyze

The CARD includes tools for analysis of molecular sequences, including BLAST and the Resistance Gene Identifier (RGI) software for prediction of resistome based on homology and SNP models.

Download

CARD data and ontologies can be downloaded in a number of formats. RGI software is available as a command-line tool. CARD Bait Capture Platform sequences and protocol available for download.

The Comprehensive Antibiotic Resistance Database (CARD)



1. Search for information about AMR genes

CARD

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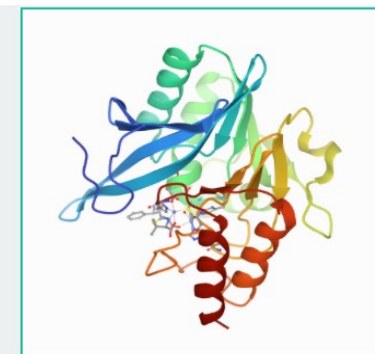
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NDM-1

NDM-1

[Download Sequences](#)



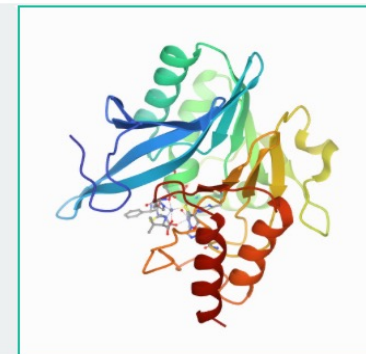
Accession	ARO:3000589
CARD Short Name	<i>NDM-1</i>
Definition	NDM-1 is a metallo-beta-lactamase isolated from <i>Klebsiella pneumoniae</i> with nearly complete resistance to all beta-lactam antibiotics.
AMR Gene Family	NDM beta-lactamase
Drug Class	penam , carbapenem , cephamycin , cephalosporin
Resistance Mechanism	antibiotic inactivation

The Comprehensive Antibiotic Resistance Database (CARD)

2. Download AMR gene reference sequences

NDM-1

Download Sequences



Detection Models

protein homolog model

Model Type: protein homolog model

Model Definition: The protein homolog model is an AMR detection model. Protein homolog models detect a protein sequence based on its similarity to a curated reference sequence. A protein homolog model has only one parameter: a curated BLASTP bitscore cutoff for determining the strength of a match. Protein homolog model matches to reference sequences are categorized on three criteria: perfect, strict and loose. A perfect match is 100% identical to the reference sequence along its entire length; a strict match is not identical but the bitscore of the matched sequence is greater than the curated BLASTP bitscore cutoff. Loose matches are other sequences with a match bitscore less than the curated BLASTP bitscore.

Bit-score Cut-off (blastP): 500

Protein

DNA

```
>gb|CAZ39946.1|-|NDM-1 [Klebsiella pneumoniae]  
MELPNIMHPVAKLSTALAAALMLSGCMPGEIRPTIGQQMETGDQRFGLVFRQLAPNVWQHTSYLDMPGFGAVASNGLIVRDGGRVLVVD  
TAWTDDQTAQILNWIKEINLPVALAVVTHAQDKMGGMDALHAAGIATYANALSNQLAPQEGMVAAQHSLTFAANGWVEPATAPNFGPL  
KVFPYGPFGHTSDNITVGIDGTDIAFGGCLIKDSKAKSLGNLGDADTEHYAASARAFGAAPFKASMIVMSSHAPDSRAAITHARMADKLR
```

COPY

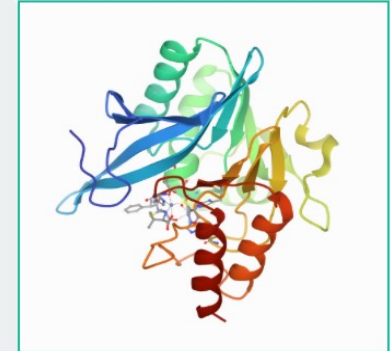


The Comprehensive Antibiotic Resistance Database (CARD)

2. Download AMR gene reference sequences

NDM-1

Download Sequences



Detection Models

protein homolog model

Model Type: protein homolog model

Model Definition: The protein homolog model is an AMR detection model. Protein homolog models detect a protein sequence based on its similarity to a curated reference sequence. A protein homolog model has only one parameter: a curated BLASTP bitscore cutoff for determining the strength of a match. Protein homolog model matches to reference sequences are categorized on three criteria: perfect, strict and loose. A perfect match is 100% identical to the reference sequence along its entire length; a strict match is not identical but the bitscore of the matched sequence is greater than the curated BLASTP bitscore cutoff. Loose matches are other sequences with a match bitscore less than the curated BLASTP bitscore.

Bit-score Cut-off (blastP): 500

Protein **DNA**

```
>gb|CAZ39946.1|-[NDM-1 [Klebsiella pneumoniae]  
MELPNIMHPVAKLSTALAAALMLSGCMPGEIRPTIGQQMETGDRFGDLVFRQLAPNVWQHTSYLDMPGFGAVASNGLIVRDGGRVLVVD  
TAWTDDQTAQILNWIQEIINLPVALAVVTHAQDKMGGMDALHAAGIATYANALSNQLAPQEGMVAAQHSLTFAANGWVEPATAPNFGPL  
KVFYYPGPGHTSDNITVGIDGTDIAFGGCLIKDSKAKSLGNLGDADTEHYAASARAFGAAPFKASMIVMSSHAPDSRAAITHARMADKLR
```

COPY



The Comprehensive Antibiotic Resistance Database (CARD)



3. Molecular Sequence Analysis Tool (BLAST)



CARD

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Analyze

BLAST

Perform standard BLAST searches against the CARD reference sequences. Results are annotated with extra information from CARD.

BLAST Basic Local Alignment Search Tool

BLAST performs similarity searches only and does not include secondary screening for mutations curated in CARD, please use [Resistome Gene Identifier](#) for SNP detection. Protein variant models may use sensitive, wild-type sequences as their reference for SNP screening, which will be included in these BLAST databases.

BLAST uses sequences stored in CARD.

Using BLAST:

Paste FASTA Query Sequence:

Upload FASTA Query Sequence:

Escolher ficheiro

nenhum ficheiro selecionado

Upload or paste a plain text file containing DNA or protein sequence(s) in FASTA format (5000 nucleotide or amino acid limit).

Select Data Type:

☒ BLASTP - Search a protein sequence against all protein sequences

☐ BLASTN - Search a nucleotide sequence against all nucleotide sequences

☐ BLASTX - Search a nucleotide sequence against all protein sequences

☐ TBLASTN - Search a protein sequence against all nucleotide sequences translated in all reading frames

☐ TBLASTX - Search a nucleotide sequence against all nucleotide sequences by translating both in all reading frames

Submit

The Comprehensive Antibiotic Resistance Database (CARD)



4. Resistance Gene Identifier (RGI) software for resistome prediction

CARD

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RGI ¹

Use the Resistance Gene Identifier to predict resistome(s) from protein, genome, or metagenomics data based on homology and SNP models.

Use RGI:

Enter a GenBank accession(s):

Nucleotide sequences will undergo ORF calling to generate predicted protein sequences. Examples: JN420336.1, AY123251.1, HQ451074.1, AL123456

Upload FASTA sequence file(s):

Upload a **plain text** file containing DNA or protein sequence(s) in FASTA format (20 Mb limit). The file can contain more than one FASTA formatted sequence, such as assembly contigs or multiple proteins. Each file will be treated as a single sample.

CARD:Live
☐ Consent, allowing CARD to collect pathogen, AMR gene list, and geotemporal data for these isolates.

If consenting, please select geographical source of isolates

The CARD:Live project collects pathogen identification, MLST, AMR gene list, date, and geographical region for genome sequences submitted to RGI online, providing a dynamic view of the antibiotic resistant isolates being analyzed around the world. **No sequence information is collected.** Full information at [CARD:Live](#).

Submit

Select Data Type:
☒ DNA sequence
☐ Protein sequence

Select Criteria:
☒ Perfect and Strict hits only
☐ Perfect, Strict and Loose hits

Nudge ≥95% identity Loose hits to Strict:
☒ Exclude nudge
☐ Include nudge

Sequence Quality:
☒ High quality/coverage¹
☐ Low quality/coverage²
¹ Complete genomes, plasmids, or high quality assemblies (includes contigs > 20,000 bp). Excludes prediction of partial genes.
² Low quality/coverage assemblies, metagenomic merged reads, small plasmids or assembly contigs (<20,000 bp). Includes prediction of partial genes.

41

The Comprehensive Antibiotic Resistance Database (CARD)



4. Resistance Gene Identifier (RGI) software for resistome prediction

Summary						
Filename	Date (UTC)	RGI Criteria	# Perfect Hits	# Strict Hits	# Loose Hits	Download
GCF_013620905.1_ASM1362090v1_genomic	June 14, 2022 12:19:27	Perfect, Strict, complete genes only	13	25	0	Download

Download and open in excel

Results								
Search: <input type="text"/>								
RGI Criteria	ARO Term	SNP	Detection Criteria	AMR Gene Family	Drug Class	Resistance Mechanism	% Identity of Matching Region	% Length of Reference Sequence
Perfect	oqxA		protein homolog model	resistance-nodulation-cell division (RND) antibiotic efflux pump	fluoroquinolone antibiotic, glycyclcycline, tetracycline antibiotic, diaminopyrimidine antibiotic, nitrofurantoin antibiotic	antibiotic efflux	100.0	100.00
Perfect	SHV-28		protein homolog model	SHV beta-lactamase	carbapenem, cephalosporin, penam	antibiotic inactivation	100.0	100.00
Perfect	Klebsiella pneumoniae KpnE		protein homolog model	major facilitator superfamily (MFS) antibiotic efflux pump	macrolide antibiotic, aminoglycoside antibiotic, cephalosporin, tetracycline antibiotic, peptide antibiotic, rifamycin antibiotic, disinfecting agents and antiseptics	antibiotic efflux	100.0	100.00
Perfect	Klebsiella pneumoniae KpnF		protein homolog model	major facilitator superfamily (MFS) antibiotic efflux pump	macrolide antibiotic, aminoglycoside antibiotic, cephalosporin, tetracycline antibiotic, peptide antibiotic, rifamycin antibiotic, disinfecting agents and antiseptics	antibiotic efflux	100.0	100.00
Perfect	LptD		protein homolog model	ATP-binding cassette (ABC) antibiotic efflux pump	carbapenem, peptide antibiotic, aminocoumarin antibiotic, rifamycin antibiotic	antibiotic efflux	100.0	100.00
Perfect	sul1		protein homolog model	sulfonamide resistant sul	sulfonamide antibiotic	antibiotic target replacement	100.0	100.00
Perfect	qacEdelta1		protein homolog model	major facilitator superfamily (MFS) antibiotic efflux pump	disinfecting agents and antiseptics	antibiotic efflux	100.0	100.00
Perfect	aadA2		protein homolog model	ANT(3")	aminoglycoside antibiotic	antibiotic inactivation	100.0	100.00
Perfect	dfrA12		protein homolog model	trimethoprim resistant dihydrofolate reductase dfr	diaminopyrimidine antibiotic	antibiotic target replacement	100.0	100.00
Perfect	CTX-M-15		protein homolog model	CTX-M beta-lactamase	cephalosporin, penam	antibiotic inactivation	100.0	100.00
Perfect	TEM-1		protein homolog model	TEM beta-lactamase	monobactam, cephalosporin, penam, penem	antibiotic inactivation	100.0	100.00
Perfect	OXA-48		protein homolog model	OXA beta-lactamase	carbapenem, cephalosporin, penam	antibiotic inactivation	100.0	100.00
Perfect	AAC(6')-Ib-cr5		protein homolog model	AAC(6')-Ib-cr	fluoroquinolone antibiotic, aminoglycoside antibiotic	antibiotic inactivation	100.0	93.48



plusieurs fichiers
d'assemblage peuvent être
lancés en même temps

<https://cge.cbs.dtu.dk/services/ResFinder/>



Center for Genomic Epidemiology

Services

Contact

ResFinder

Version

4.5.0 ▼

ResFinder identifies acquired genes and/or finds chromosomal mutations mediating antimicrobial resistance in total or partial DNA sequence of bacteria.

ResFinder software: (2024-03-22)

ResFinder database: (2024-03-22)

PointFinder database: (2024-03-08)

DisinFinder database: (2023-05-31)

ResFinder

Chromosomal point mutations:

Threshold for %ID

90%



Minimum length

60%



- ☐ Show unknown mutations
- ☐ Ignore premature stop codons:
- ☐ Ignore frameshift indels:

Acquired antimicrobial resistance genes:

Threshold for %ID

90%



Minimum length

60%



Species and input data type:

Select species

Other



Select input type

FASTA (Assembled Genome/Contigs)



Disinfectant:

☐ Run disinfectant

Threshold for %ID

90%



Minimum length

60%



Upload and submit job:

Email (Get email, when finished - Optional):

Enter your email address...

Files (The sum of uploaded file sizes cannot exceed 1 gb):

Escolher ficheiro nenhum ficheiro selecionado

Escolher ficheiro nenhum ficheiro selecionado

Submit Job



Center for Genomic Epidemiology

Services

Contact



Your job is running. Please wait...

Session ID: ikdev85gqdhk33xmu9gh5fgzazr3l9so

1. Table with predicted phenotype based on genotype

Antimicrobial	Class	WGS-predicted phenotype	Genetic background
streptomycin	aminoglycoside	Resistant	aadA1;;4;;JQ480156
spectinomycin	aminocyclitol	Resistant	aadA1;;4;;JQ480156
trimethoprim	folate pathway antagonist	Resistant	dfrA1;;8;;X00926
gentamicin	aminoglycoside	No resistance	

2. Table with AMR genotype presented according to antibiotic class

Acquired AMR gene hits

Hide

Resistance gene	Identity	Alignment length/gene length	Position in reference	Contig or depth	Position in contig	Phenotype	PMID	Accession no.	Notes
aadA1	100.00%	789 /	1...789	NZ_CP022457.1 Shigella sonnei strain 2015C-3566 chromosome, complete genome	1314198...1314986	['streptomycin', 'spectinomycin']	22486636	JQ480156	Alternative name ant(3'')-Ia
dfrA1	100.00%	474 /	1...474	NZ_CP022457.1 Shigella sonnei strain 2015C-3566 chromosome, complete genome	1315663...1316136	['trimethoprim']	6308574	X00926	

AMR detection available only for some species

GCF_018885245.1_ASM1888524v1_ge...  Pathogenwatch
Campylobacter coli

MLST - Multilocus sequence typing
<https://pubmlst.org/campylobacter/>

Sequence type

1145

[View all ST 1145](#)

Profile							
aspA	glnA	gltA	glyA	pgm	tkr	uncA	
33	39	30	82	104	44	17	

AMR - Antimicrobial resistance
[PAARSNP AMR - Library 194 version 0.0.16](#)

Agent	Inferred resistance	Known Determinants
Ciprofloxacin	Resistant	gyrA_T86I



PAGE
Pathogenwatch AMR

- [Campylobacter sp.](#)
- [Candida auris](#)
- [Enterococcus faecium](#)
- [Neisseria gonorrhoeae](#)
- [Salmonella Typhi](#)
- [Staphylococcus aureus](#)
- [Streptococcus pneumoniae](#)
- [Vibrio cholerae](#)

Time to discussion

Spotlight

Antimicrobial susceptibility prediction from genomes: a dream come true?

Guido Werner^{1 4 5}  , Hege Vangstein Aamot^{2 4 5},
Natacha Couto^{3 4 5}

Genome-based diagnostics provides relevant information to guide patient treatment and support pathogen and resistance surveillance. Recently, Coll et al. introduced a curated database for predicting antimicrobial resistance (AMR) from *Enterococcus faecium* genomics data, offering excellent predictive values for susceptibility to important antimicrobials. Challenges to predict resistance to last-resort antimicrobials remain.

Keywords: AMR genotypes; AMR prediction; antibacterial; antimicrobial therapy.

<https://pubmed.ncbi.nlm.nih.gov/38355048/>

https://docs.google.com/forms/d/e/1FAIpQLSc7Ruzi2p3v2qv-r924SKDDNoPmLM0FLvj-3vbAR_NXFfxKQQ/viewform

Expression of Interest to join ESGEM-AMR working group

We are forming a new working group within ESGEM, called ESGEM-AMR (ESCMID Study Group for Epidemiological Markers - Antimicrobial Resistance Working Group).

The working group will be led by Prof Kat Holt (LSHTM) and Dr Natacha Couto (ESGEM Chair), and will be open to ESGEM members and others with relevant expertise. Active working group members will be encouraged to note their membership on their CV, and will be invited to co-author outputs.

Purpose

The overall purpose of the group is to capture expert knowledge on the relationship between antimicrobial resistance (AMR) genotypes and antimicrobial susceptibility testing (AST) phenotypes in bacterial pathogens. The initial focus of the ESGEM-AMR working group will be expert curation of interpretive standards for AMR genotypes, but may expand in future to include other activities/projects including generating matched genome-phenotype data to support AMR genomics.

Process

Please use this form to register your interest in joining the working group, **by 2 June 2024**.

Acknowledgements

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