

A petri dish containing a bacterial culture with several antibiotic discs. The discs are labeled with numbers and letters, including '1000', '100', '1000', '1000', and '1000'. The culture shows varying degrees of inhibition around the discs.

The impact of antimicrobial resistance on enteric infections in Vietnam

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Outline

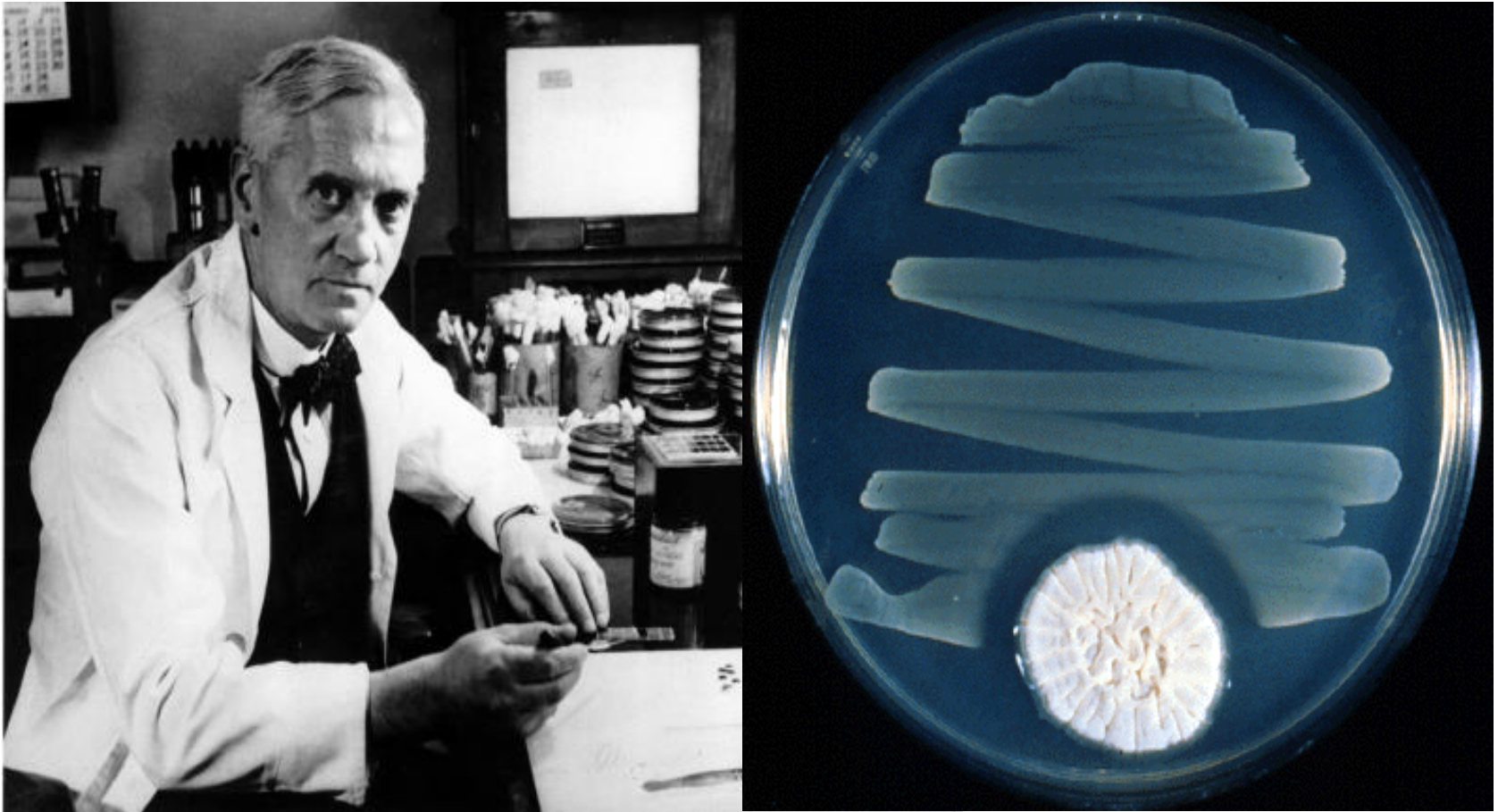
- The impact of antimicrobial resistance
- The drivers of antimicrobial resistance
- (Fluoro)quinolone resistance in typhoid
- ESBL producers
- Resistance in commensal organisms
- Carbapenemases
- Preventative measures

Microorganisms



We live in a
microbial
world

From the miracle.....



1928.....1942.....1947

.....To This

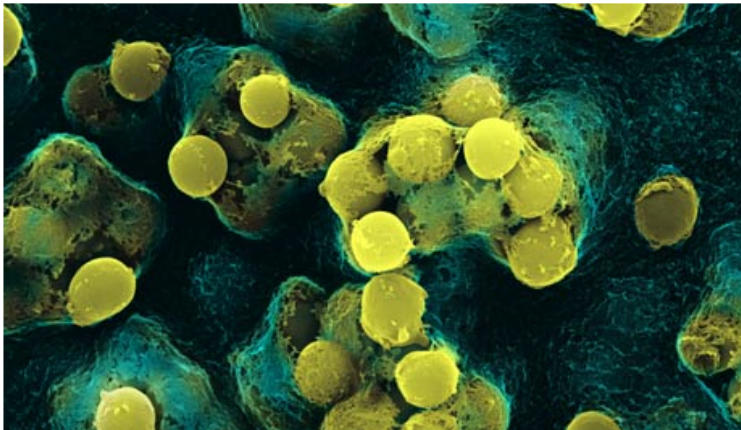
News Society Antibiotics

Are you ready for a world without antibiotics?

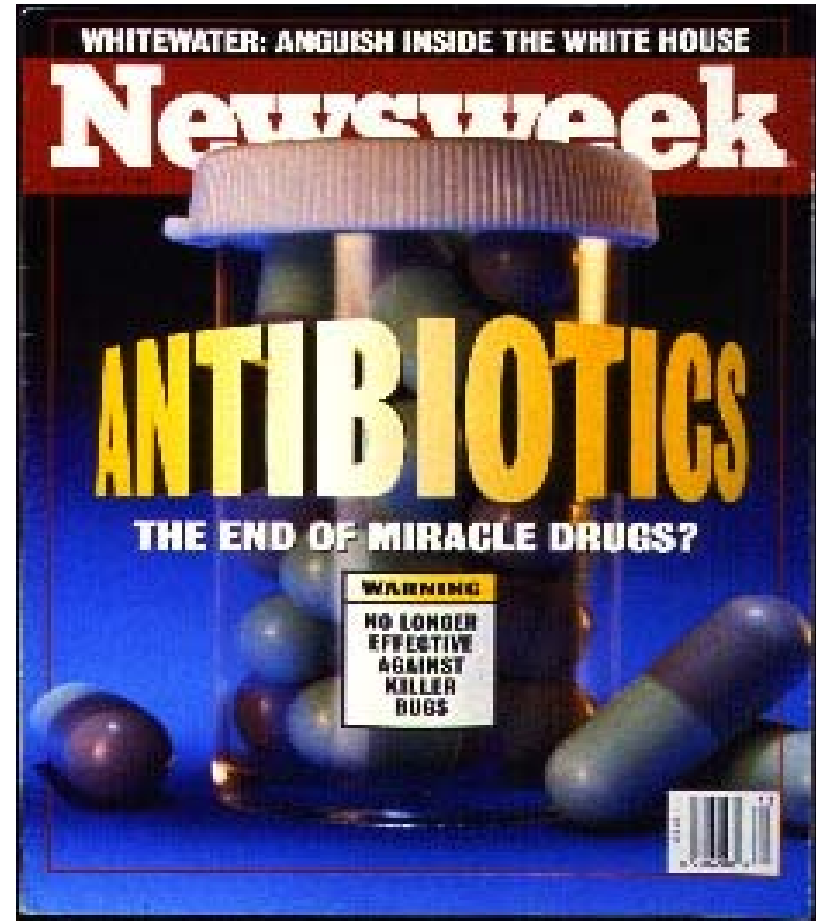
Antibiotics are a bedrock of modern medicine. But in the very near future, we're going to have to learn to live without them once again. And it's going to get nasty



Sarah Boseley
The Guardian, Thursday 12 August 2010
[Article history](#)



Streptococcus pyogenes bacteria. Photograph: S Lowry/University of Ulster/Getty Images



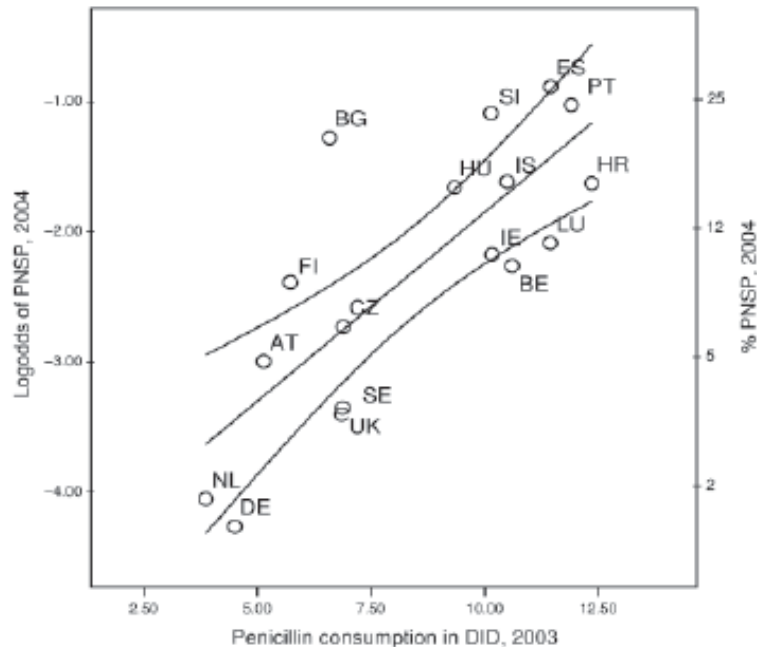
In less than 50 years

Impact of resistance

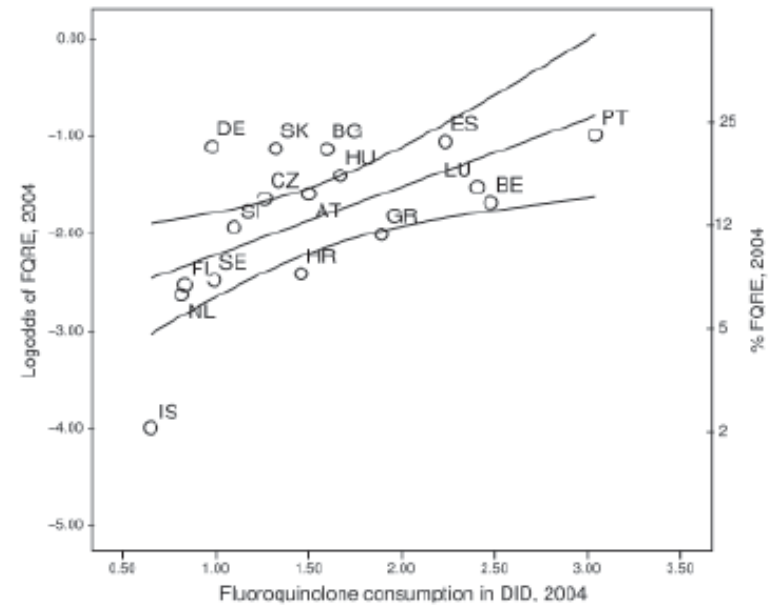
- 70% of neonatal sepsis cannot be treated with antibiotics recommended by WHO due to resistance. *Lancet 2005*.
- 67% died with resistant bacteria as compared to 26% with sensitive. *BMC Pediatrics 2010*.
- Antimicrobial resistance has global health implications
- Pathogenic bacteria that exhibit antimicrobial resistance are a widespread phenomenon and arguably constitute an uncontrollable global epidemic.

Occurrence of antimicrobial resistance is associated with antimicrobial usage

Data for primary blood culture isolates of *S. pneumoniae* and *E. coli*



Occurrence of penicillin-nonsusceptible *Streptococcus pneumoniae* (PNSP) plotted against outpatient use of penicillins in 17 European countries including 95% confidence intervals. DID, defined daily doses per 1,000 inhabitants



Occurrence of fluoroquinolone-resistant *Escherichia coli* (FQRE) plotted against outpatient use of fluoroquinolone antimicrobial agents in 17 European countries including 95% confidence intervals. DID, defined daily doses/1,000 inhabitants.

MRSA - Methicillin resistant *Staphylococcus aureus*

S. aureus is a common bacterium that can be found on the skin of many healthy people
Typically it causes only minor infections, in “pimples” but can also cause serious diseases (e.g. pneumonia)

First report of resistance to penicillin in 1947
MRSA is also resistant to ampicillin and other penicillins, erythromycin, tetracycline
can only be treated with Vancomycin
Vancomycin-resistant strains have already been found and isolated




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NHS superbug death rate doubles

The number of deaths in which the superbug MRSA has been cited as a cause has doubled in four years, official statistics show.

The Office for National Statistics said in 2003 MRSA was mentioned on 955 death certificates - up from 487 in 1999.

But the figures suggested some of the rise may be down to better reporting of the bug.

Other statistics revealed the number of HIV diagnoses seems to have levelled off after a decade of increases.

However, it was the MRSA figures which have proved most controversial.

Mortality rates were highest among older people with more men than women dying.



Some of the MRSA increase could be down to better reporting

“ No other country has seen the super bug infection take over its hospitals in the same way as we have in Britain ”

BBC NEWS:VIDEO AND AUDIO

What hospitals are doing to stop the spread of MRSA

VIDEO

BBC iCAN



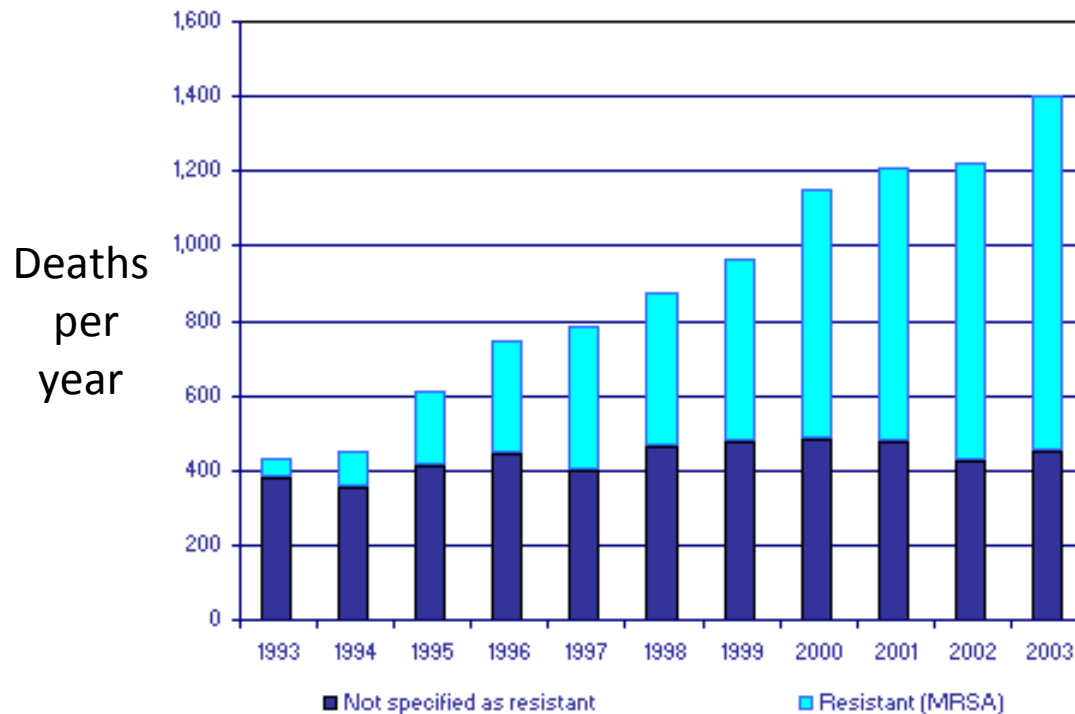
MRSA infections

What can you do about the hospital 'superbug'?

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10 Feb 05 | Health
- ▶ ['Clean yourself' advice on MRSA](#)
26 Jan 05 | Health
- ▶ [NHS targets 'to blame for MRSA'](#)
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24 Jun 04 | Health
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13 Dec 02 | Health

MRSA in the UK



Source: Health Protection Agency

Antimicrobial development

Lack of development of new antimicrobial drugs: a potential serious threat to public health

J. Roger Kirby, Cal Gilliland, and Roger Finch, for the European Society of Clinical Microbiology and Infectious Diseases (ESCMID)

Antimicrobial resistance is threatening the management of infections such as pneumonia, tuberculosis, malaria, and AIDS. In the past, resistance could be handled by development of new drugs active against resistant microbes. However, the pharmaceutical industry has reduced its research efforts in infectious genomics; hence it has delivered the anticipated novel therapeutic; new regulatory requirements have increased costs; antibiotic use in common infections—eg, bronchitis and sinusitis—is questioned; and, compared with other drugs, return on investment is lower for antimicrobials. To avoid a serious threat to public health, academia, biotechnology and pharmaceutical industry, regulators, and healthcare providers must find solutions to this problem. Academia should concentrate on technologies to unlock new drug targets, and industry on drug candidates. In addition, regulators and pharmaceutical companies should agree on new clinical-trial designs so that information on therapeutic efficacy is generated in fewer patients—eg, by studying pharmacodynamics of antimicrobials in patients with defined infections.

Since the development of sulphonamides in the 1930s and penicillin in the 1940s, many new classes of antibacterial compounds have been developed. Drugs active against fungi, parasites, and viruses have also been introduced. Within the field of antibiotics, the emergence of resistance was soon realized to represent a considerable clinical problem. However, until the end of the 20th century, the pharmaceutical companies were consistently able to develop new antibiotics with activity against most resistant bacterial strains.

During the past 10–15 years, antibiotic-resistant organisms have steadily increased, and now present a threat to disease management. Examples include methicillin-resistant staphylococci, pneumococci resistant to both penicillin and macrolides, vancomycin-resistant enterococci, multidrug-resistant Gram-negative organisms, and multidrug-resistant strains of *Mycobacterium tuberculosis*. Development of multidrug resistance is now gathering pace and contributing more substantially to the problem. For instance, penicillin-resistant *Streptococcus pneumoniae* was not a major problem until the same organism also became resistant to macrolides. Viruses, particularly HIV, have also developed resistance. Fungi may become resistant but, by contrast with bacteria, resistance cannot be transferred between fungal cells. Resistance has also become a major problem in the treatment of, and prophylaxis against, malaria.

The European Society of Clinical Microbiology and Infectious Diseases (ESCMID) has noted with great concern that we now seem to have entered a new era where very few novel antimicrobial drugs are being developed.¹ For example, of the new antibiotics introduced during the past decade or that are under development, none has improved activity against multidrug-resistant Gram-negative pathogens, or against mycobacteria (table 1). As a consequence of this lack of new drugs, organisms resistant to most existing antimicrobials may emerge. The result could be that common infections become untreatable, and even lethal.

This threat is most obvious in the fields of bacterial infections (including tuberculosis), parasitic infections (especially malaria), and HIV infections.

This article highlights a selection of the issues discussed at an ESCMID symposium on Antimicrobial Treatment in the 21st Century, held in Stockholm in June 2004 (http://www.escmid.org/symposium_fair04/pam-3.1.5). We provide an analysis of the reasons for the current lack of development of new anti-infective drugs, and give some suggestions as to how the problem might be tackled.

The roles for academic research, the biotechnology industry, and the pharmaceutical industry

In the past, antibiotics—eg, penicillin, cephalosporins, and streptomycin—were developed by screening natural sources for products. The modern development of a new antimicrobial drug starts by identification of a target that is essential for the microorganism but, preferably, is not present in human beings. This process should, in theory, be facilitated by modern genomic technologies; the complete genomes of more than 100 microorganisms are today mapped. Less than 20% of well-known essential targets have been exploited.² However, a genomic-based approach has, so far, failed to deliver novel therapeutics.³ In fact, in the past three decades,

See website for 2005
S 217–23

ESCMID is the Swedish Institute for Infectious Disease Control, Umeå, Sweden. CM is of the Department of Life Science Medicine, University Hospital, Lundholm University Hospital, Huddinge, Stockholm, Sweden, and RW is of the Department of Microbiology and Infectious Diseases, The City Hospital, Nottingham, UK.
Correspondence to: Professor J. Roger Kirby, Swedish Institute for Infectious Disease Control, SE-17123 Solna, Sweden.
roger.kirby@smi.se

Antibiotic	Class	Main target and mechanism of action
Quinolones	Quinolones	Gram-positive, including MRSA, MSSA, MSSA
Tetracyclines	Tetracyclines	Gram-positive, including MRSA, MSSA
Linezolid	Oxazolidinones	Gram-positive, including MRSA, MSSA
Daptomycin	Lipopeptides	Gram-positive, mainly MRSA
Moricapron	Fluoropyridones	Gram-positive, mainly MRSA
Gatifloxacin	Fluoropyridones	Gram-positive, mainly MRSA
Relaxin	Coligomers	None

All Microbials shown (table 1) are currently FDA-approved. All other drugs shown are under development.

Table 1. ANTIBIOTIC CLASSIFICATION 2005

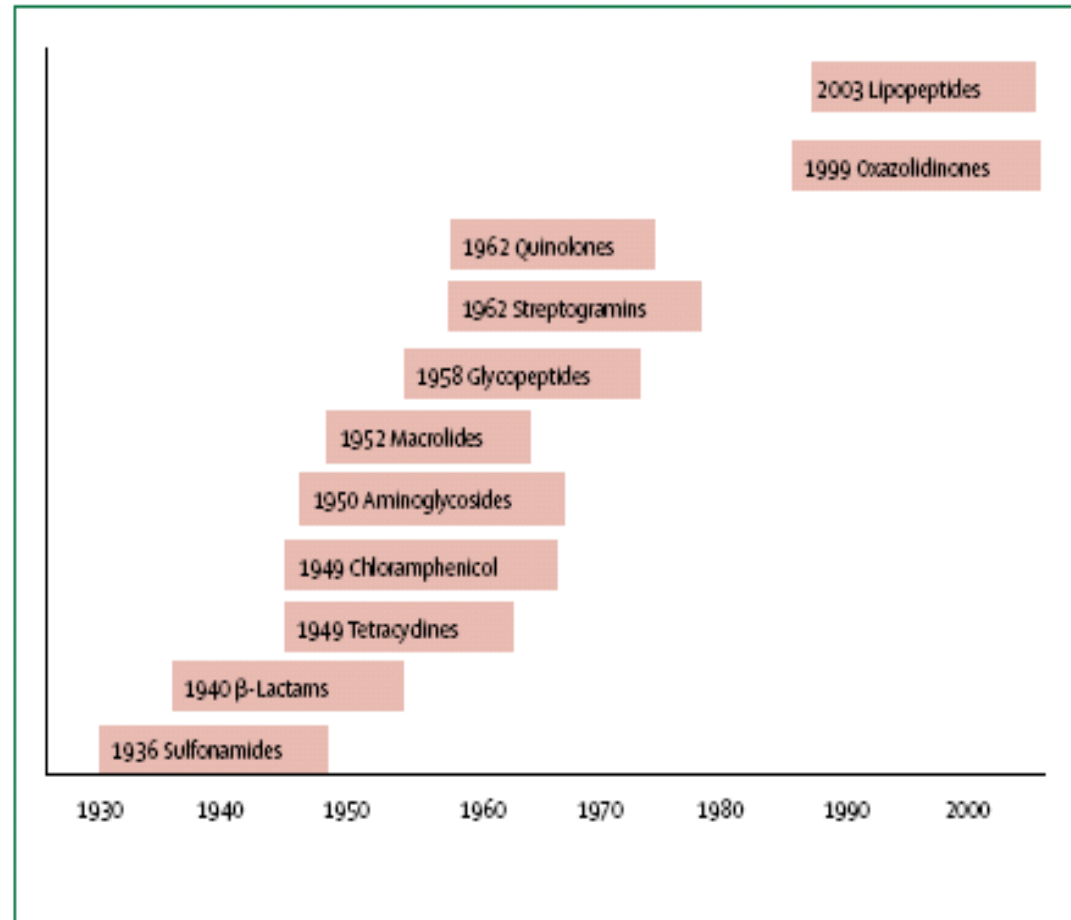


Figure: Development of new antibiotics over time

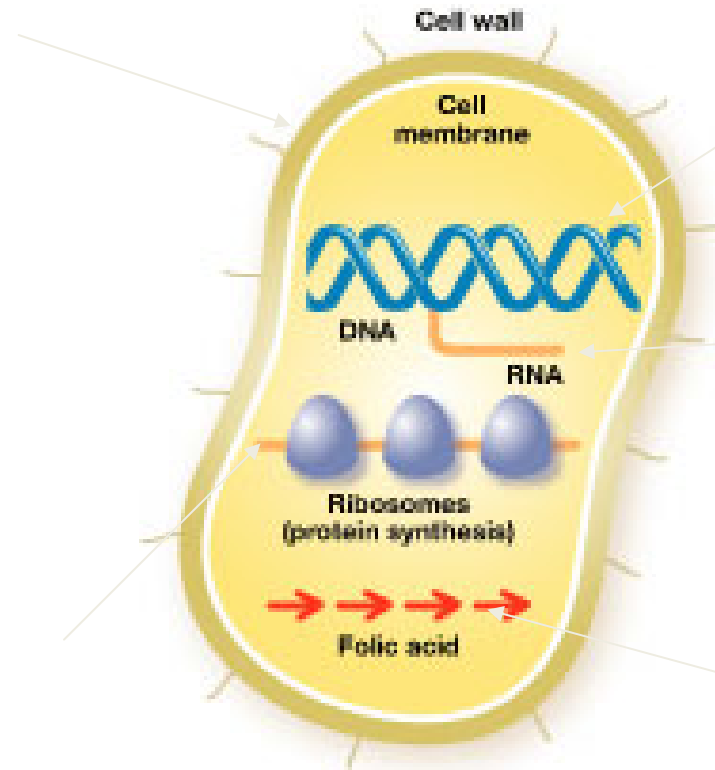
Targets of Antimicrobials

Inhibition of Cell wall synthesis

Penicillins
Cephalosporins
Carbapenems
Daptomycin
Glycopeptides

Protein synthesis

Macrolides
Chloramphenicol
Tetracycline
Aminoglycosides



DNA synthesis

Fluoroquinolones

RNA synthesis

Rifampicin

Folic acid synthesis

Sulfonamides
Trimethoprim

A lack of novel targets for new antimicrobials?

Impact of resistance in Vietnam

- Lack of antimicrobial legislation
- Inappropriate community usage
- Inadequate therapy or therapy not required
- Forcing a selective pressure on bacterial populations
- Failing of hospital therapy for severe infections
- Prospect of antimicrobials becoming useless....

Emergence of Antimicrobial Resistance

Prescribers

- lack of time
- convenience
- patient expectations
- economic incentives
- advertisement
- lack of knowledge
- no updated guidelines

Pharmacies

- patient expectations
- economic incentives
- advertisement
- lack of knowledge
- no law enforcement

Inappropriate antibiotic use

Resistant infections

Treatment failures
Increased morbidity
Increased mortality
Increased costs

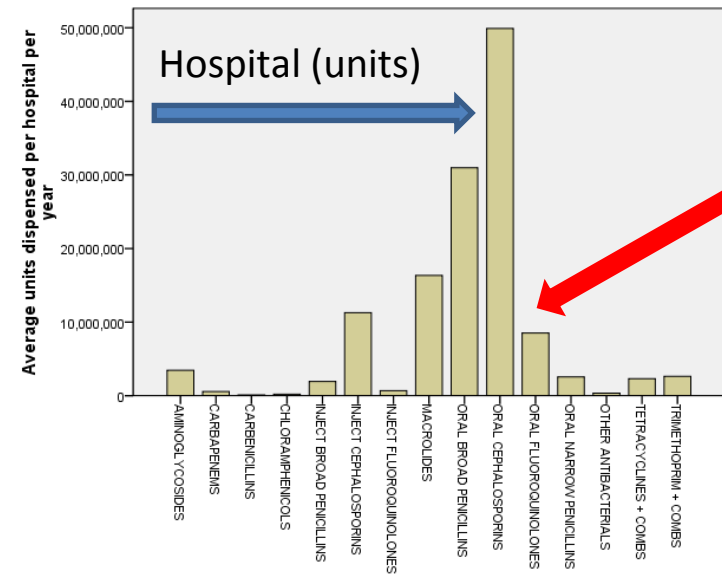
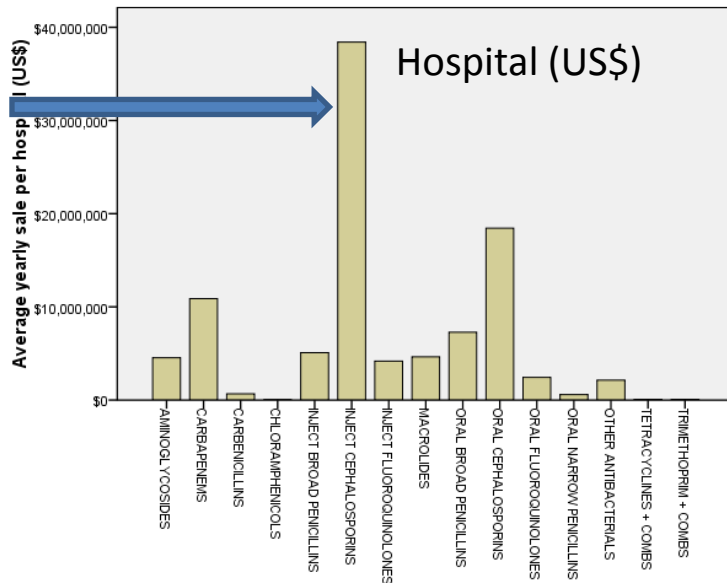
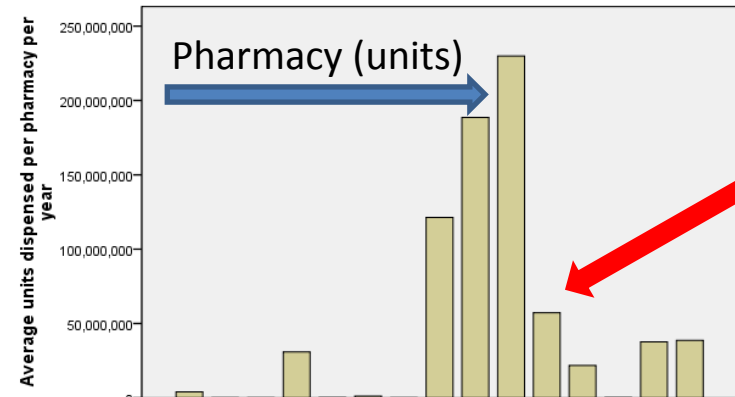
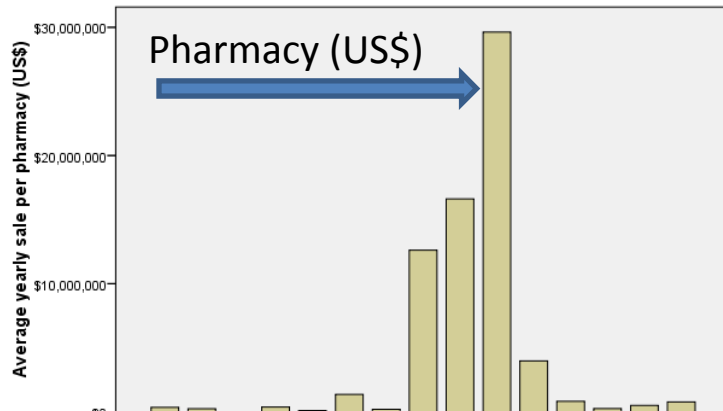
Important drivers of AB consumption

- High out-of-pocket health expenditure
- Mostly self-medication as is cheaper and quicker
- Despite regulation, AB dispensed without prescription
- No law enforcement

Important drivers of AB consumption

- Lack of knowledge: patient, pharmacist, doctor
- Financial incentives: patient, pharmacist, doctor
- Financial incentives health facilities
- Lack of time doctor
- Lack of good diagnostics
- Frequently used for mild ARI
- Advertising

Antibiotic use pattern is some pharmacies and hospitals in Vietnam



Source: GARP report 2010

Quinolones

- Family of broad-spectrum antibiotics.
- The majority of quinolones in clinical use belong to the subset of Fluoroquinolones (FQ).
- Inhibit topoisomerases/DNA synthesis
 - DNA gyrase/topo II (*gyrA* and *gyrB*)
 - Primary target in Gram-negatives
 - Topoisomerase IV (*parC* and *parE*)
 - Primary target in Gram-positives

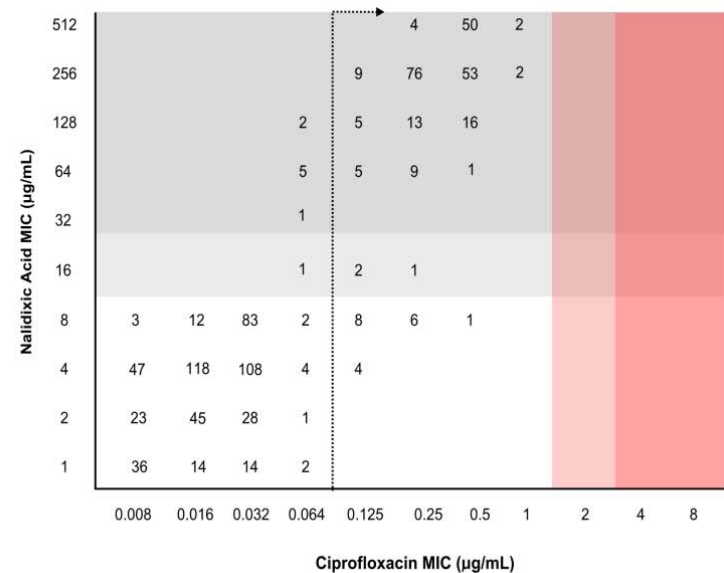
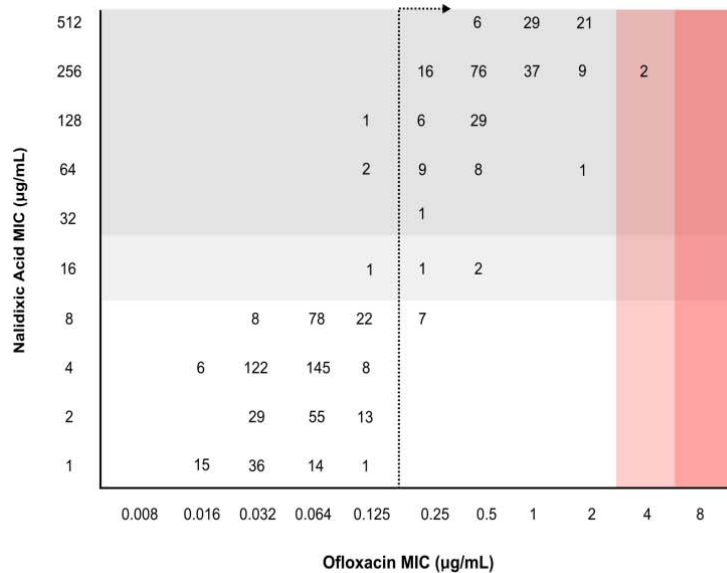
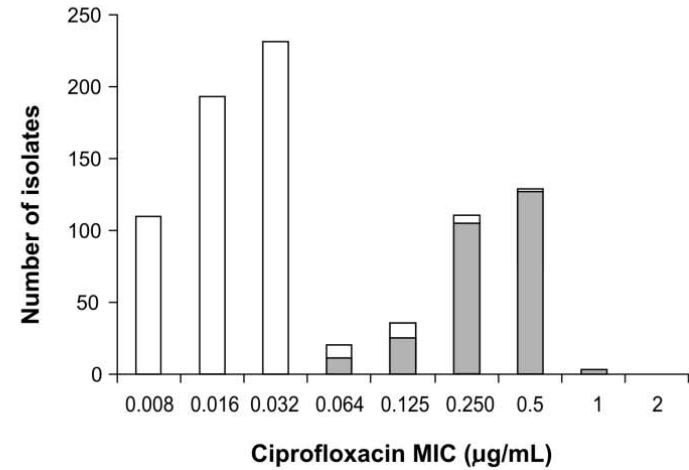
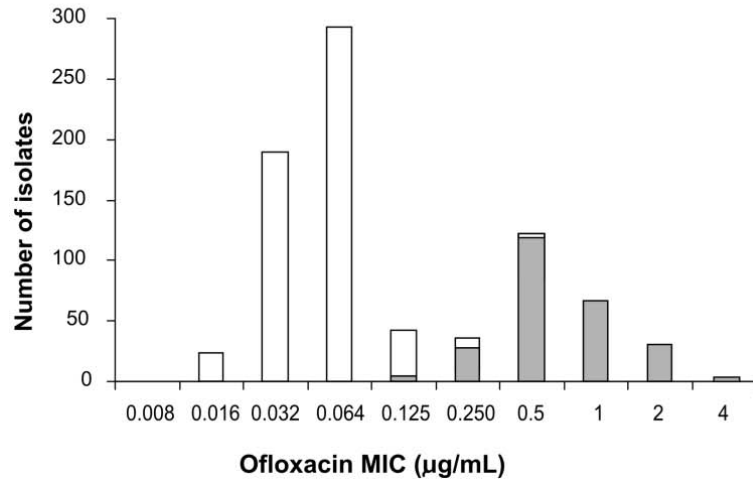
Resistance to Quinolones

- Mutations in DNA gyrase and topo IV subunits
- Stepwise increase in resistance results from sequential mutations
 - Quinolone resistance determining region(QRDR) is a hotspot for mutation
 - *gyrA* codons 83 and 87 in *Salmonella*
 - Amino acid substitutions within QRDR
 - Hydroxyl group hydrophobic group
 - Changes in binding site conformation and/or charge

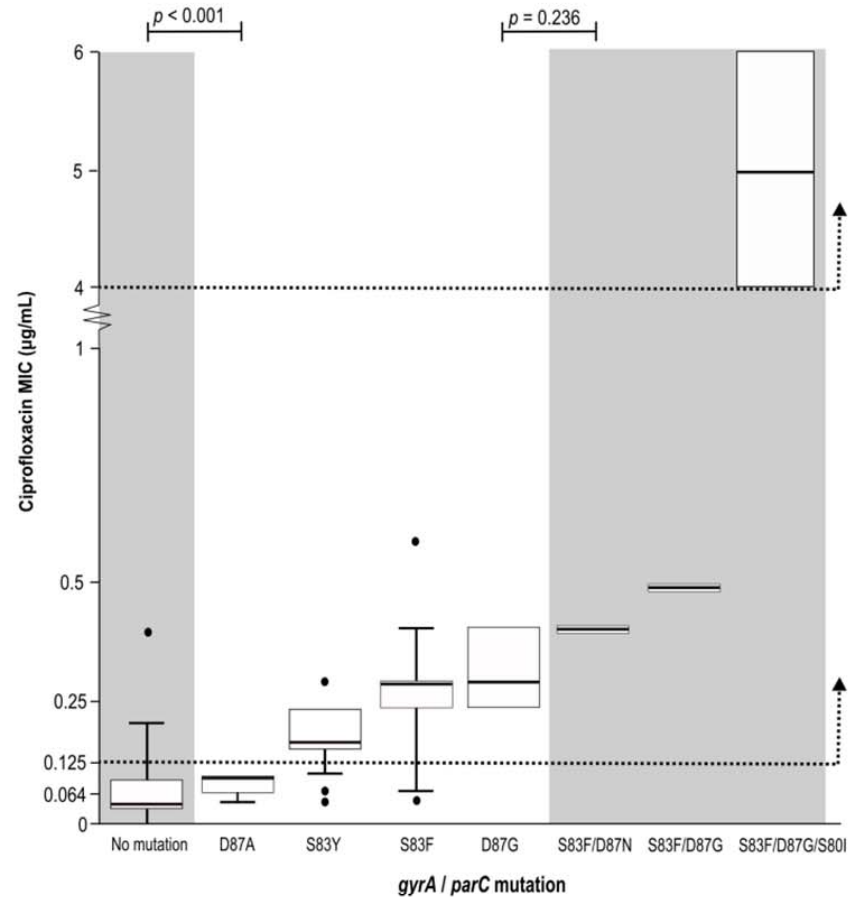
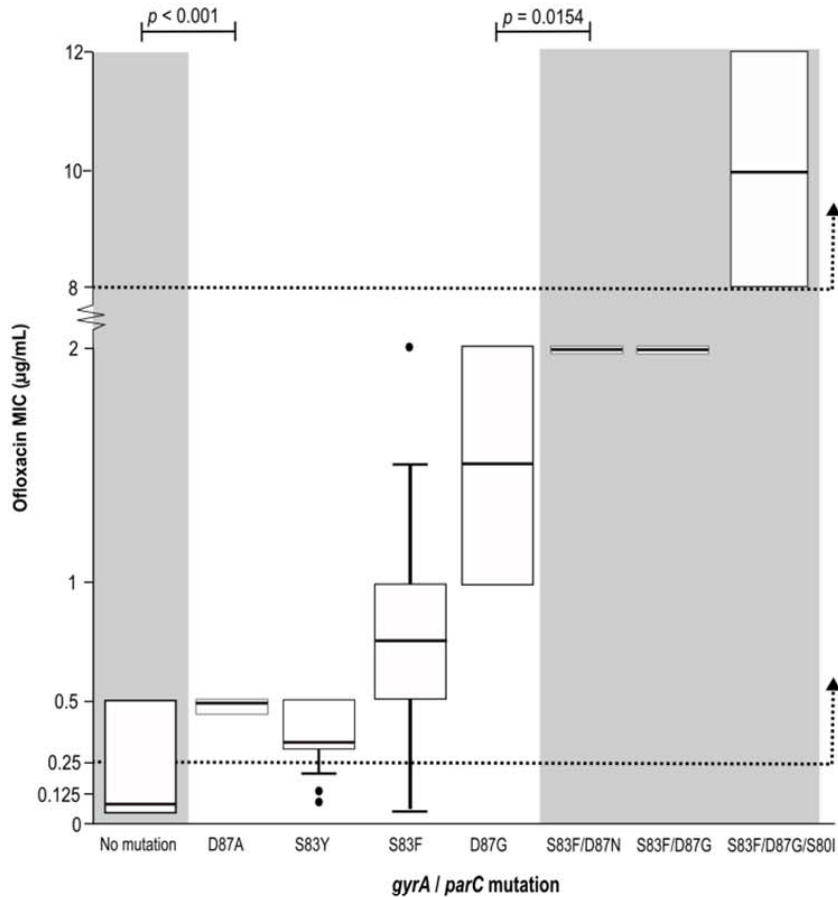
Plasmid-mediated FQ resistance

- Plasmid-mediated FQ resistance (*qnrA, B, S*)
- Significant as previously FQ resistance only spread vertically!
- Protects DNA gyrase from ciprofloxacin (CIP) inhibition.
- Nalidixic acid resistance, reduced susceptibility to FQ's
- Association with ESBL producers (*qnrA, B*).

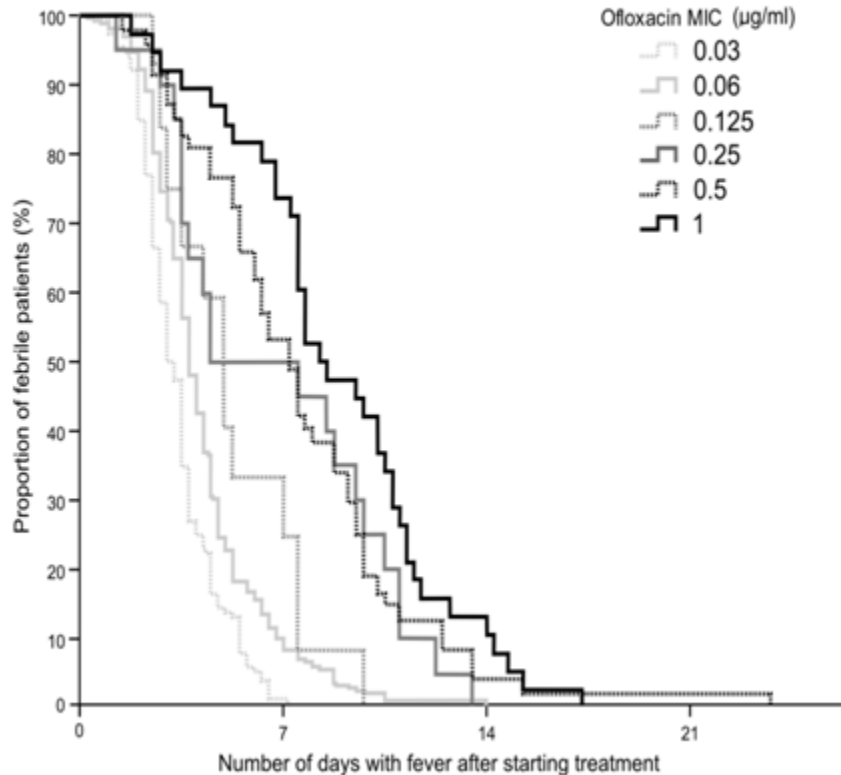
Fluoroquinolones in Typhoid in Vietnam



Fluoroquinolones in Typhoid



Clinical typhoid response

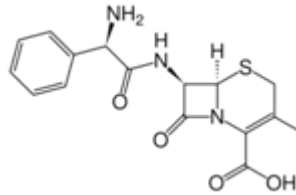


Breakpoint value	Number successfully treated/ total number treated (%)	Odds ratio (95% CI)
Ofloxacin MIC < 0.06 $\mu\text{g/ml}$	148/152 (97.4 %) 144	5.47 (1.95-21.20)
Ofloxacin MIC \geq 0.06 $\mu\text{g/ml}$	338/388 (87.1 %) 314	
Ofloxacin MIC < 0.12 $\mu\text{g/ml}$	406/423 (96.0 %)	11.05 (5.71-21.88)
Ofloxacin MIC \geq 0.12 $\mu\text{g/ml}$	80/117 (68.4 %)	
Ofloxacin MIC < 0.25 $\mu\text{g/ml}$	417/435 (95.9 %)	12.09 (6.24-23.81)
Ofloxacin MIC \geq 0.25 $\mu\text{g/ml}$	69/105 (65.7 %)	
Ofloxacin MIC < 0.50 $\mu\text{g/ml}$	432/455 (94.9 %)	10.78 (5.6-20.77)
Ofloxacin MIC \geq 0.50 $\mu\text{g/ml}$	54/85 (63.5 %)	
Ofloxacin MIC < 1.00 $\mu\text{g/ml}$	466/502 (92.8 %)	11.65 (5.26-25.36)
Ofloxacin MIC \geq 1.00 $\mu\text{g/ml}$	20/38 (52.6 %)	
Nalidixic acid susceptible	417/434 (96.1 %)	13.15 (6.74-26.20)
Nalidixic acid resistant	69/106 (65.1 %)	

Cephalosporins

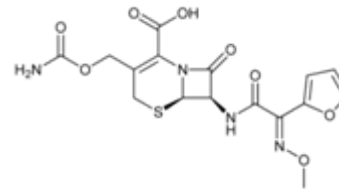
1st Generation

e.g. Cephalexin



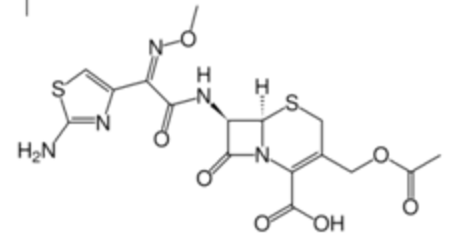
2nd Generation

e.g. Cefuroxime, cefoxitin



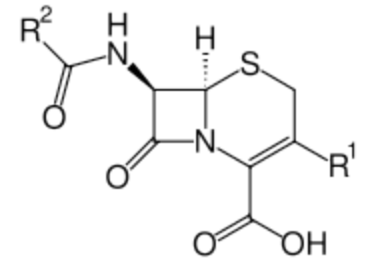
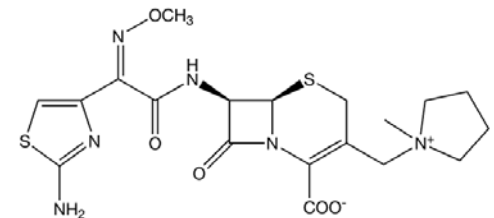
3rd Generation

e.g. Cefotaxime, cefpodoxime, ceftriaxone, cefoperazone, ceftazidime



4th Generation

Cefopime, Cefquinome



What Are ESBLs?

- Molecular class A or D β -lactamases
- Hydrolyse oxyimino cephalosporins
- Have an active site serine
- Generally inhibited by β -lactamase inhibitors
(clavulanic acid, sulbactam, tazobactam)
- Most often associated with *E.coli* and *Klebsiella pneumoniae* but can be produced by other enteric bacilli
- >170 types



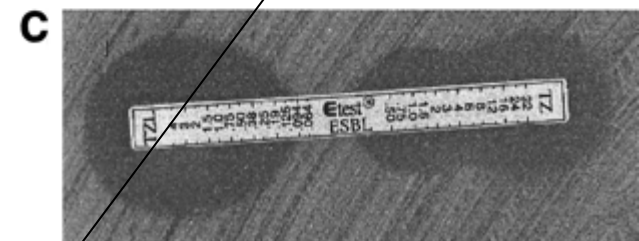
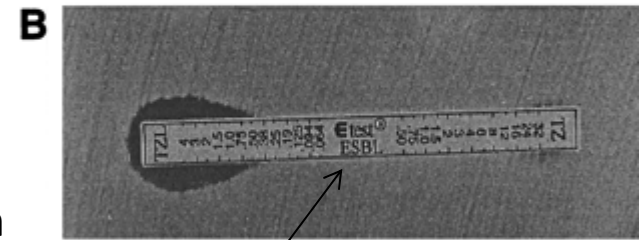
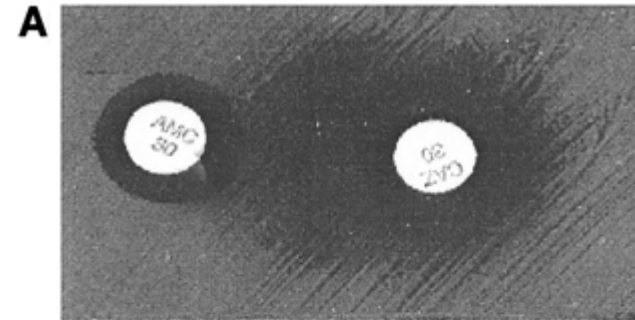
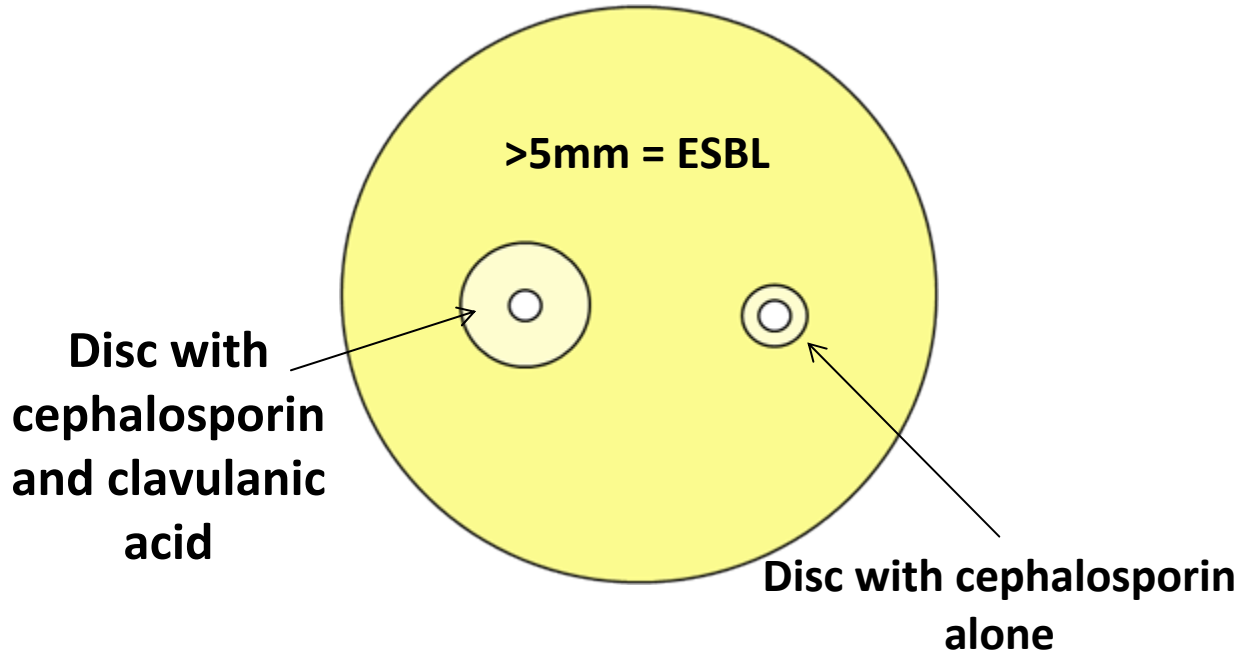
Extended-spectrum β -lactamases

- Plasmid-mediated enzymes found in *Enterobacteriaceae*
- Hydrolyze 3rd generation cephalosporins
 - But not carbapenems or cephamycins (cefoxitin)
- Encoded on large plasmids (>100Kb)
 - Multi-drug resistance
- Mostly Ambler class A
 - TEM, SHV, CTX-M
- More rarely
 - Ambler Class D
 - OXA (can also be resistant to cefipime)
 - VEB, PER (resistant to β -lactamase inhibitors)

Laboratory Detection

- Increased global reporting of resistant Enterobacteriaceae
 - AmpC
 - ESBL
- Many labs still fail to routinely test for ESBLs
- No methodology without its problems

ESBL detection



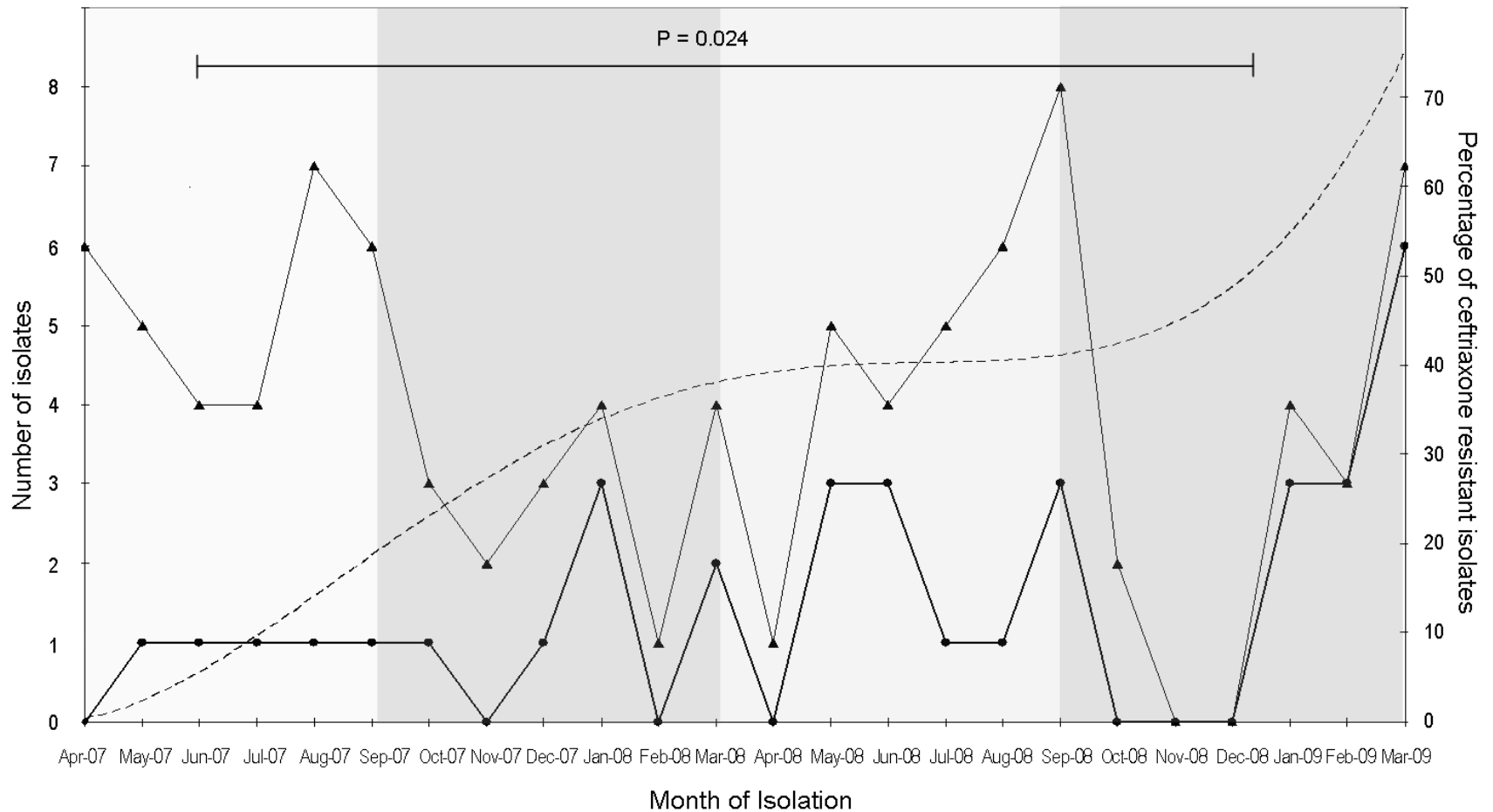
3-fold reduction of
MIC=ESBL

- Double disc synergy
- Combination disc test
- E-test

Laboratory detection

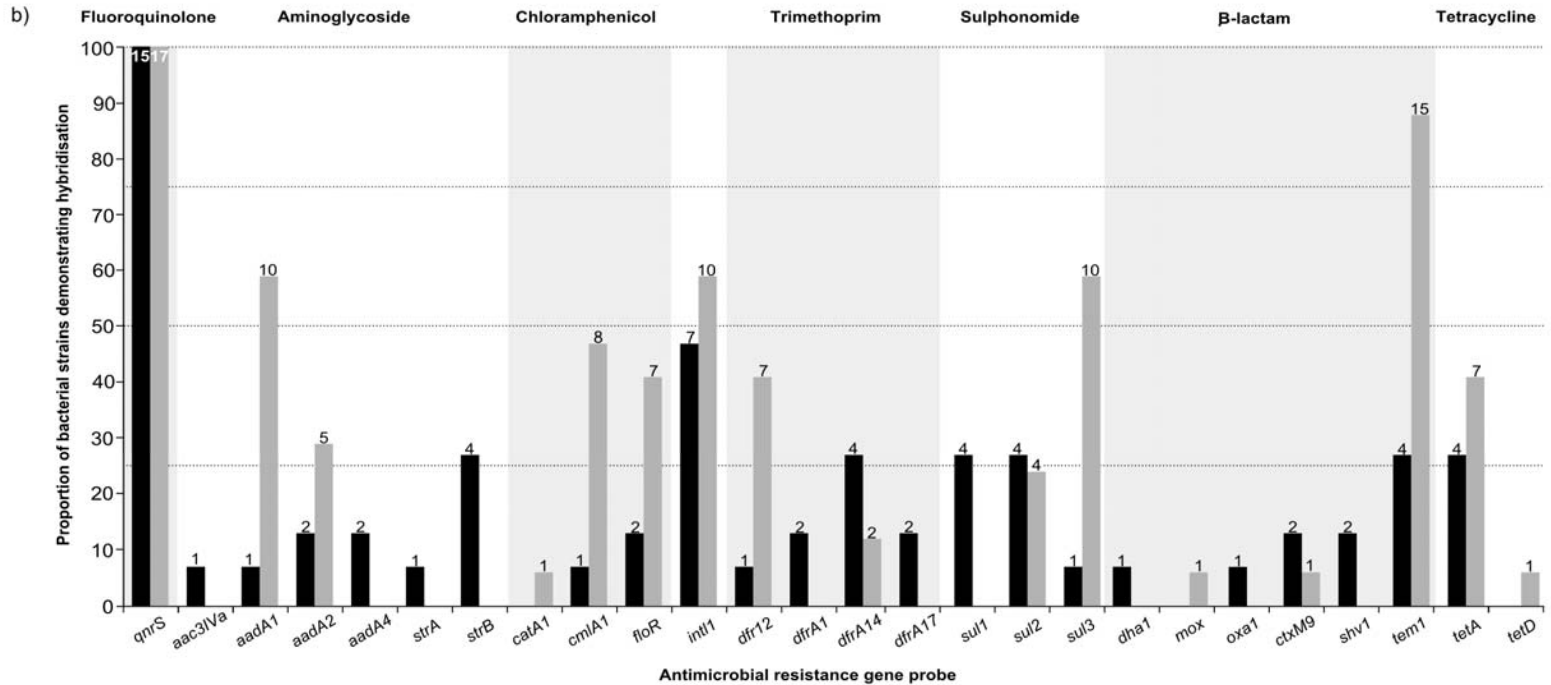
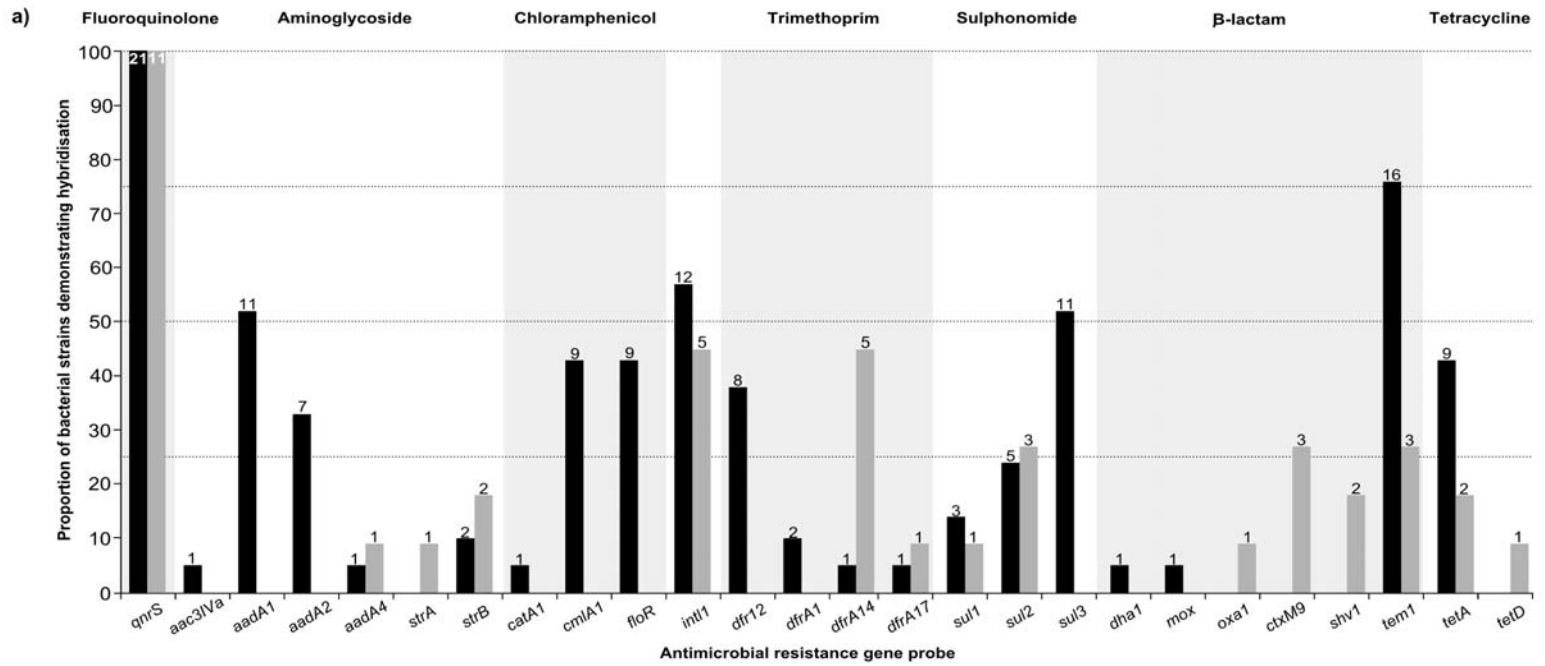
- Initial decreased susceptibility to oxyamino cephalosporins
 - Will not detect all ESBLs (TEM7,TEM12,SHV2)
- Further phenotypic (and genotypic) testing of isolates for ESBL production
- Testing with ceftazidime alone may miss CTX-M isolates
- Cefoxitin susceptibility will exclude the presence of AmpC-type beta-lactamase

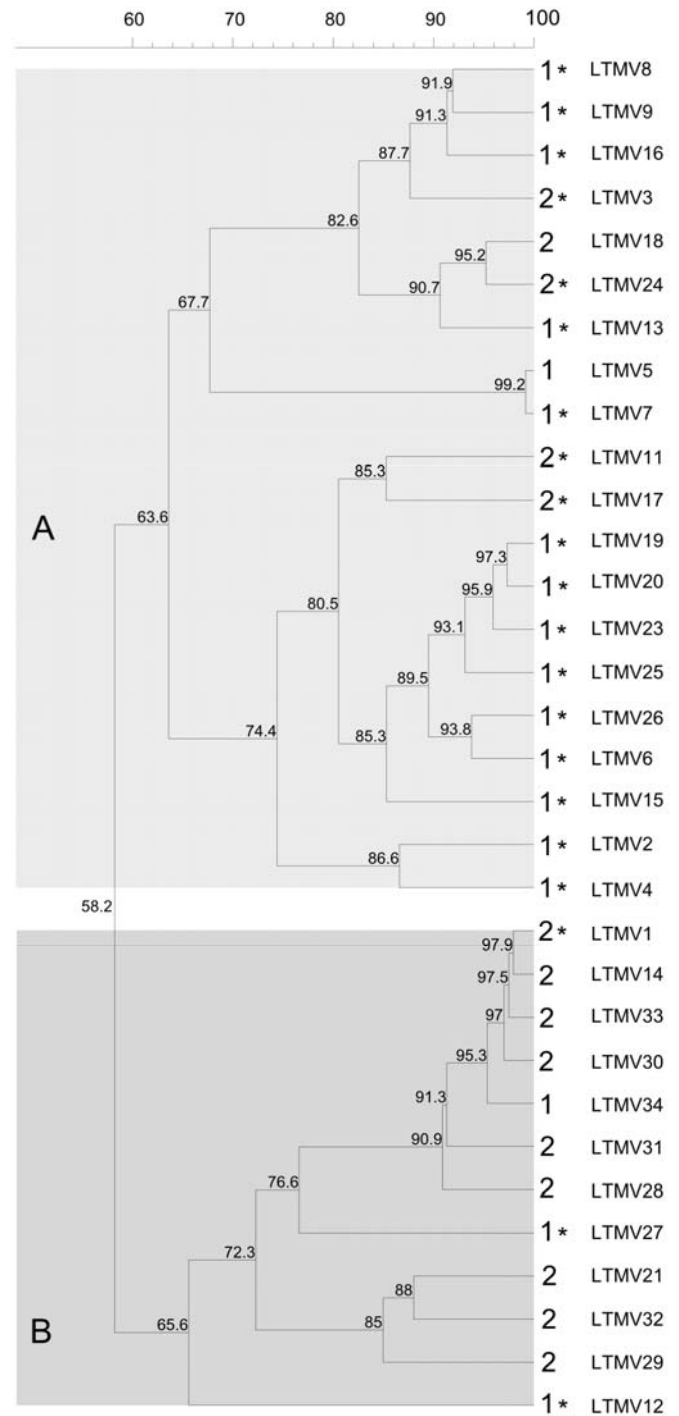
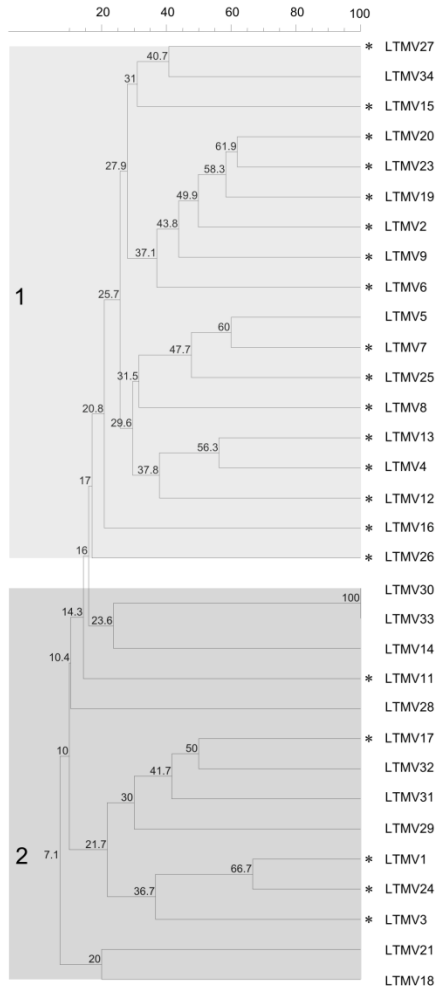
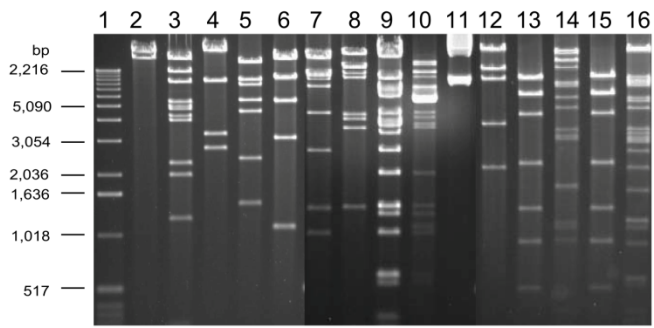
Extended-spectrum β -lactamases in *Shigella* in Ho Chi Minh City



Resistance in commensal enteric bacteria

	Antimicrobial tested								
	AMP	GEN	CHL	TET	SXT	CRO ^c	FEP ^c	KAN	TIC
Number of resistant organisms (from 32) [n (%)]	23 (71.9)	21 (65.6)	18 (56.3)	15 (46.9)	15 (46.9)	6 (18.8)	5 (15.6)	2 (6.3)	2 (6.3)
Resistant <i>E. coli</i> (from 17) [n(%)]	13 (76.5)	9 (52.9)	13 (76.5)	8 (47.1)	8 (47.1)	1 (5.9)	1 (5.9)	2 ² (11.8)	1 (5.9)
Resistant <i>K. pneumoniae</i> (from 15) [n(%)]	10 (66.7)	13 (86.7)	4 (26.7)	7 (46.7)	6 (40.0)	5 (33.3)	4 (26.7)	1 (6.7)	1 (6.7)
<i>p</i> value ^a	0.6989	0.0605	0.0118*	1	0.7345	0.0755	0.1609	1	1
Resistant organisms community (from 21) [n(%)]	15 (68.2)	11 (50.0)	17 (77.3)	12 (54.5)	11 (50.0)	0 (0.0)	0 (0.0)	2 (9.1)	1 (4.5)
Resistant organisms hospital (from 11) [n(%)]	8 (72.7)	10 (90.9)	1 (9.1)	3 (27.3)	4 (36.4)	6 (54.5)	5 (45.5)	0 (0.0)	1 (9.1)
<i>p</i> value ^b	1	0.0273*	0.0005*	0.2659	0.712	0.0004*	0.0019*	0.5417	1





Carbapenemases

- Class A
 - Chromosomally-encoded IMI, NMC-A and SME
 - Plasmid-encoded KPC and GES
 - Clavulanic acid-inhibited
- Class B
 - Metallo- β -lactamases (inhibited by EDTA)
 - IMP, VIM, NDM-1
 - Integron encoded (transposon and plasmid)
- Class D
 - OXA types (mostly *Acinetobacter baumannii*)
 - Sensitive to β -lactamase inhibitors

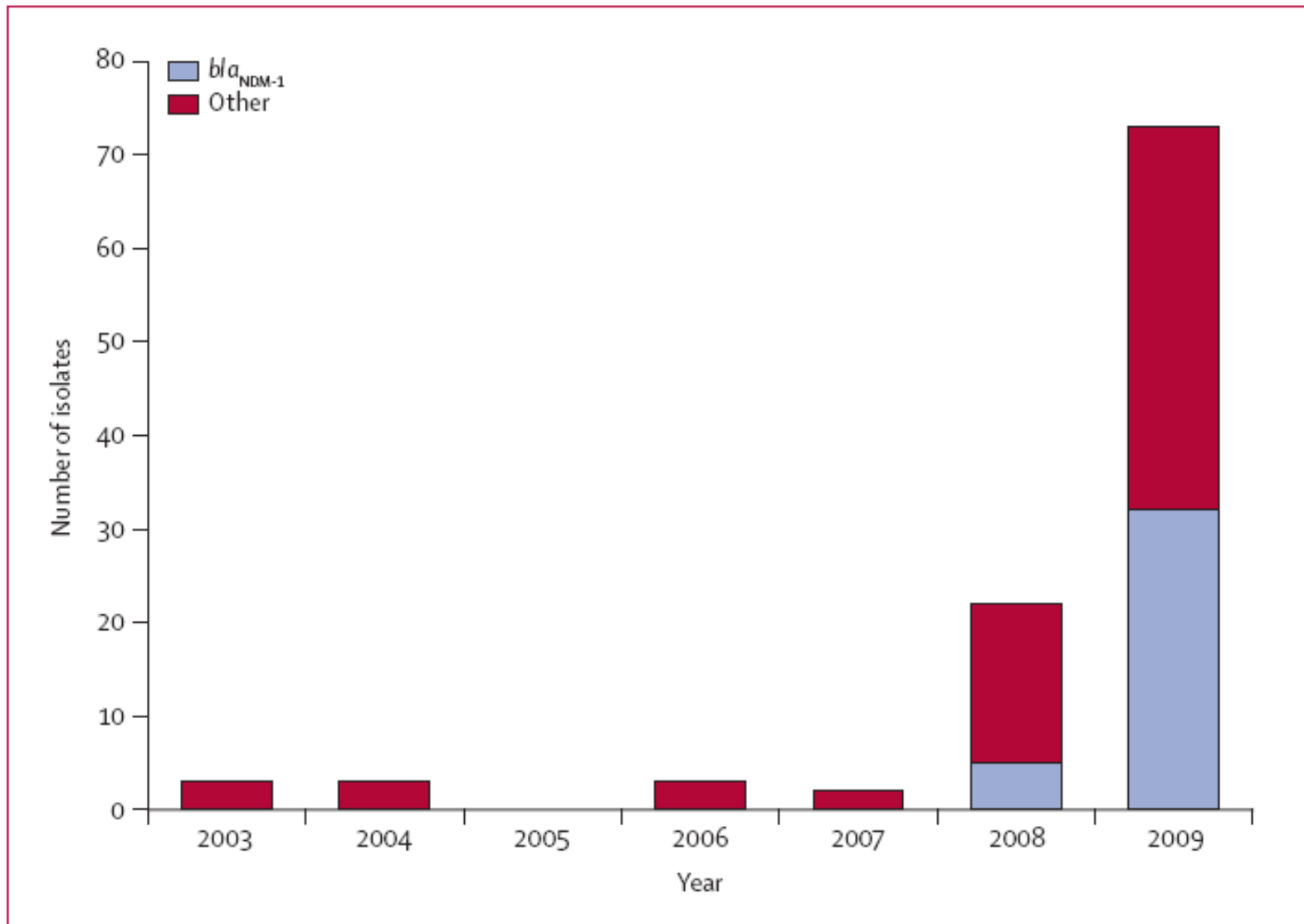


Figure 1: Numbers of carbapenemase-producing Enterobacteriaceae referred from UK laboratories to the UK Health Protection Agency's national reference laboratory from 2003 to 2009

The predominant gene is *bla*_{NDM-1} which was first identified in 2008. The other group includes diverse producers of KPC, OXA-48, IMP, and VIM enzymes.

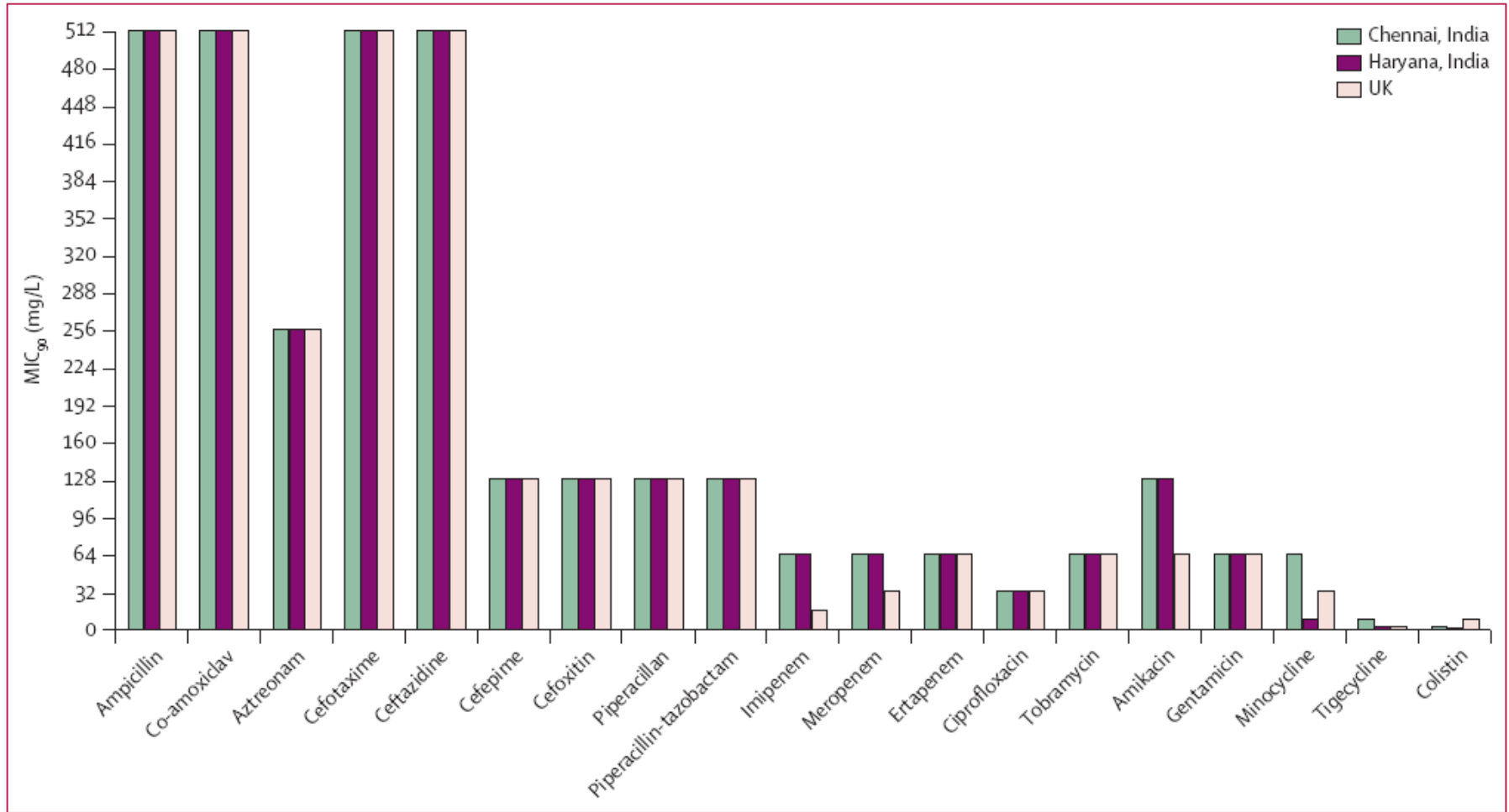
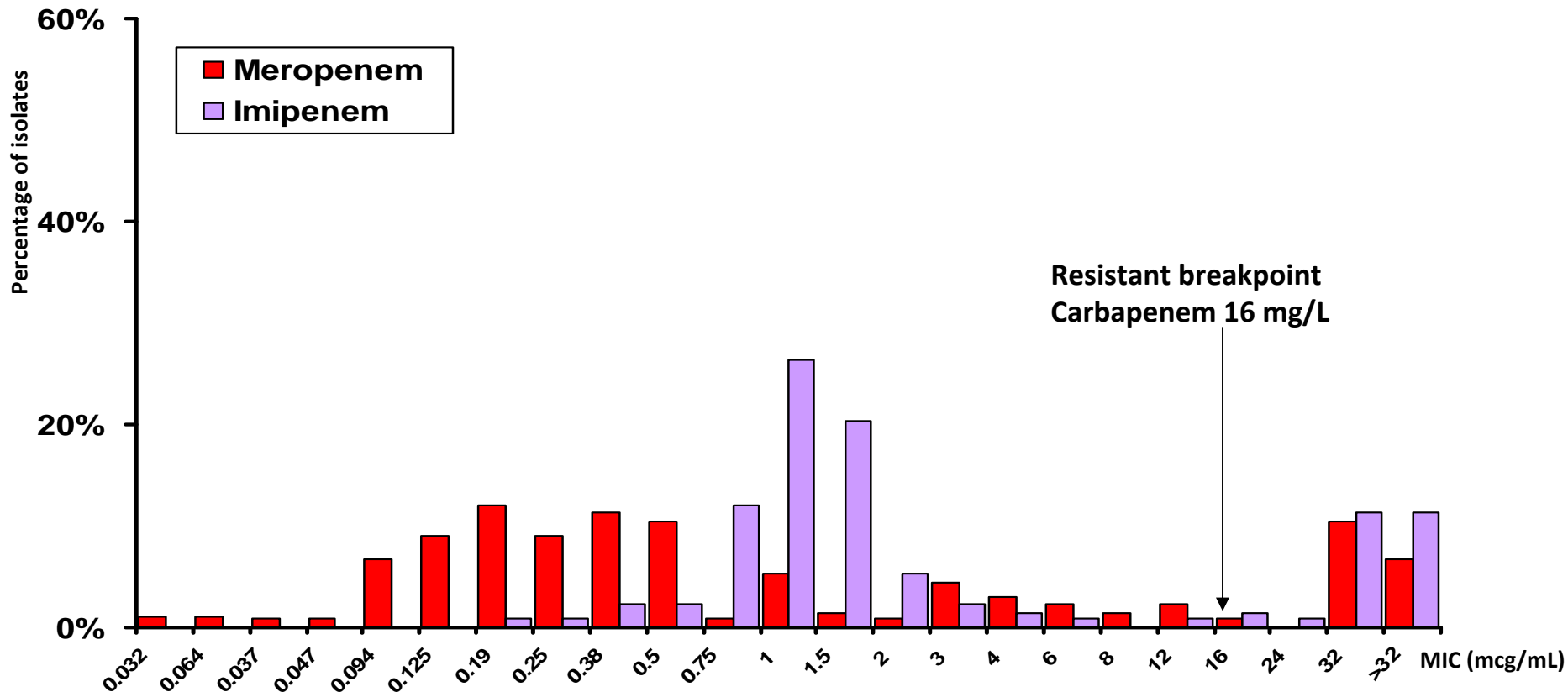


Figure 2: 90% minimum inhibitory concentration (MIC₉₀) for Enterobacteriaceae from Chennai and Haryana, India, and the UK

Carbapenem resistance *P. Aeruginosa* Cause of hospital pneumonia

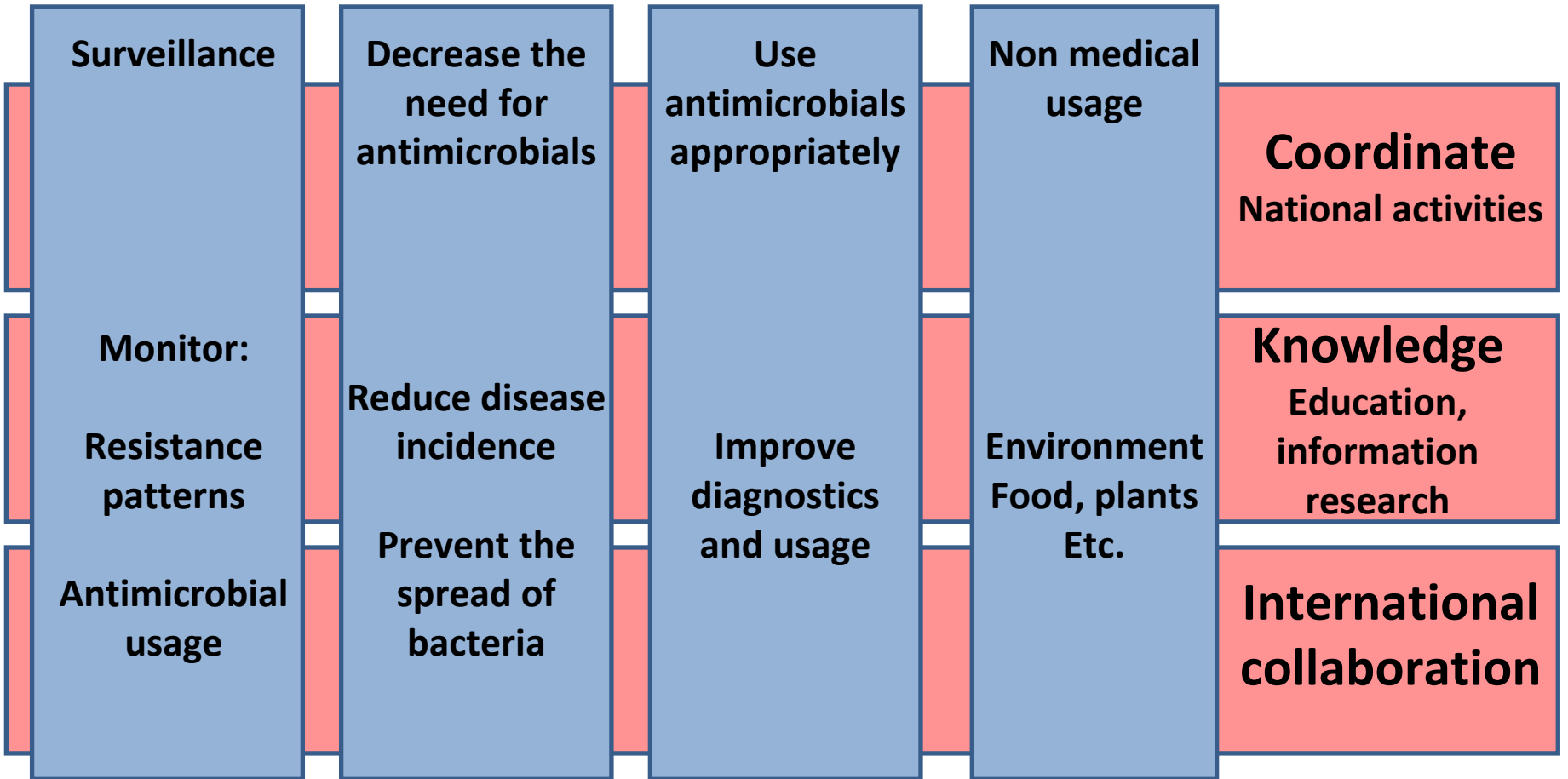
(133 strains isolated in 6 hospitals - 2008)

► Emerging carbapenem resistance



Source: Dr Doan Mai Phuong, Bach Mai Hospital

Tools to control use and resistance



What surveillance can be done now?

- **Antibiotic consumption surveillance**
 - main driving force for development of resistance
 - Surveillance provides data to implement interventions
 - Hospital, community, agriculture

- **Antibiotic resistance surveillance**
 - Monitor of prescribing practices and interventions
 - Early warning of important resistance trends
 - Helps prescribers to give the right antibiotic
 - Hospital, community, agriculture

Proposals to Combat Antimicrobial Resistance

- Speed development of new antibiotics
- Develop alternatives
- Track resistance data nationwide
- Restrict antimicrobial use
- Directly observe dosing (TB)
- Use more narrow spectrum antibiotics
- Use antimicrobial cocktails

In addition

- Education
- Guidelines and Pathways
- Antimicrobial cycling
- Antimicrobial order forms
- Combination therapy
- De-escalation of therapy
- Dose Optimisation
- IV/Oral
- Controlling community usage.....

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