

AMR at human animal interface: PGIMER research updates



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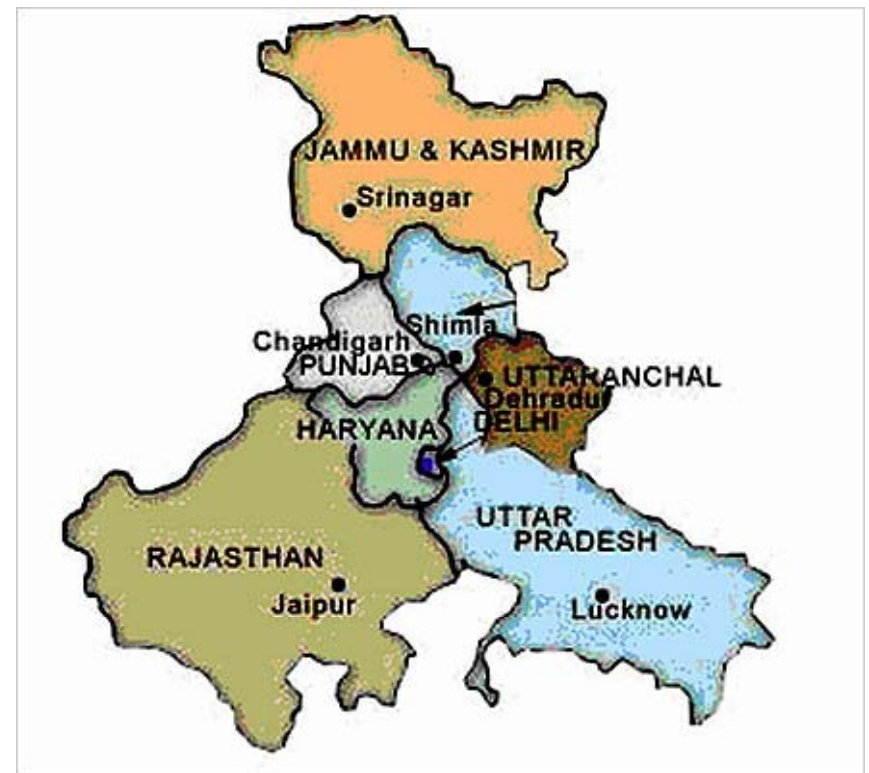
PGIMER

2000 bed tertiary care referral centre in Chandigarh, North India

Caters to patients from seven adjoining States (Chandigarh, Punjab, Haryana, Himachal Pradesh, Jammu and Kashmir, western parts of Uttar Pradesh, Uttaranchal, and some parts of Rajasthan) thus representing a large geographical area

2,42,3501 outpatients and 87973 admission in 2016

8.2017



Enteric Lab

Diagnostic (conventional as well as molecular)

- Urine and Stool samples
- Load- 45000 /year
- NABL accreditation

Surveillance and referral services investigating and managing outbreaks of cholera, and food poisoning in this geographic area

Research in the field of diarrhea, food borne infections and urinary tract infections with special focus on epidemiology and drug resistance and pathogenesis

Antimicrobial resistance in Enteric and Uro pathogens is being studied at community and hospital level by both phenotypic and molecular assays

Conventional Culture for Salmonella, Shigella, Vibrio cholerae, Campylobacter, STEC and Yersinia, C. difficile

Antigen detection for STEC, Campylobacter, C. difficile

Molecular tests

- Multiplex PCR for diarrhoeagenic *E. coli*
- *Shigella* PCR
- STEC PCR
- Campylobacter PCR

Rapid dipstick for cholera and dysentery

Food borne Pathogens

Vibrios, Bacillus cereus, Shigella, Aeromonas, Pleisomonas, Yersinia, Campylobacter, *Staphylococcus aureus*, Listeria, testing of milk samples by total plate counts, methylene blue test, turbidity test, coliform tests for milk, full water testing for coliforms, *E coli*, Enterococci, *V. cholerae*, testing of water directly for diarrhoeagenic *E.coli* using in house protocols (PCR).

Molecular assays to detect directly from food samples

Special food (RUTF) which was developed to treat malnutrition was tested by us for component analysis and shelf life of the prepared food

Receive request from Government labs for testing commercial food and water samples

Capacity for molecular epidemiology

- AFLP
- PFGE
- MLVA
- Ribotyping
- Plasmid typing
- Rep-PCR and RAPD
- MLST
- WGS

Public Health Contribution

Public health role and surveillance

Investigated 25 outbreaks of cholera and gastroenteritis.

Visit the area and collect water samples, stool samples and study the factors responsible for cholera.

Due to fast identification of source of water contamination, we could control the cholera outbreaks in a week .

We are also studying the molecular epidemiology of *V. cholerae* causing the recent epidemics in our region by AFLP, ribotyping and PFGE.

WHO APW project and DFC



Strengthening district public health laboratories for laboratory surveillance of communicable diseases of outbreak potential Announcement of phase 1

To assist in capacity building of the district laboratories.

- Punjab-Moga, Bhatinda, Hoshiarpur, **Sangrur**
- Haryana-Ambala, Faridabad, Bhiwani, **Panchkula**
- Uttarakhand-Dehradun, Haridwar, Tehri Garhwal, **Pauri**

To assist in technical operations & provision of resources needed to ensure required quality of laboratory procedures.

To formulate a framework for establishment of quality control & quality assessment schemes in these laboratories.

To periodically visit the laboratories at district level & monitor the progress

WHO APW project and DFC-Phase 2



Stool referral system :A total of 336 stool samples were collected and submitted from the following centers- Moga (N=58), Ambala (N=38), Sangrur (N=17), Panchkula (N=72) and Pauri (N=32) DPHLs. These samples were collected from PHC and DPHL level by active surveillance

Most of the samples (231, 68%) were sent by local couriers and 95% were received in proper conditions, though some were not sent in double packaging

Outbreaks of cholera were reported from Ambala, Moga and Panchkula ,samples were also submitted from suspected cases from Sangrur , Uttarakhand and Chandigarh for confirmation .

Fourteen outbreaks of diarrhoea / food poisoning occurred in 2010 and 2011 followed by 4 outbreaks each of dengue chickenpox, measles and viral fever , 3 of jaundice , 2 of typhoid one each of viral encephalitis and rubella .

Tool for assessment of biosafety in laboratory

The culture facilities were established at the following centres- Ambala, Bhiwani, Haridwar , Pauri.

Quality assurance panels were sent and responded

Food borne illnesses

Foodborne illness are of serious concern to public health worldwide

90% bacterial infections followed by parasitic and viral

Major bacterial pathogens : *Campylobacter*, *Salmonella*, *Diarrhoeagenic coli*, *Listeria*, *Yersinia*, *Shigella*, *Vibrio*, etc.

Salmonella is the leading cause of death followed by *Campylobacter* (C Alert;2008)

Both occur in intestinal tract of sheep, goat, pigs and poultry

E. coli is commensal microbiota but some may be pathogenic strains
i.e. **EPEC**, **ETEC**, EAEC, EIEC, STEC

Transfer of virulence genes can occur through lateral gene transfer

Diarrhoeagenic *E. coli* caused maximum hospitalizations

Contaminated food and water are main sources of infections

Indian scenario

Burden of foodborne diseases is unknown

No surveillance system

No national database of epidemiology of common food borne pathogens

Foodborne infections occur as sporadic cases and also as outbreaks

Underreporting of foodborne outbreaks and cause is rarely established. Foodborne gastroenteritis is clubbed with acute diarrhoea and is not notifiable

In our region too foodborne illnesses are very common but not investigated or reported

In a study conducted by us, in collaboration with WHO, we found that every year 1,400 to 31,000 cases of suspected food- and-water-borne infections were being reported at the district public health laboratories (DPHLs) across Punjab, Haryana and Uttarakhand

Every year one to three outbreaks of food poisoning reportedly occurred at the DPHLs (Unpublished data PGIMER) Almost all of these go uninvestigated

How antibiotics in livestock affect us

used for prophylactic, therapeutic and growth promotion

suppress gut flora leaving more nutrients to be absorbed by animal leading to greater gain in weight

Most of the antibiotic classes are the ones used for humans

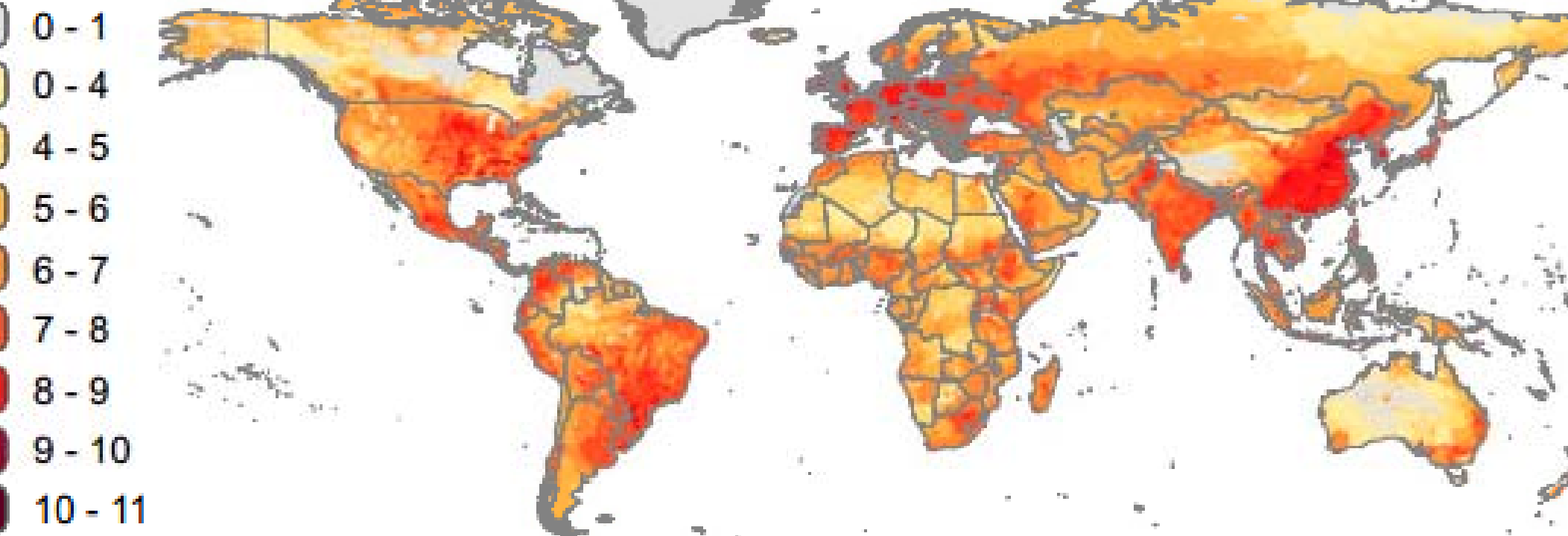
Overuse has led to emergence of antibiotic resistance

Residues of these antibiotics remain active in animals for certain time and are also excreted in faeces

Consumption of trace levels of these residues in foods may alter human intestinal microflora and cause resistance gene transfer

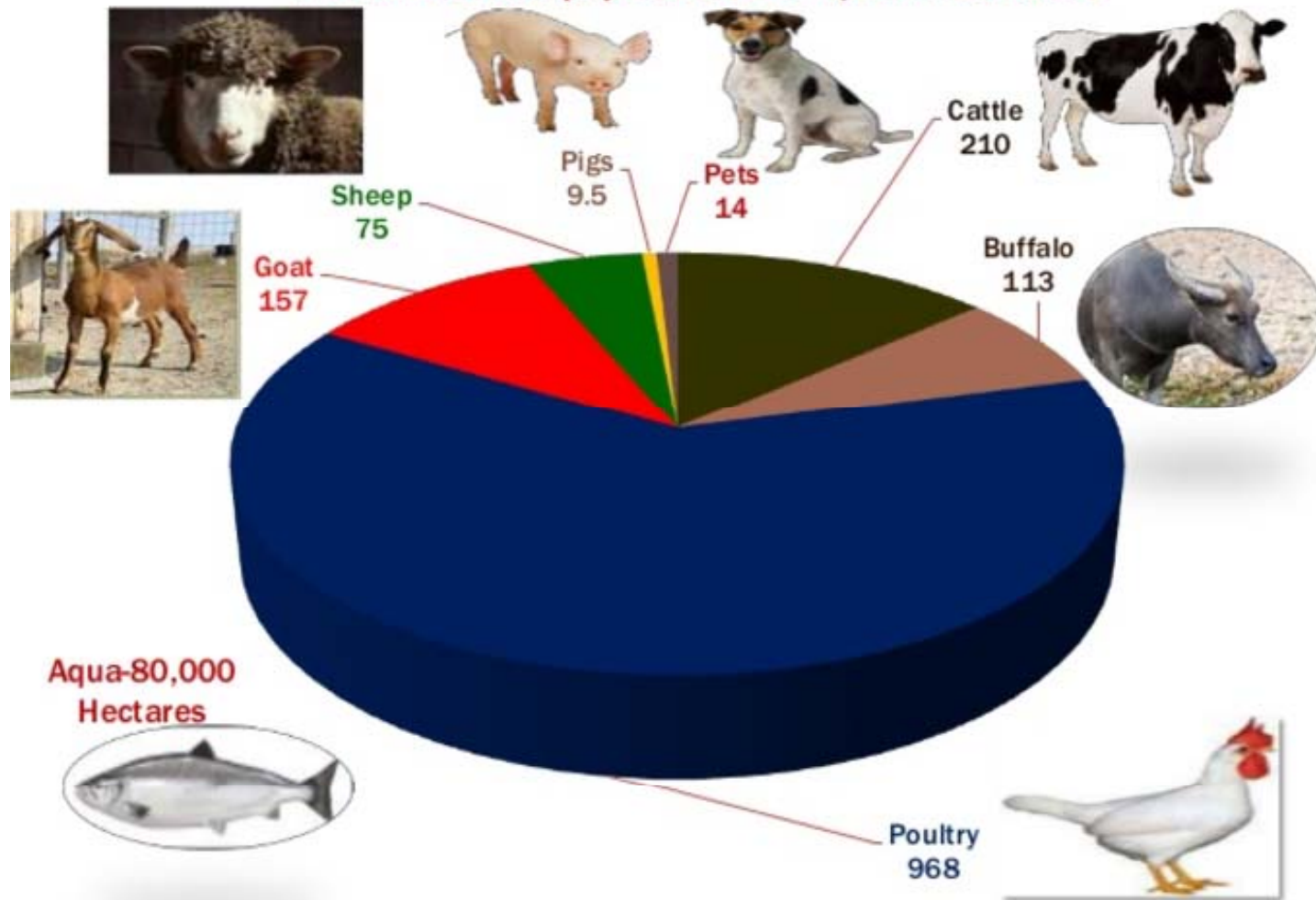
Low levels of abs released in environment accumulate and affect bacteria and cause transfer of resistance genes

10 [(mg/pixel)+1]



Global antimicrobial consumption in livestock (Van Bockerel; 2015)

Indian Livestock population: 2011(in Million Heads)



K.S.Niranjan

Source: FAOSTAT

What we lack in India

Guidelines on antibiotic use in feed are available, but not implemented

Antibiotics used for human disease treatment are used in growth promoters

No monitoring of residue limits in food meat in Indian markets

We do not know the antibiotic resistance pattern or resistance gene pool in food animals

We are unaware of the rate of transmission of antibiotic resistance from humans

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Antibiotics	Class / active compound	
Furazolidone	Nitrofuran	Human + veterinary
Bacitracin	Peptides from B. licheniformis	Human (topical) + veterinary
Neomycin + doxycycline	Aminoglycoside + tetracycline	Human + veterinary
Colistin	Polymyxin E	Human + veterinary
Amoxicillin	Penicillin	Human + veterinary
Levofloxacin	Fluoroquinolone	Human + veterinary
Colistin + doxycycline	Polymyxin E + tetracycline	Human + veterinary
Neomycin + doxycycline	Aminoglycoside + tetracycline	Human + veterinary
Neomycin + oxytetracycline	Aminoglycoside + tetracycline	Human + veterinary
Neomycin + sulphadiazine	Aminoglycoside + sulphonamide	
Avilamycin	Orthosomycin	
Oxytetracycline	Tetracycline	Human + veterinary
halquinol	chloroxine	
Tilmicosin	macrolide	veterinary
Perfloxacin	quinolone	Discontinued in human Used in Veterinary
Tiamulin	Pleuromutilin (inhibit protein synthesis by binding to 50S subunit of ribosomes)	Veterinary
Oxyclozanide	salicylanilide anthelmintic	Veterinary
Enrofloxacin	Fluroquinolone	Veterinary
Chlorotetracycline	Tetracycline	
Ceftiofur	Third generation cephalosporin	Veterinary
Amikacin	Aminoglycoside	Veterinary + human
Tylosin	Macrolide	Veterinary
Flumequine	Fluoroquinolone	Discontinued in human Used in Veterinary

One Health Approach



WHO-AGISAR Project

Monitoring the Antimicrobial resistance profile of
bacterial food borne pathogens in Humans, food
animals and retail meat in India

Human Samples

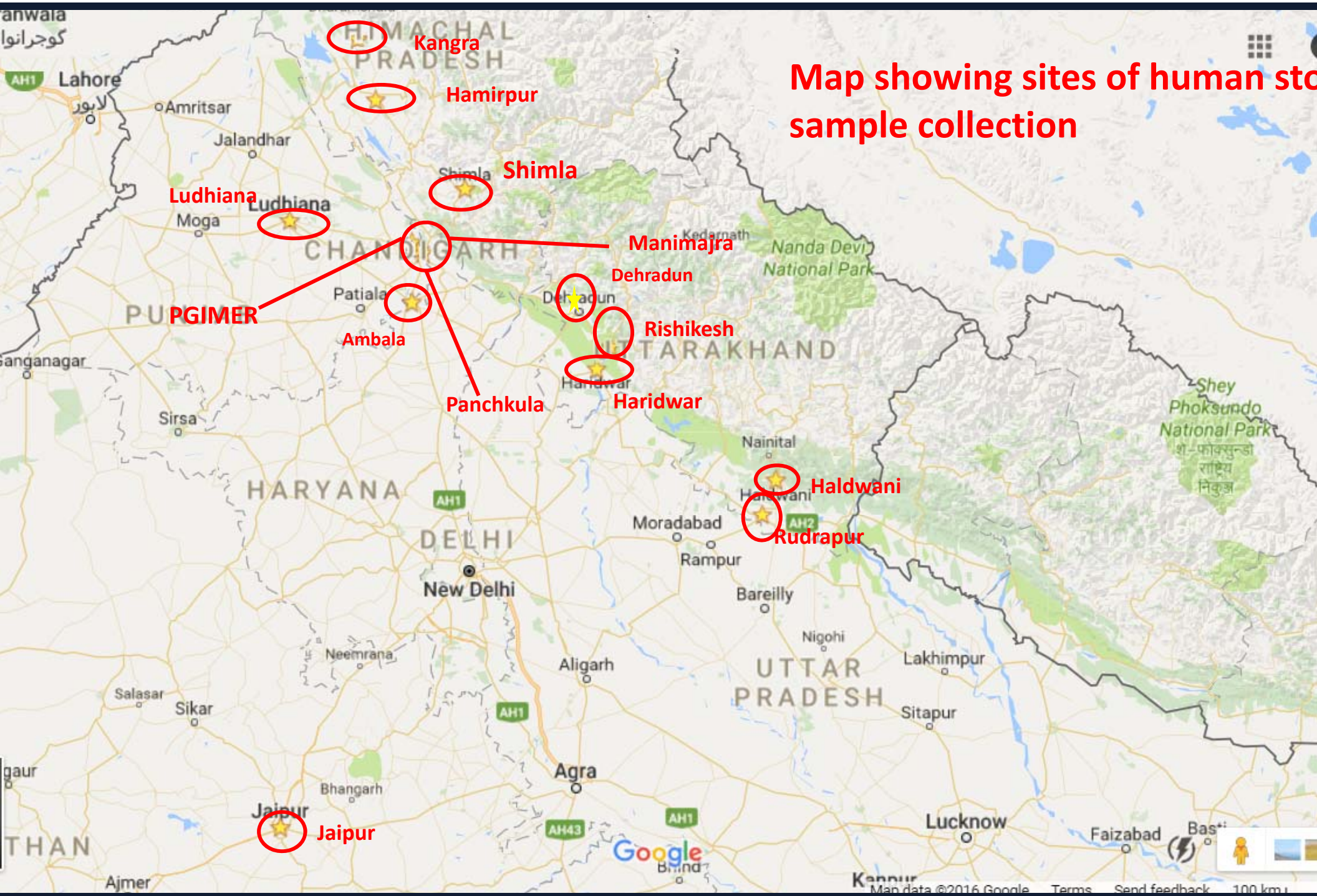
Sample collection

Total samples collected = 1968

proforma for history was filled

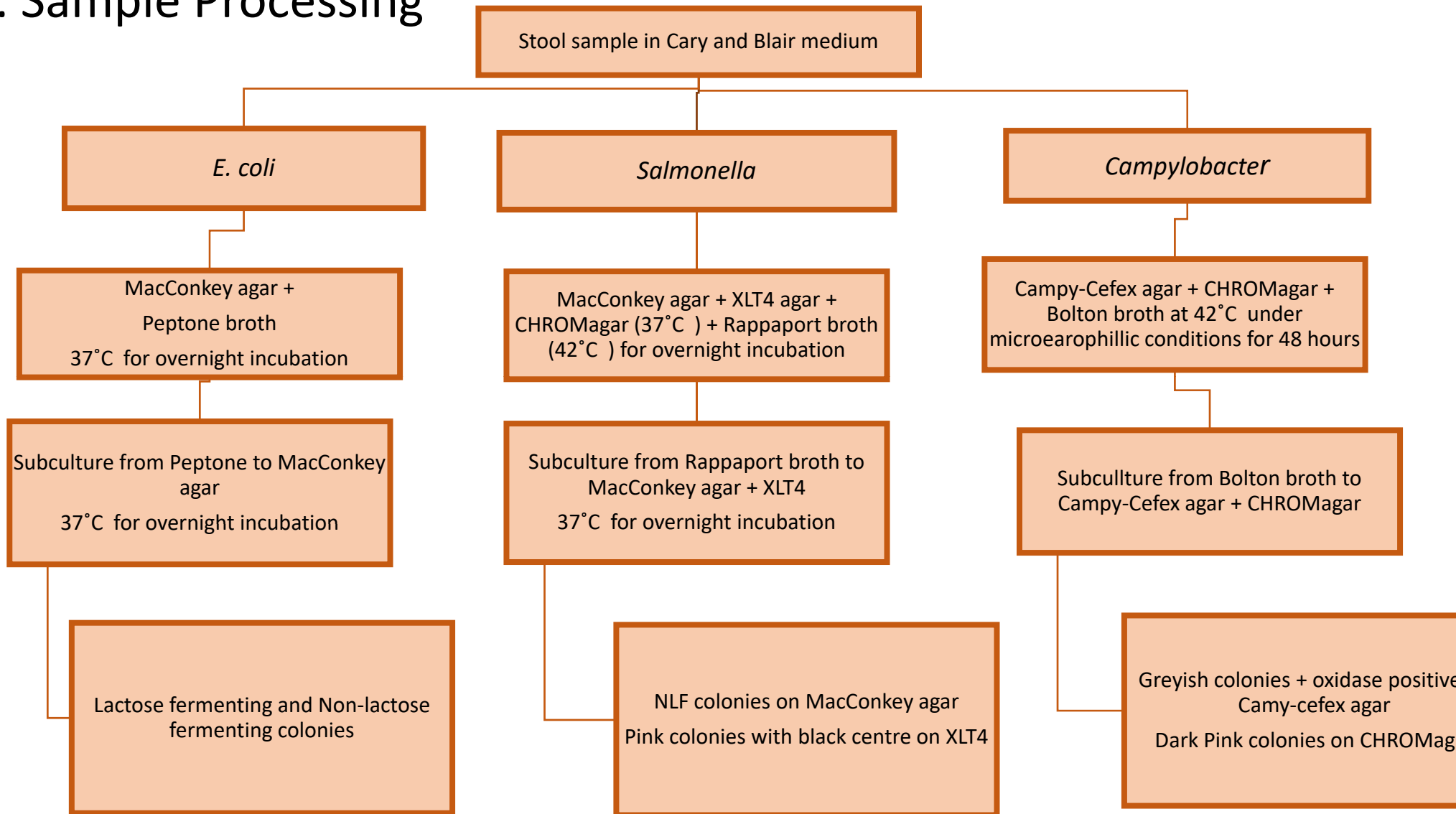
Diarrheal stool samples were collected & transported
in Cary and Blair transport medium





Map showing sites of human stool sample collection

2. Sample Processing



Colonies were identified by MALDI-TOF *

- *Salmonella* identified up to genus level
- Further serotyping to be done

Animal samples

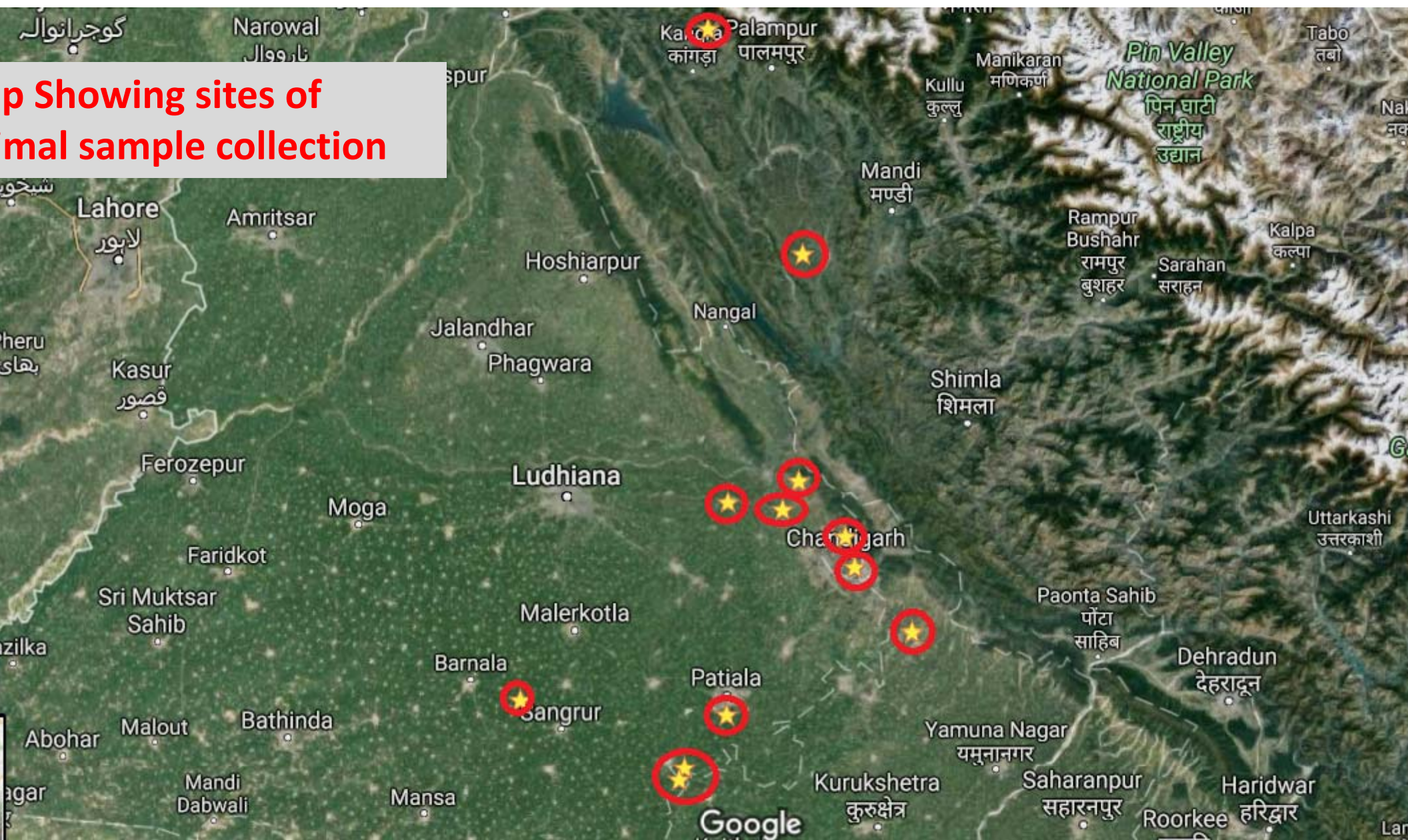
mples collected: 839

ol: 487

at: 352



Map Showing sites of
mal sample collection



Animal samples

Animal (goat, sheep, pig) meat and stool samples were collected from slaughter house, Chandigarh which receives animals from Chandigarh and nearby areas of Panchkula, Manimajra, Mohali and Punjab

Poultry stool samples were collected from farms in and around Chandigarh

These samples were processed for *Campylobacter*, Non-Typhoidal *Salmonella* and *E. coli* detection by culture methods

animal sample processing

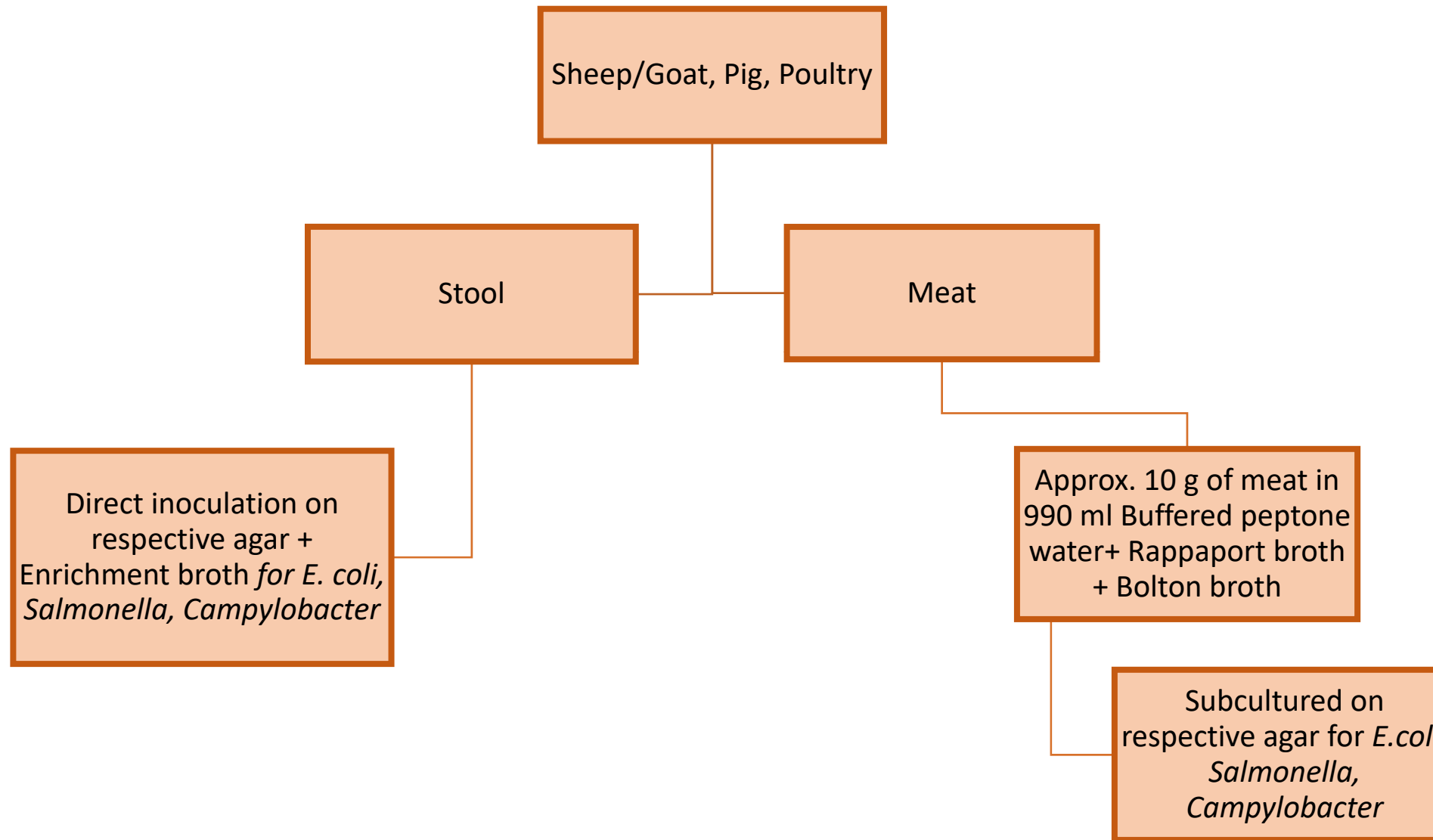


Table showing compiled results from all animals

Source	Sample (n)	Campylobacter (%)	Salmonella (%)	E. coli (%)
Pig	Stool (90)	MALDI identified species <ul style="list-style-type: none"> <i>Campylobacter jejuni</i> (38.79%) 	7 (7.78)	Multiplex PCR identified pathotypes EAEC (1%) EPEC (8%) STEC/EHEC (4.5%) ETEC (5.5%)
	Meat (191)		3 (1.57)	
Goat	Stool (57)	<ul style="list-style-type: none"> <i>Campylobacter coli</i> (58.41%) 	22 (38.6)	
	Meat (151)		29 (19.21)	
Chicken	Stool (340)	<ul style="list-style-type: none"> <i>Campylobacter hyointestinalis</i> (2.33%) 	38 (11.18)	
	Meat (10)		0	
Total	839		99 (11.8)	

5% samples has both *Campylobacter* and *Salmonella*

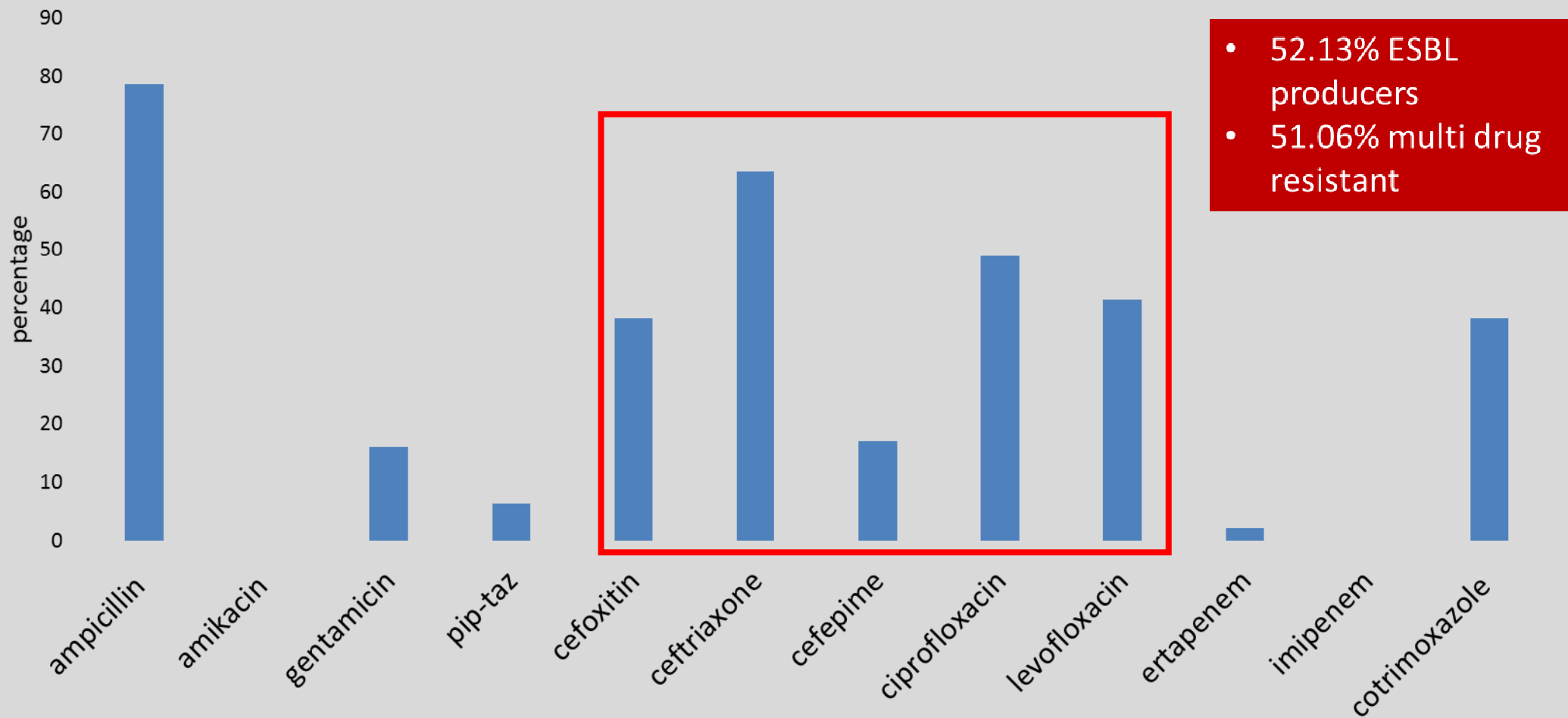
Table showing results of human stool samples

State	Locations	Number of samples	Campylobacter	Salmonella	DEC E. coli Pathotypes		
					EAEC	EPEC	ETEC
Chandigarh	PGIMER	850	10	13	36	26	32
Haryana	Panchkula	35	4	0	5	6	2
	Manimajra	745	12	9	13	21	23
	Ambala	29	2	0	5	4	4
Uttarakhand Pradesh	Kangra	8	0	0	0	1	1
	Shimla	70	3	1	7	10	5
	Hamirpur	11	1	0	2	2	3
Uttarakhand	Rudrapur	19	3	0	2	2	0
	Haldwani	13	0	0	3	1	4
	Rishikesh	86	4	1	6	6	7
	Dehradun	4	0	0	1	0	1
	Haridwar	38	3	0	7	3	6
Rajasthan	Jaipur	24	3	0	8	1	5
Punjab	Ludhiana	8	0	0	3	0	1
Total		1941	45 (2.32%)	24 (1.24%)	98 (5.05%)	83 (4.28%)	94 (4.84%)

Antibiotic usage and residues

Antibiotic susceptibility

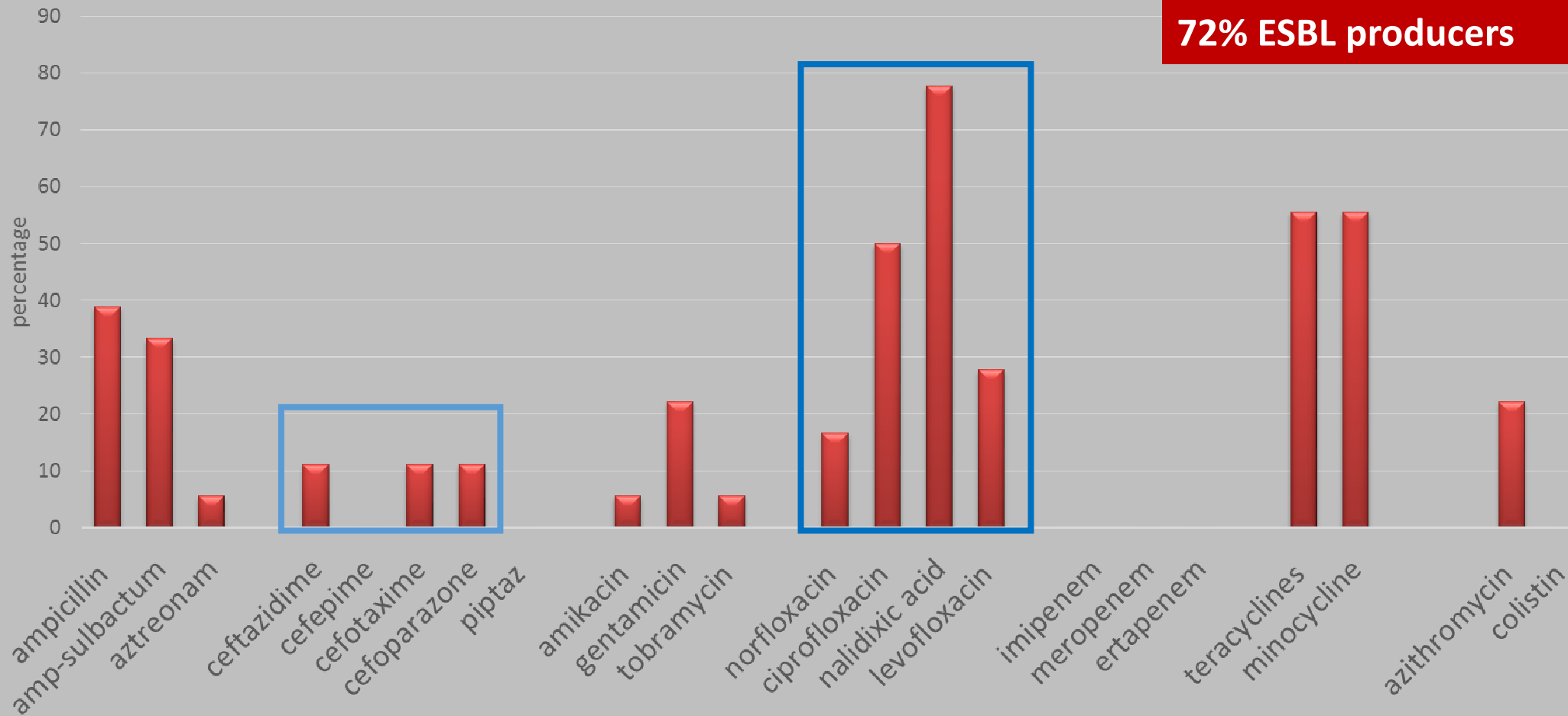
Antibiotic resistance profile of ETEC in humans (n=94)



High frequency of resistance to cephalosporins and fluoroquinolones

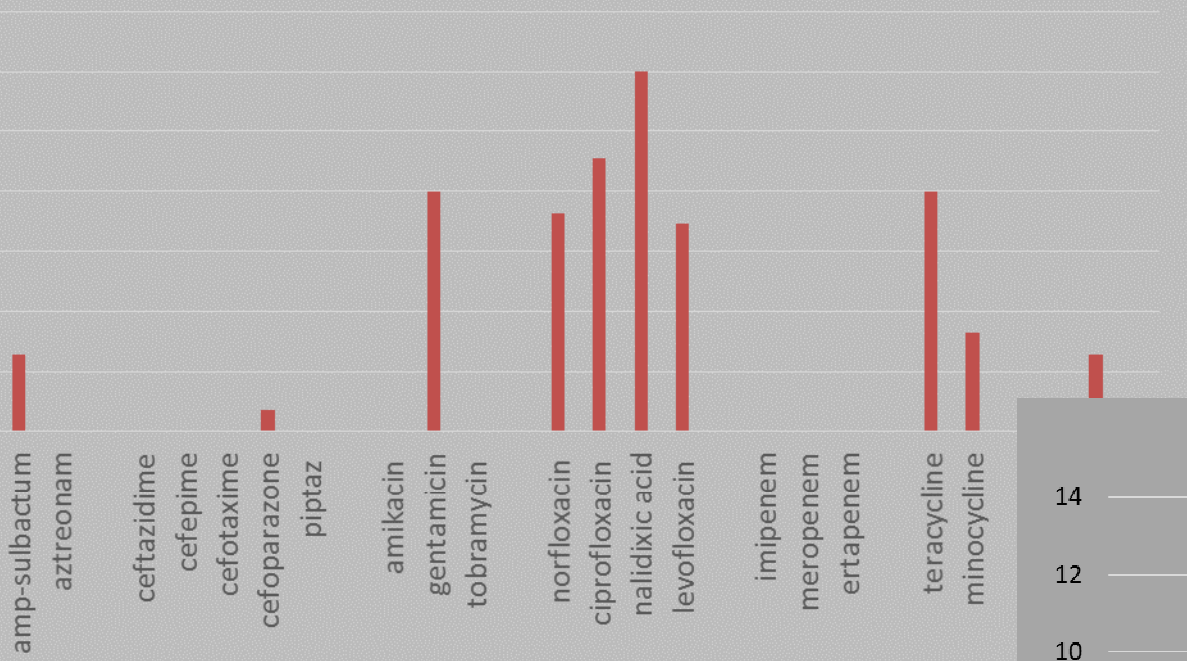
Antibiotic resistance profile in *Salmonella* from Humans (n=24)

72% ESBL producers



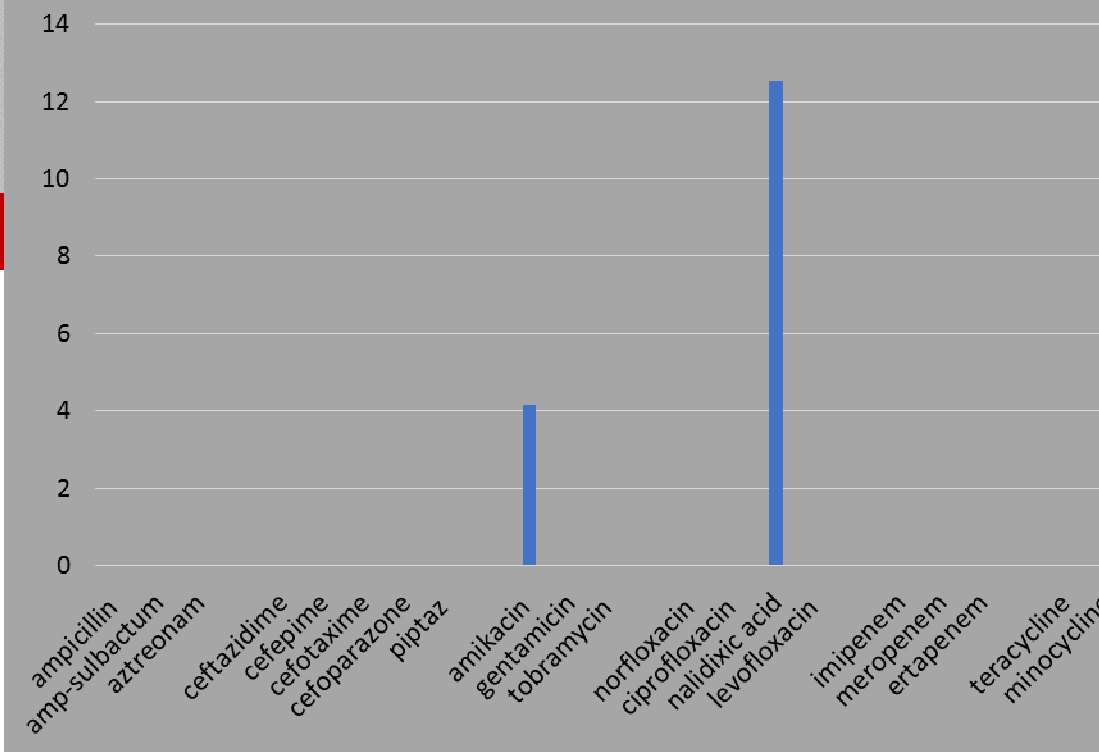
- High frequency of resistance to fluoroquinolones
- Resistance seen against 3rd generation cephalosporins
- No resistance to carbapenems

Resistance in Salmonella strains isolated from animal stool



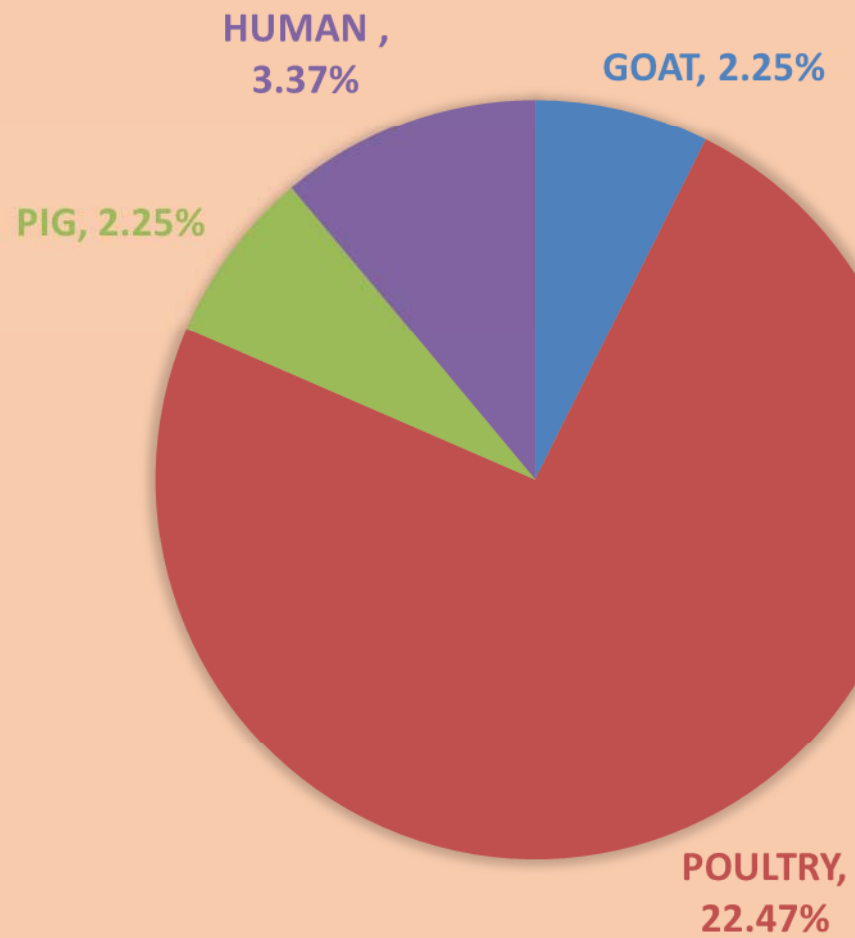
Resistance to fluroquinolones

Resistance in Salmonella strains isolated from animal meat

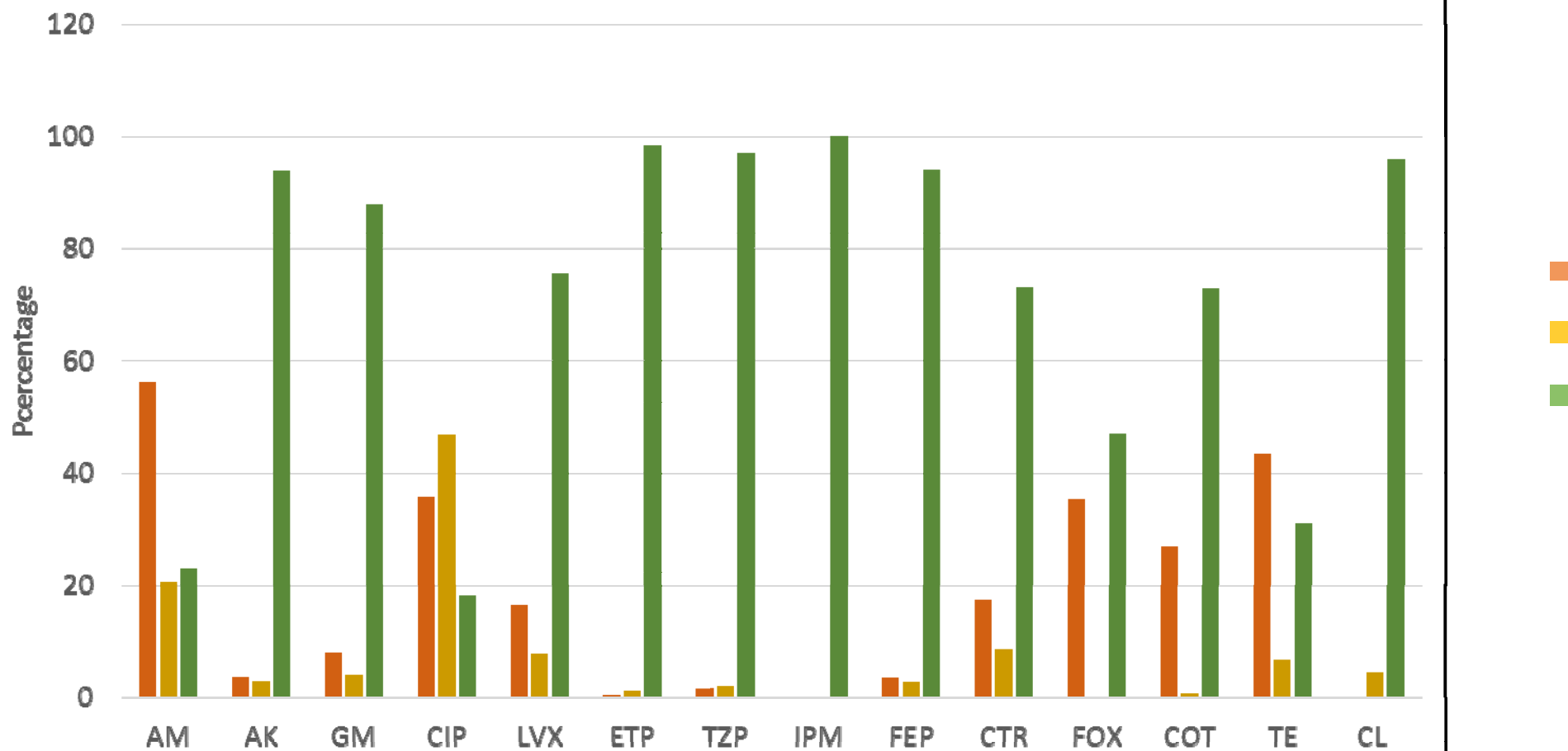


Low resistance was detected

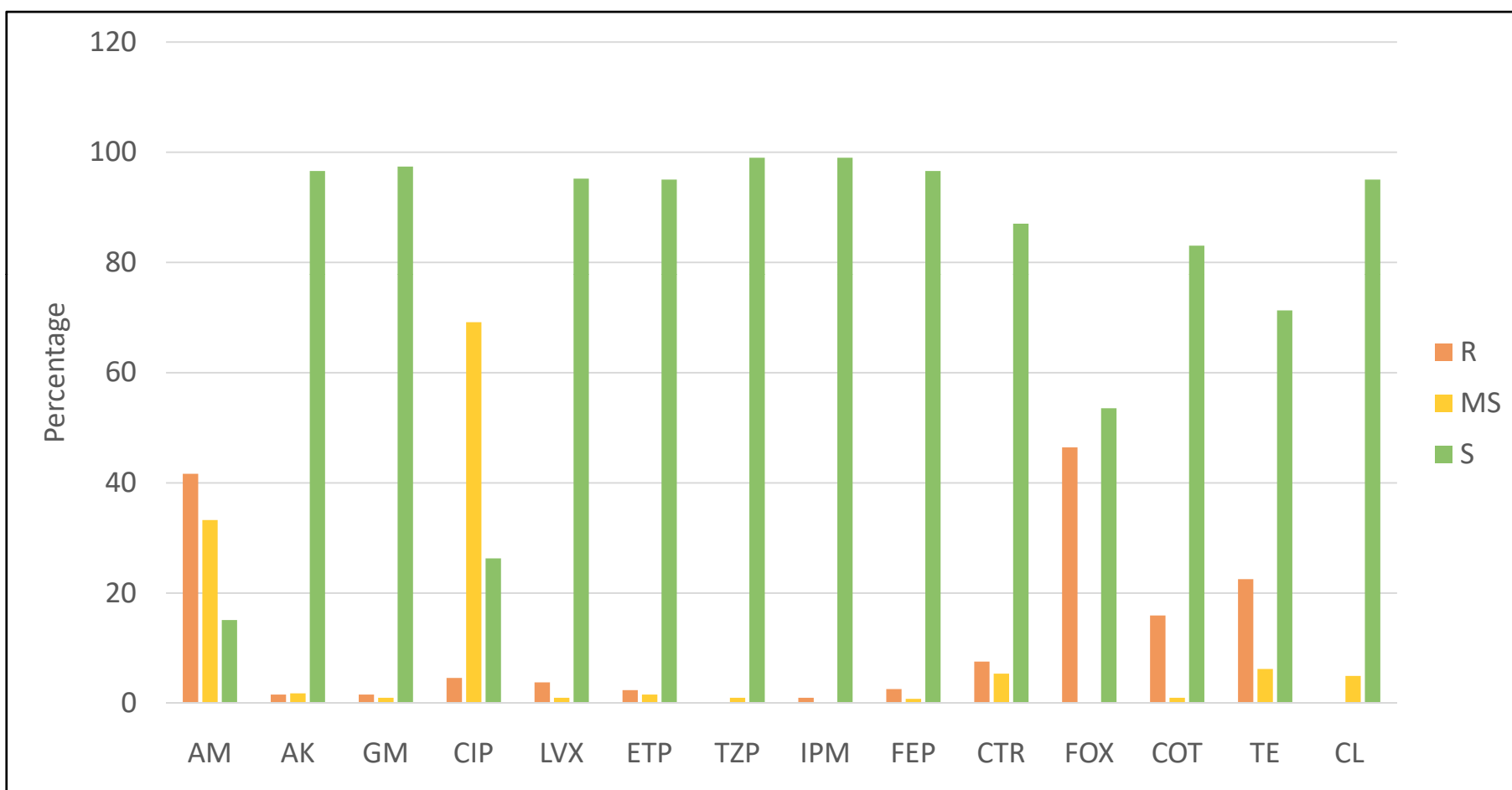
MULTI DRUG RESISTANT SALMONELLA



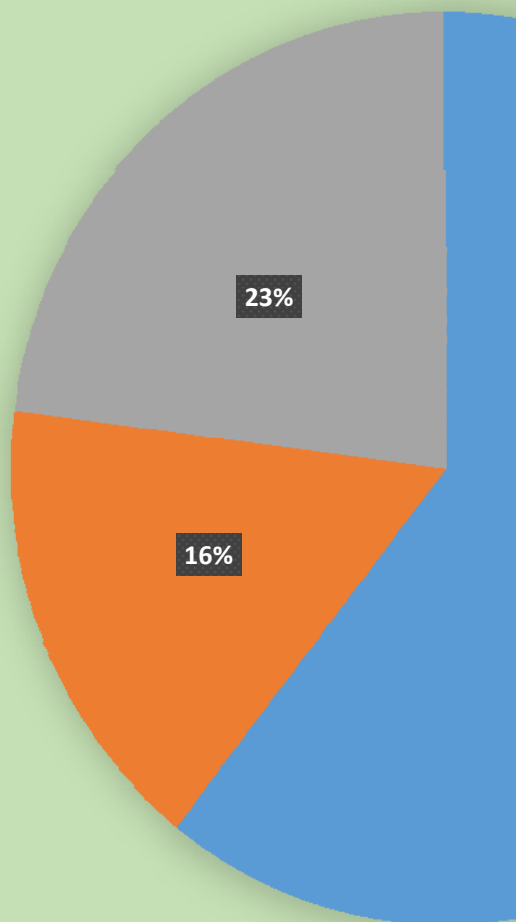
Antimicrobial susceptibility in commensal *E. coli* from animal stool samples



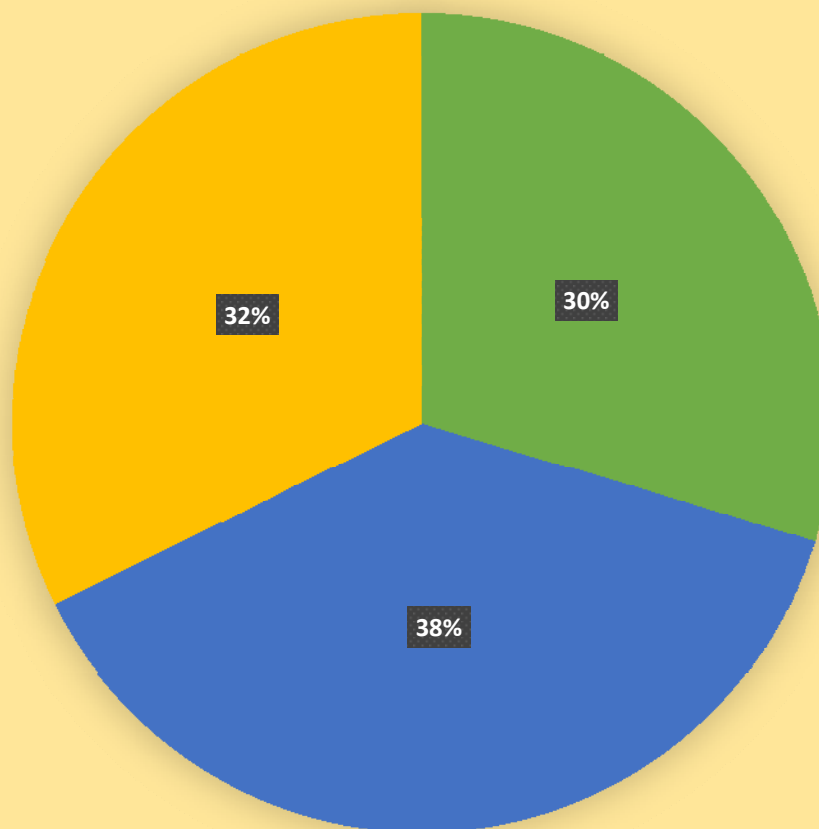
Antimicrobial susceptibility in commensal E. coli from meat samples



MDR Commensal *E. coli*



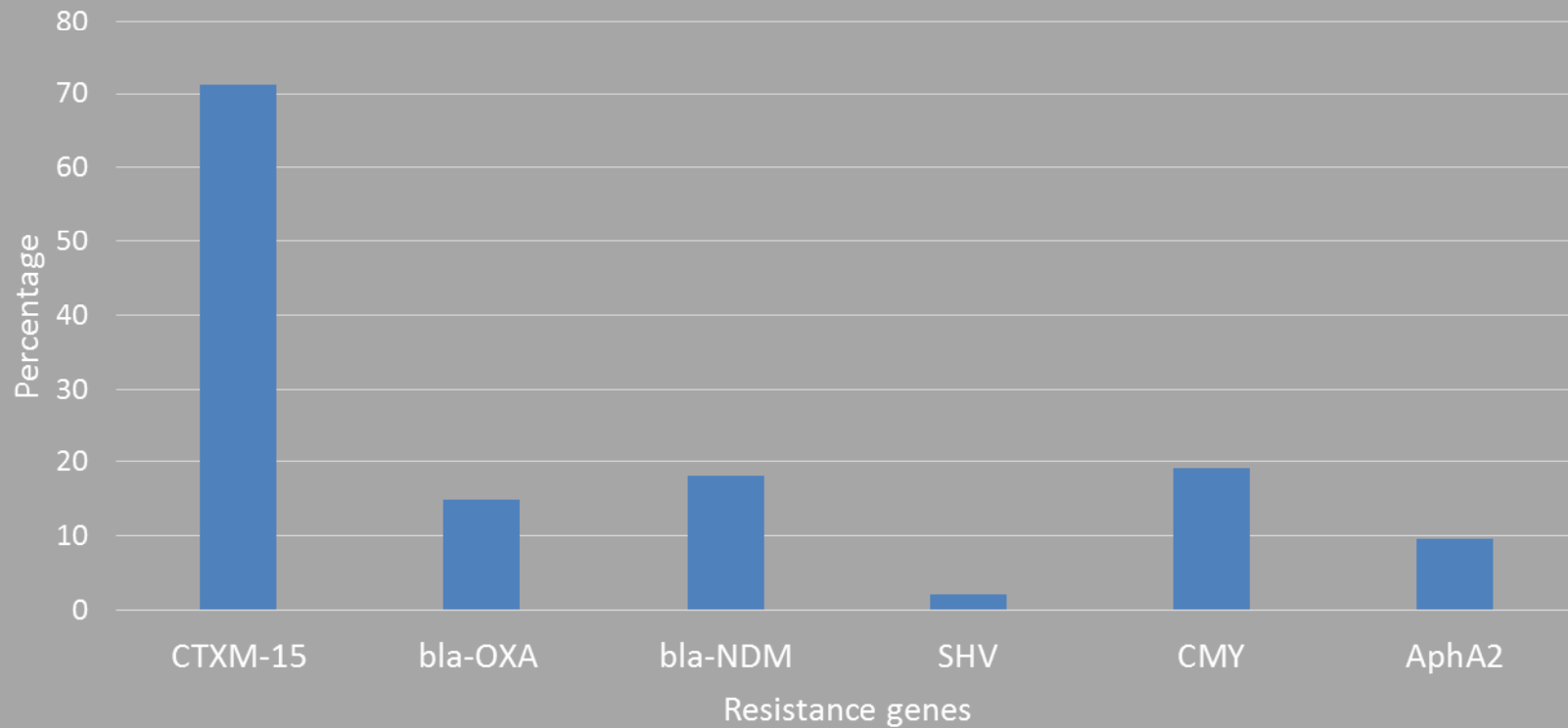
ESBL producing *E. coli*



■ chicken
■ goat
■ pig

Antibiotic resistance genes

Prevalence of resistance genes in ETEC isolates



MLST of ETEC isolates

One of the ETEC strain belongs to ST131 complex and some new sequence types have been identified

ST131 has emerged worldwide and is linked to *bla*_{CTX-M-15}. Extensive studies investigating the association of the multilocus sequence typing (MLST) clonal complex ST131 and *bla*_{CTX-M-15} have been reported from Canada, India, Kuwait, France, Switzerland, Portugal, Spain, Korea and Japan; worldwide dissemination of *bla*_{CTX-M-15} seems to be linked to this clonal complex, which is situated in the phylogenetic group B2. This demonstrates the need for constant surveillance in developing countries to prevent the spread of these multiresistant isolates

Another ETEC strain belong to ST 117 strains isolated worldwide (such as Brazil, USA, Egypt, Denmark, Sri Lanka, and South Korea) have ColV related plasmids, were involved in osteomyelitis and arthritis cases

These STs are commonly shared by APEC and human ExPEC strains

These hypothetical hybrid strains could have the potential to infect humans and birds.

Many new STs are found

Future work

Serotyping of *Salmonella* isolates

Perform MIC testing of *Campylobacter*, *Salmonella* and *E. coli* pathotypes isolates using sensititre plates

Estimate Antibiotic residue levels in meat samples by LC-MS-MS
Farm environments, water sewage using one health approach

Perform Whole Genome Sequencing of isolates to understand the transmission dynamics and determine AMR with more precision

Team Members



Dr. Balvinder Mohan, Dr. Chandra Deo, Harpreet, Naveen, Vinay Modgil, **Jaspreet Mahindroo**, Vishal, Varun Shahi, Meenakshi, Yousuf, Pinki Shankar, Ritu Verma, Bhaskar Samaui, Dhananjay

Acknowledgements

Dr Awa Adriana Kane (WHO-AGISAR) for funding

Dr Sidharth Thakur, Dr Paula, Dr Ruby

Network partners

Dr Bhavneet and Dr Surjit Singh

My lab and team mates

ICMR for funding

HOD Medical Microbiology for his support