CAPTURA's Approach for AMR Data Analysis and Capacity Building

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CAPTURA
Capturing data on Antimicrobial resistance Patterns and Trends in Use in Regions of Asia

MOTT MACDONALD

UKaid
from the British people

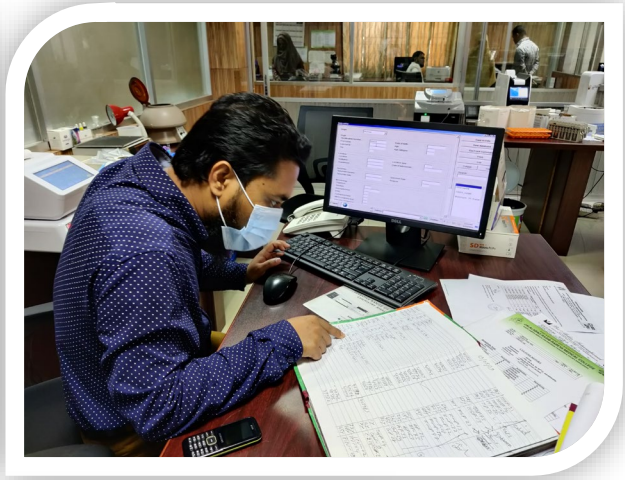
The Fleming Fund
Regional Grants

Table of Contents

CAPTURA Data Collection and Curation

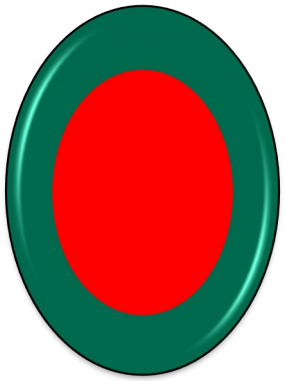
CAPTURA DATA: Collection and Curation

- Laboratory Log-books
  - Data source identification
  - WHONET training
  - Digitalization using WHONET
  - Upload to CAPTURA warehouse
- Laboratory Information Systems
  - Support data extraction
  - BacLink training
  - Data curation
  - Upload to CAPTURA warehouse



Key AMR Highlights

CAPTURA's AMR Engagement (SA and SEA)

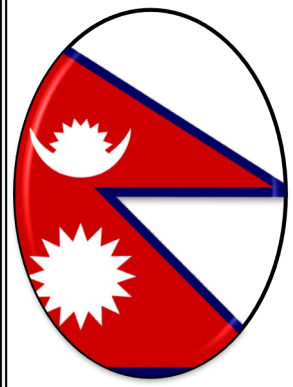


34 labs

1040166 rows

Positive: 288,851

Negative: 751,315



28 labs

663601 rows

Positive: 155,756

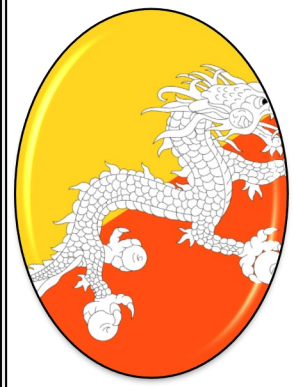
Negative: 507,845

3 labs

496222 rows

Positive: 140,382

Negative: 355,840

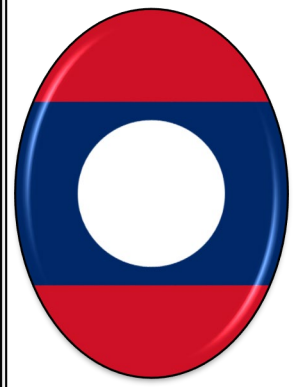


4 labs

126319 rows

Positive: 47,866

Negative: 78,453



*1 labs

29729 rows

(centrally collected from 30 labs)

Positive: 6,685

Negative: 23,044

1 lab

12334 rows

Positive: 12,334

1 lab

1808 rows

Positive: 1,288

Negative: 520

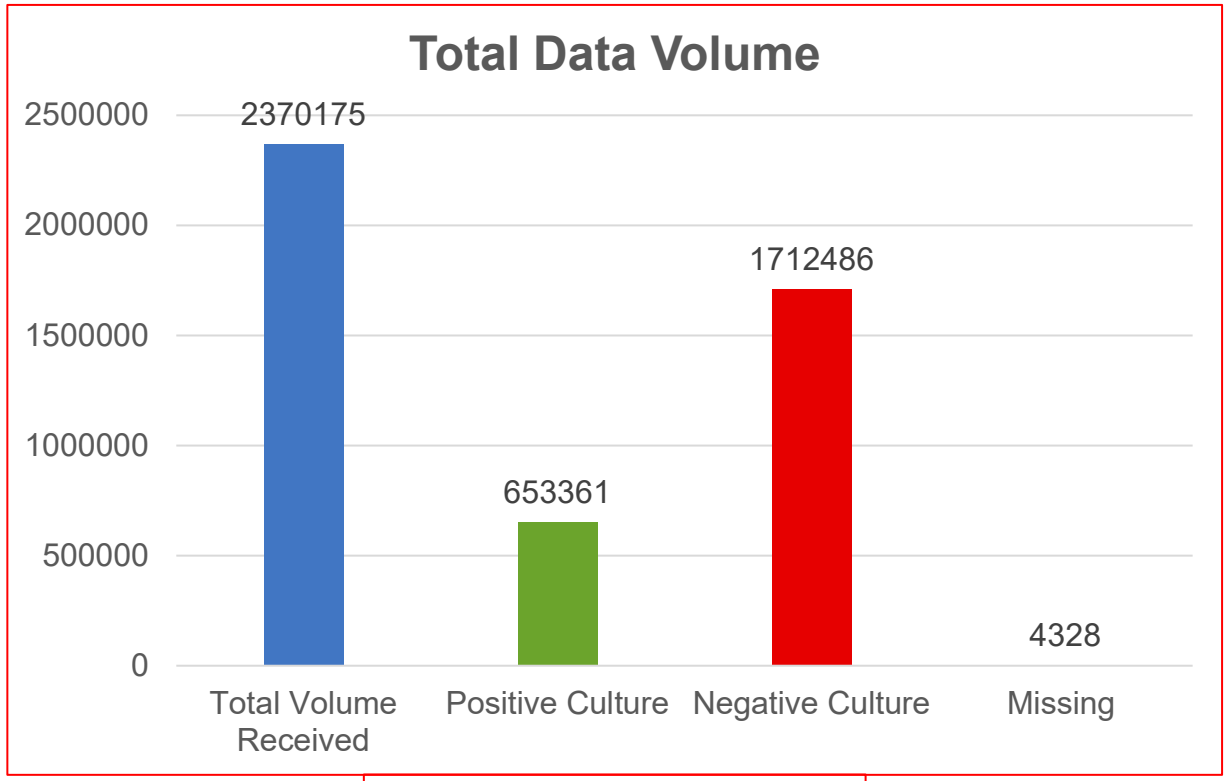
3 lab

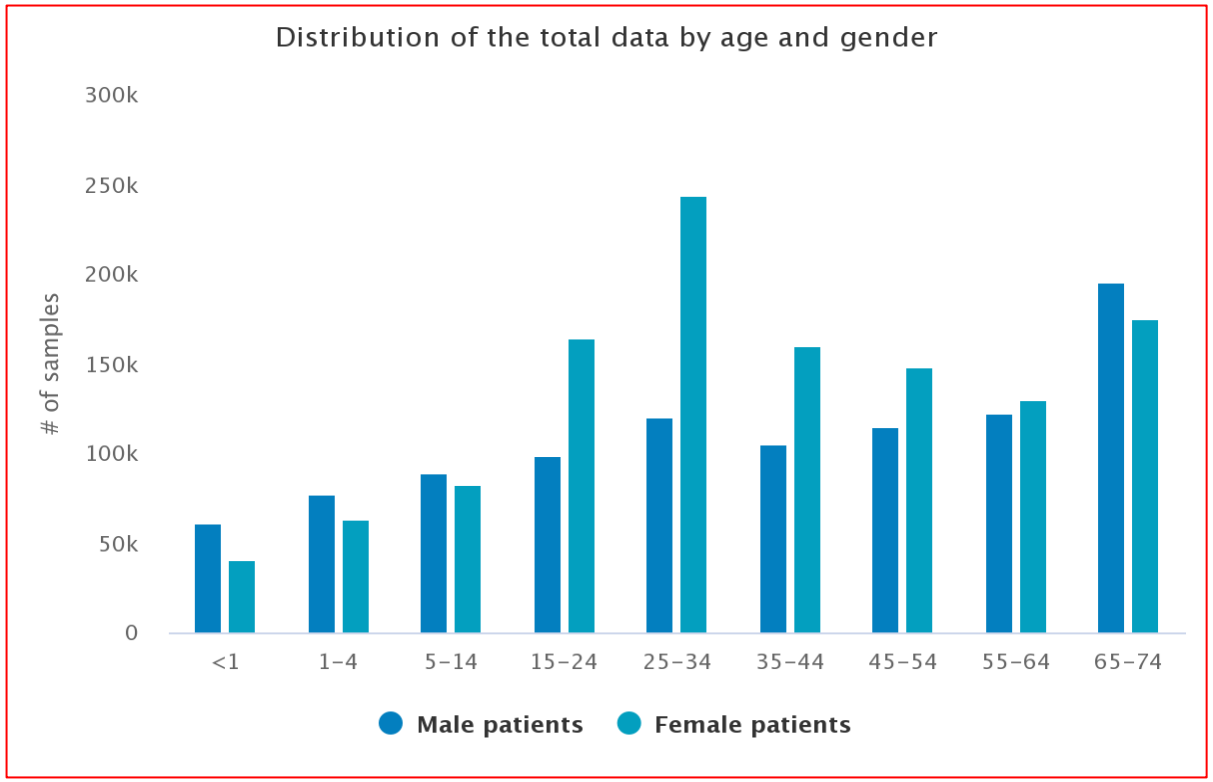
Antibiogram

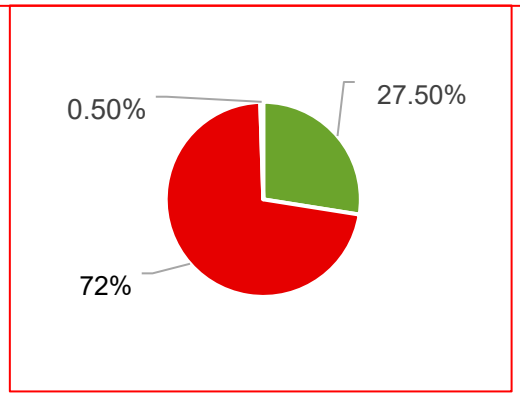
Country Engagement Period: May 2019 till March 2022

Identified/Collated 2,370,175 rows of AMR data from 71 labs

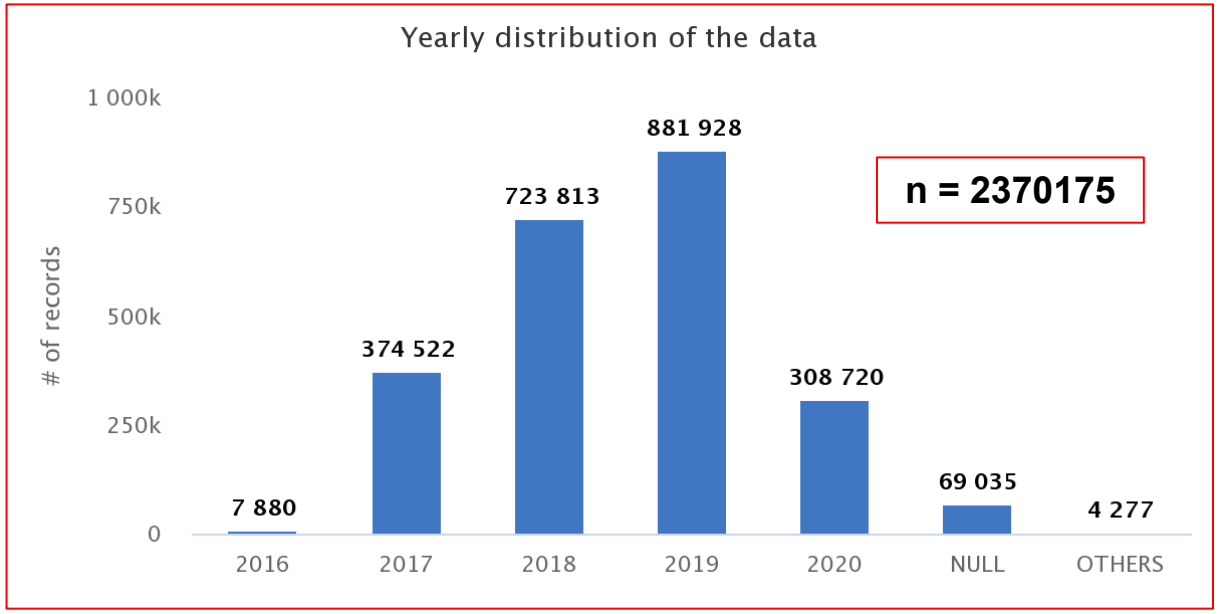
Descriptive Statistics – Aggregated for 7 countries

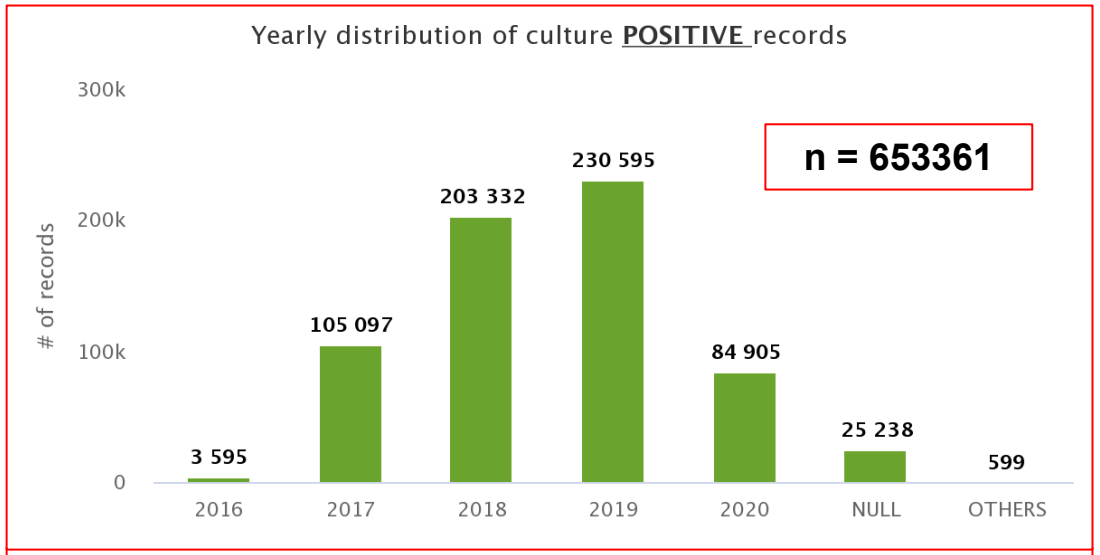


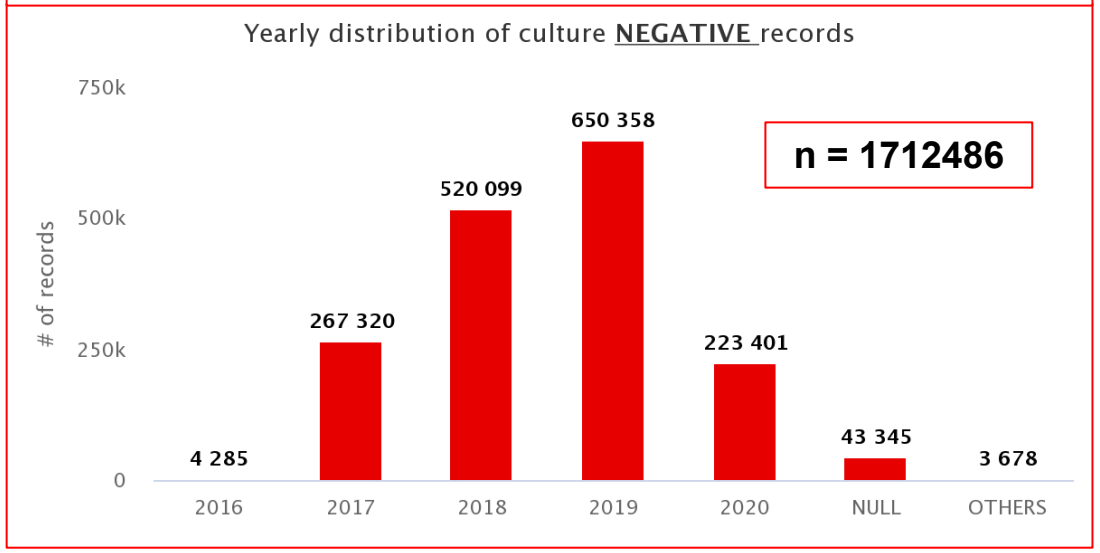




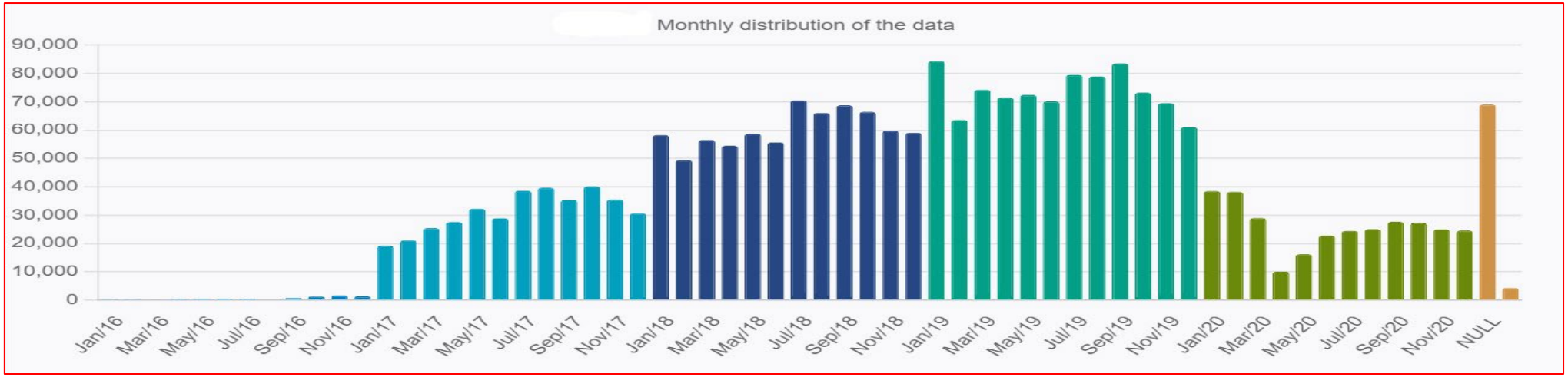
Descriptive Statistics – Culture Results



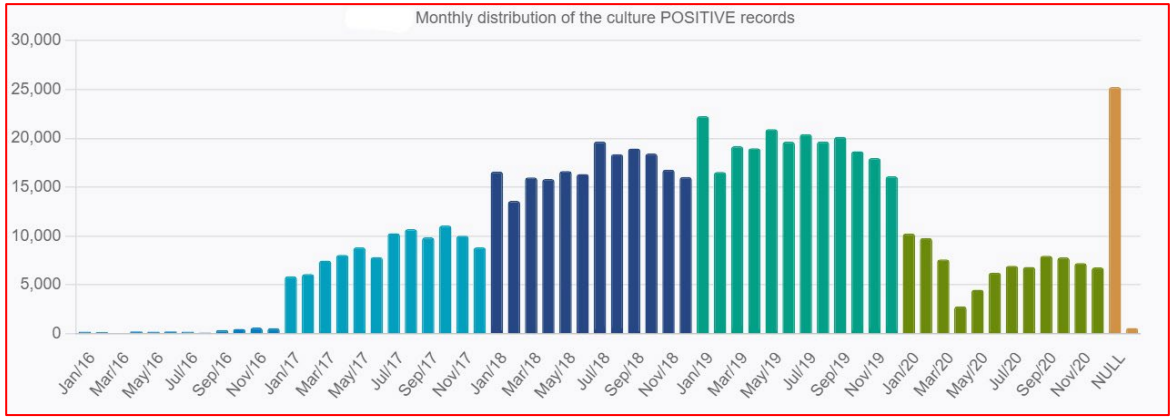




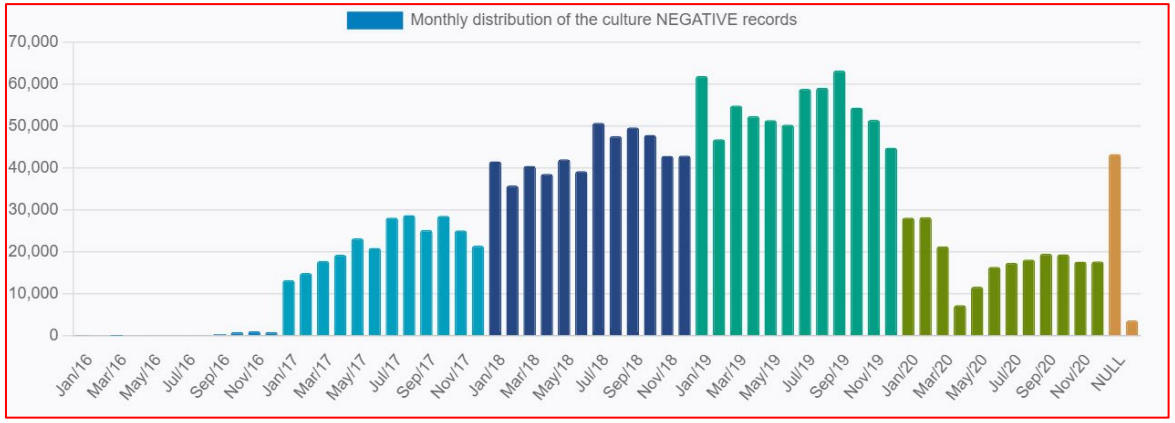
Descriptive Statistics – Monthly distribution of collected records



Total records

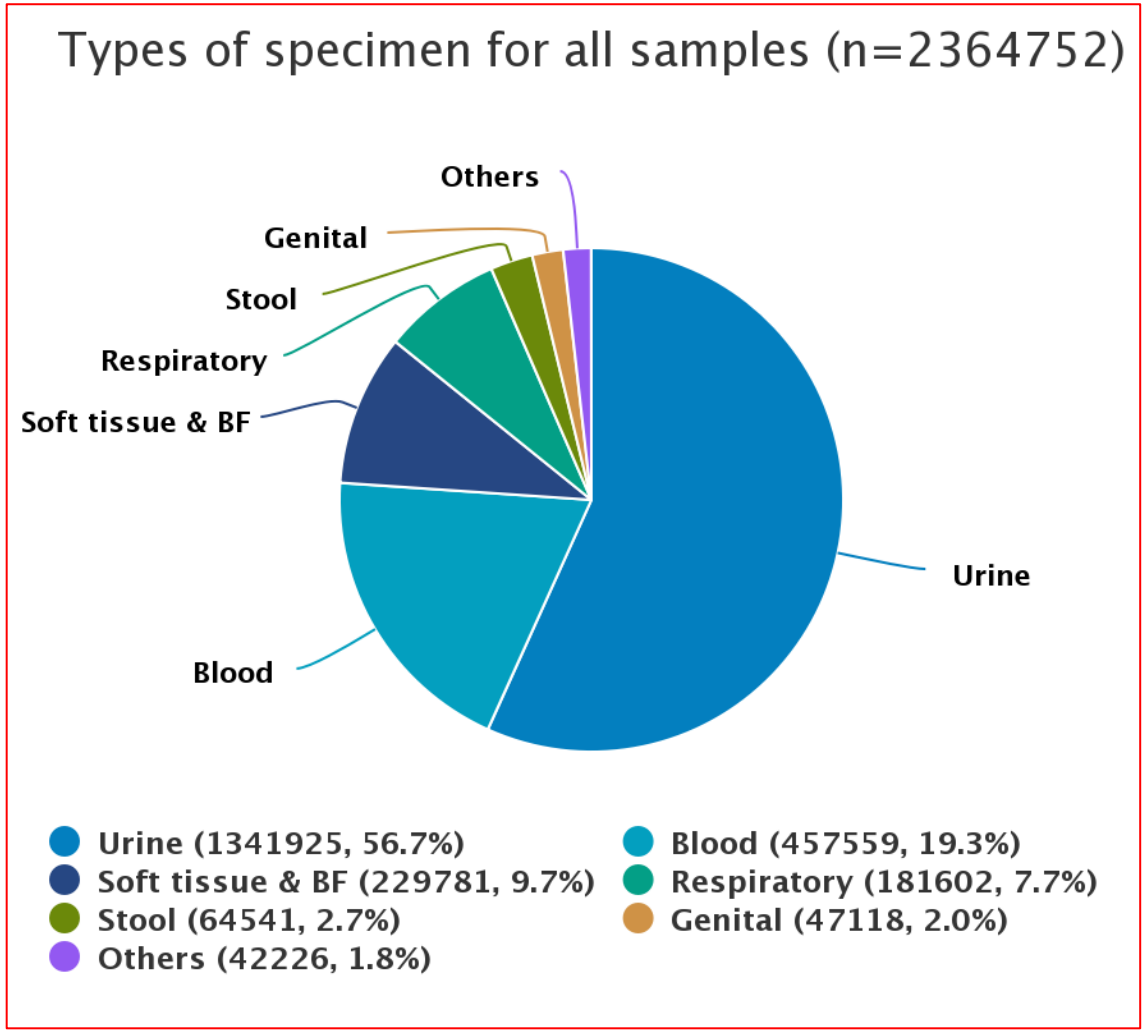


Culture positive records

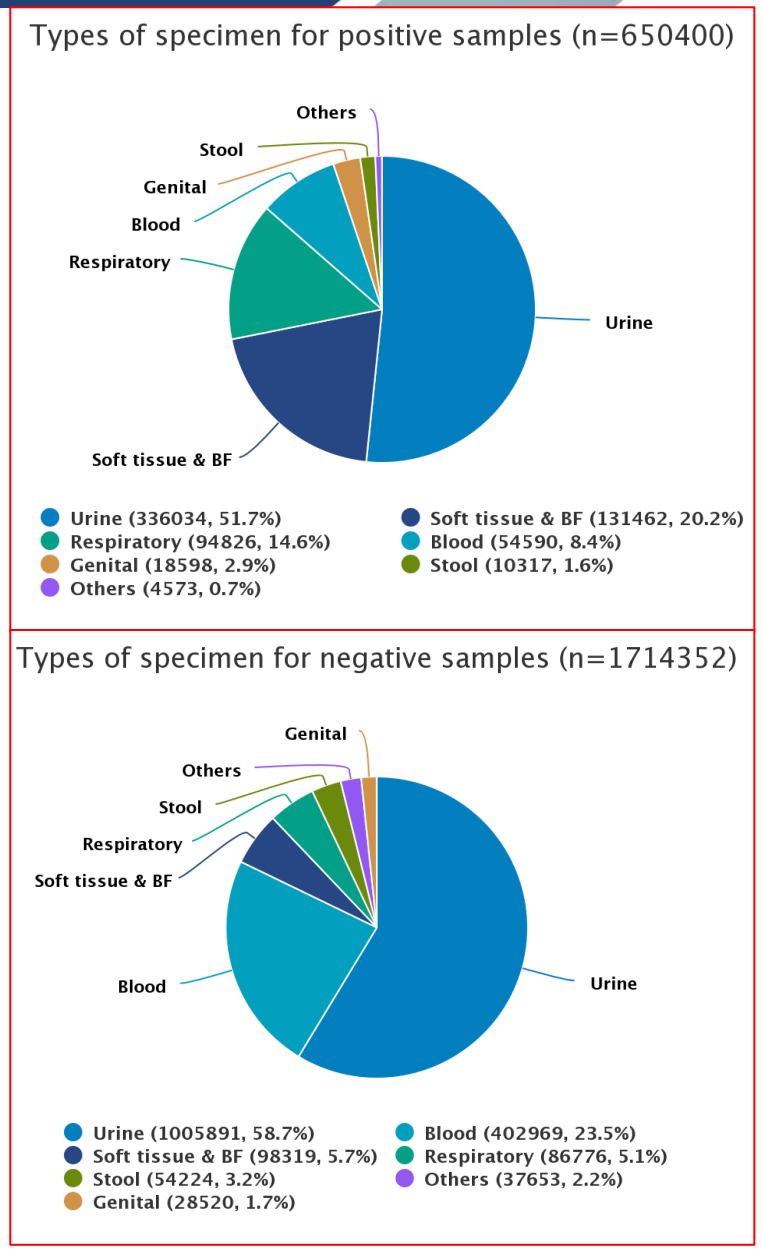


Culture negative records

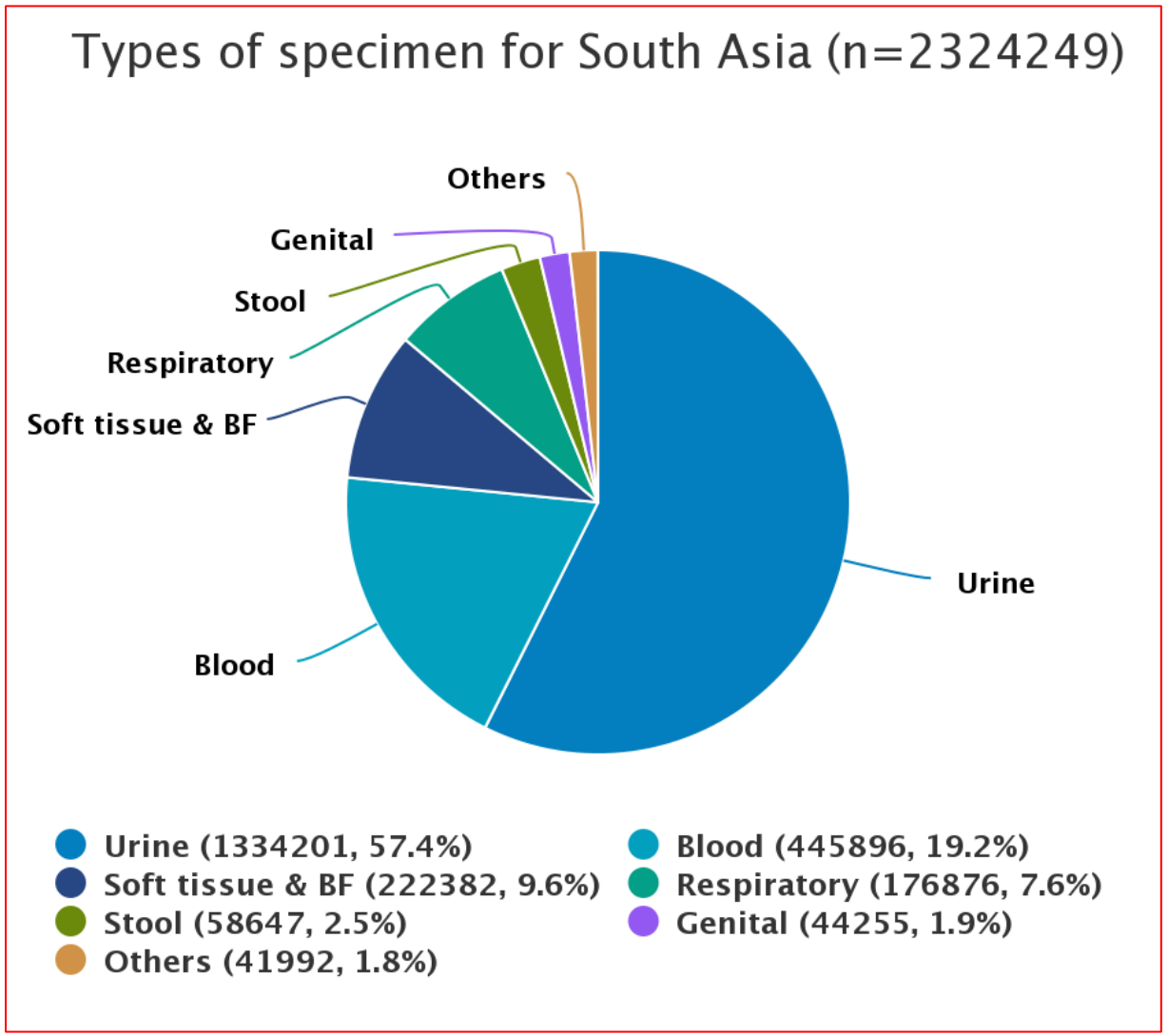
Descriptive Statistics – Specimen processed

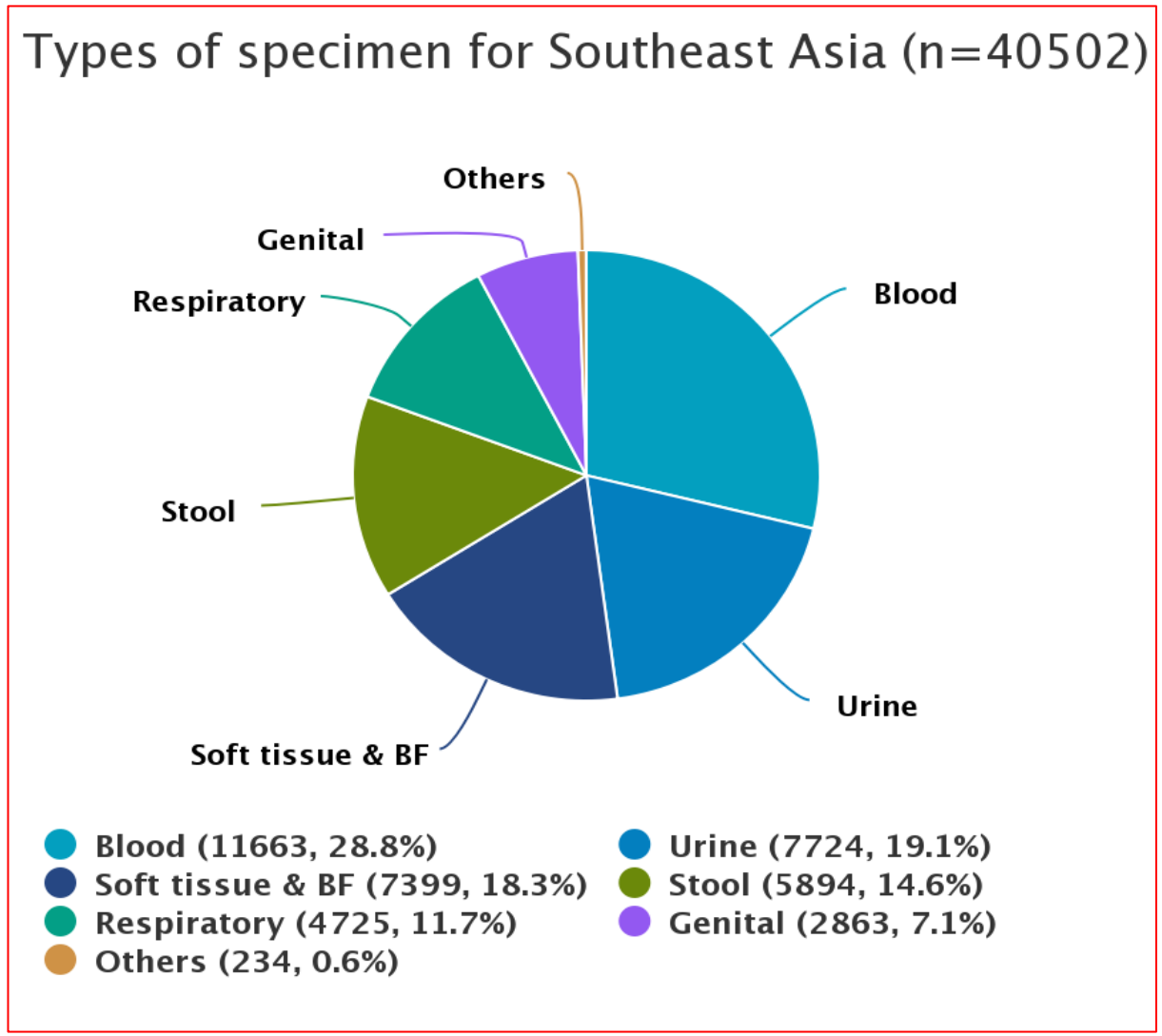


Note: Total specimen with no type defined : 5,423

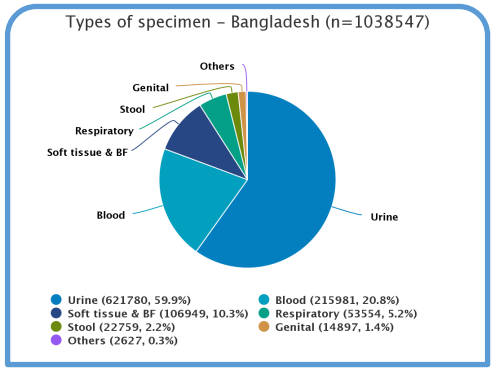


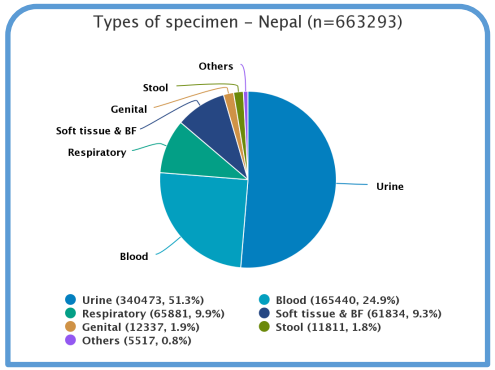
Descriptive Statistics – Specimen processed by region

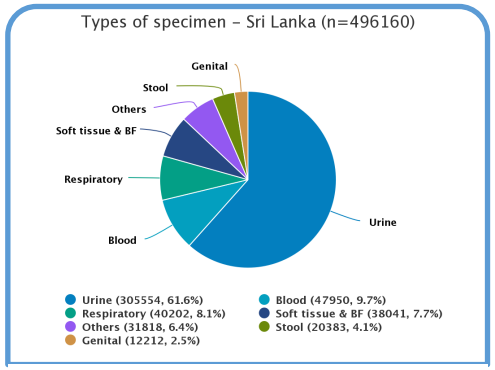


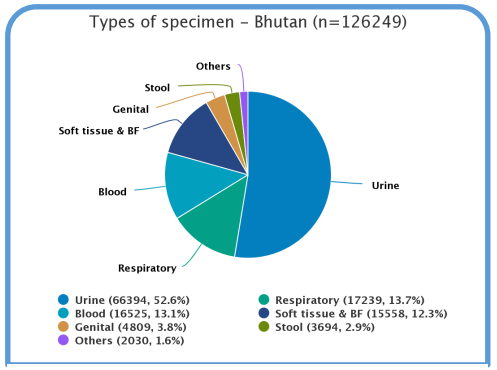


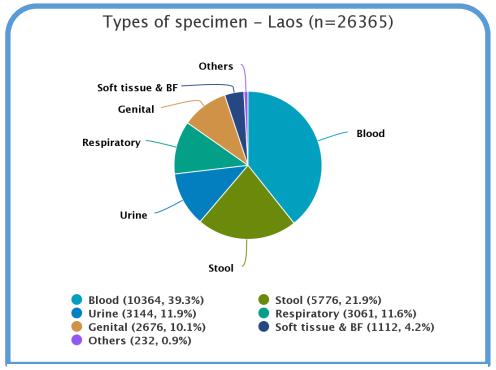
Descriptive Statistics – Specimen types by country

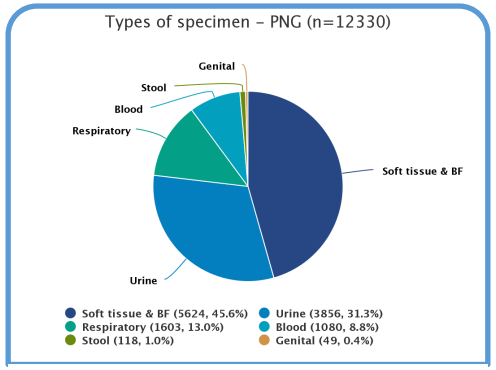


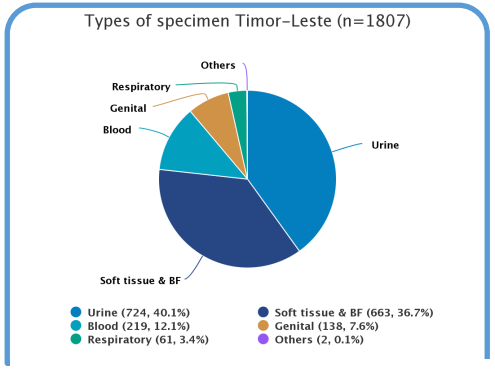




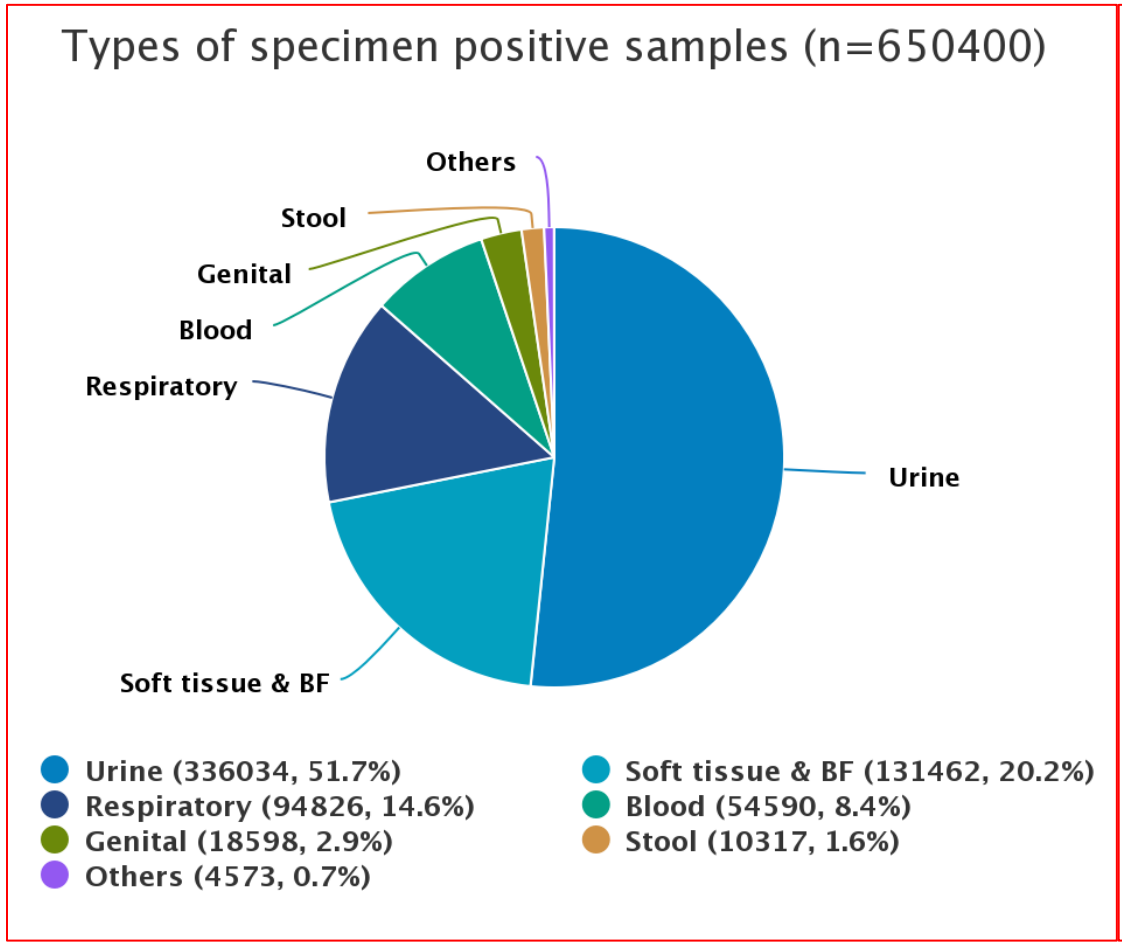


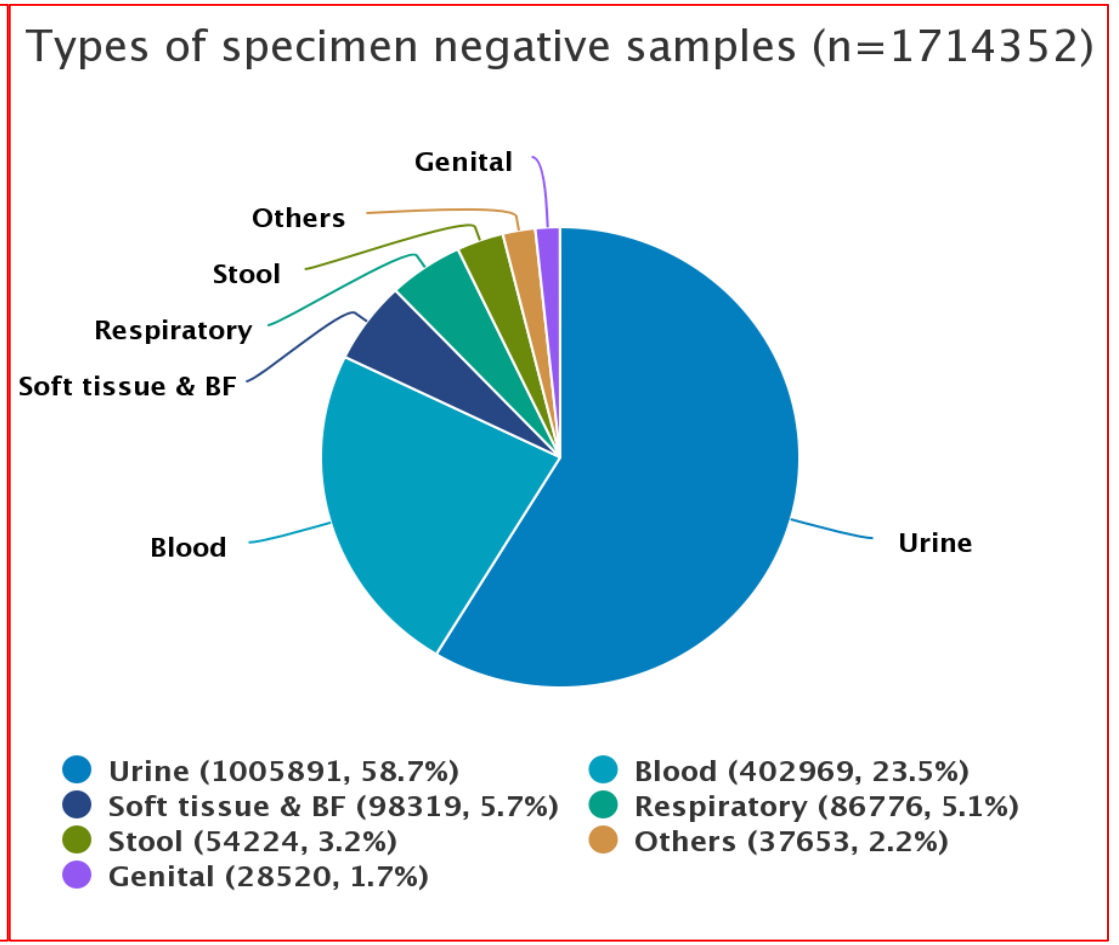




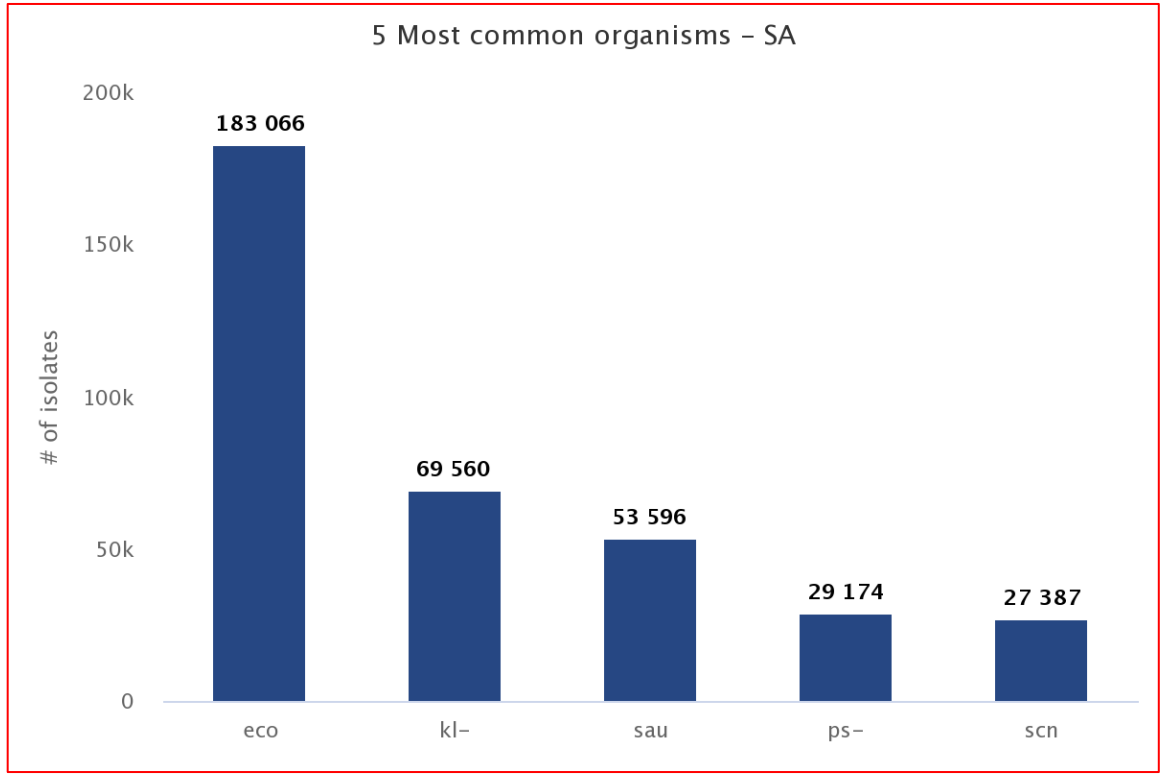


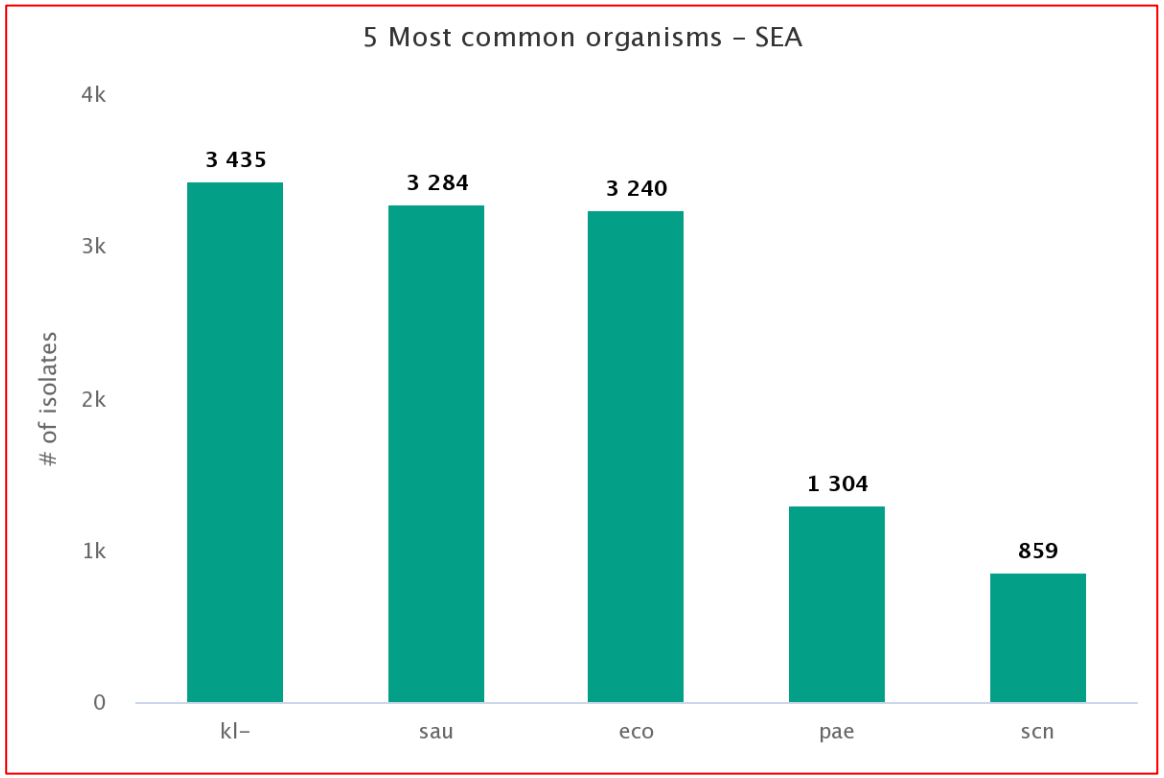
Descriptive Statistics – Sample distribution





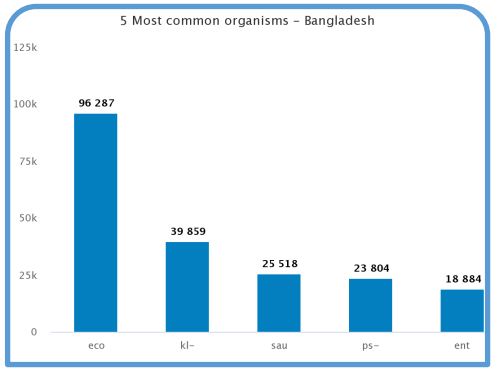
Top 5 Organism – All Specimens (SA/SEA)

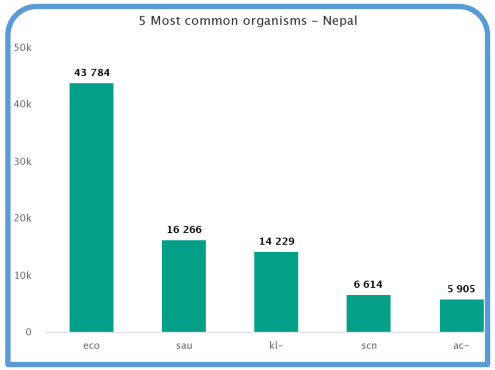


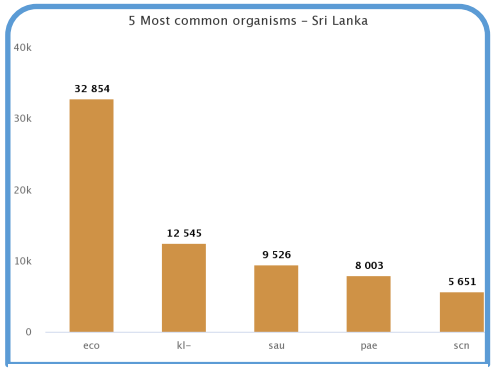


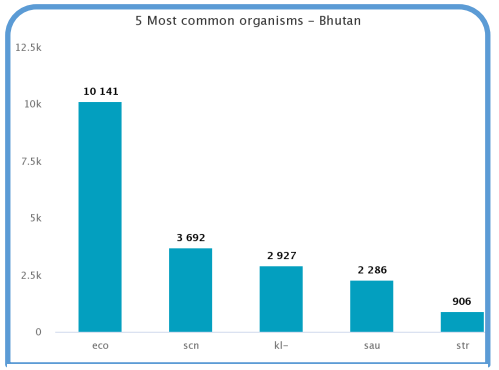
eco	Escherichia coli	ps-	Pseudomonas sp.
kl-	Klebsiella sp.	scn	Staphylococcus, coagulase negative
sau	Staphylococcus aureus	pae	Pseudomonas aeruginosa

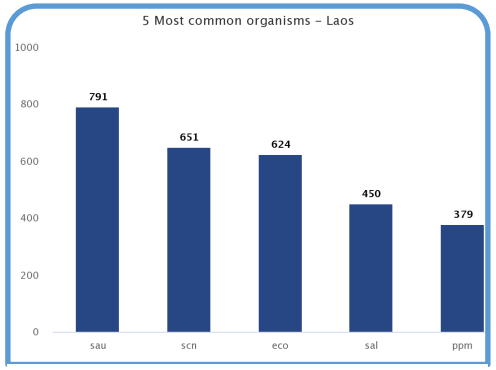
Top 5 organism – Country Specific

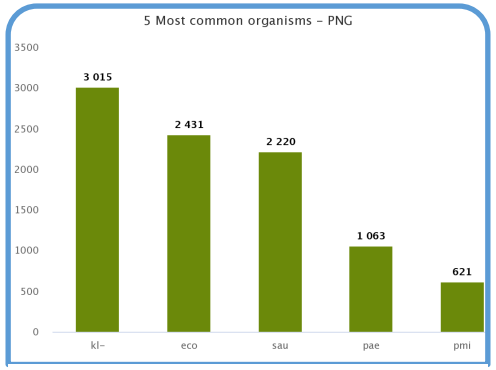


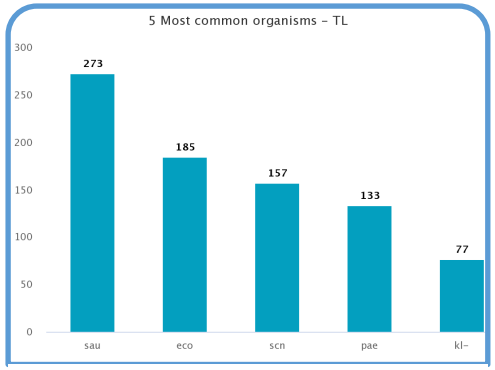




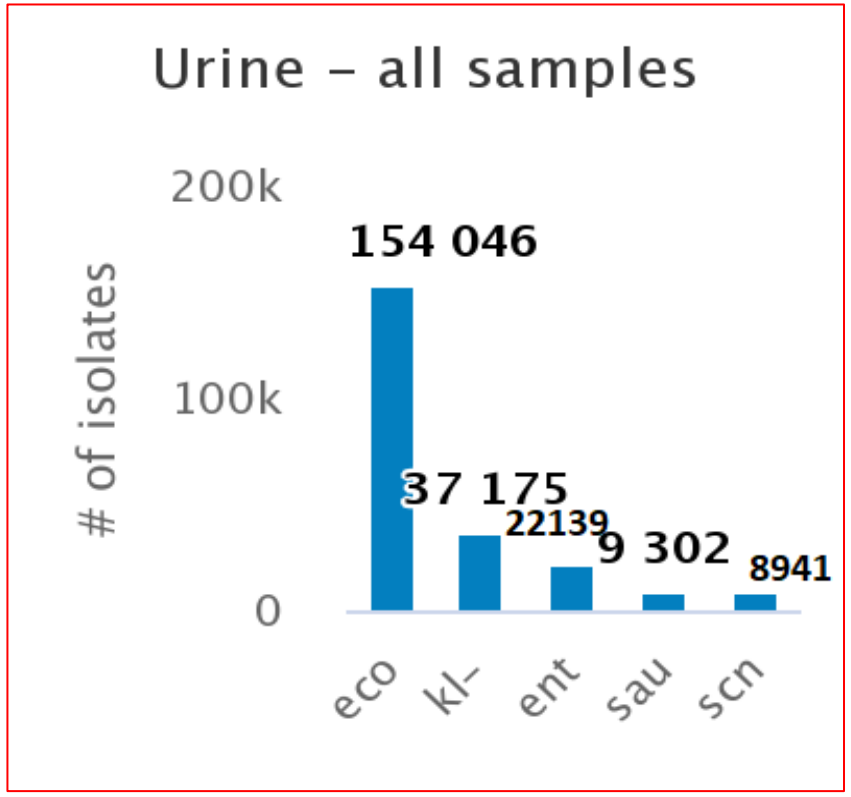


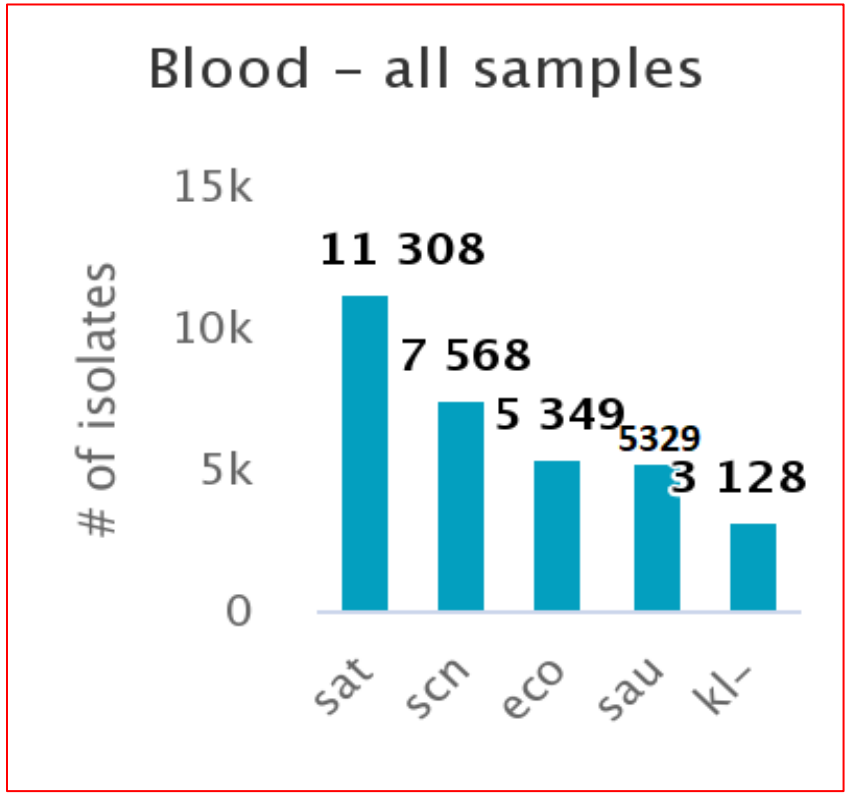






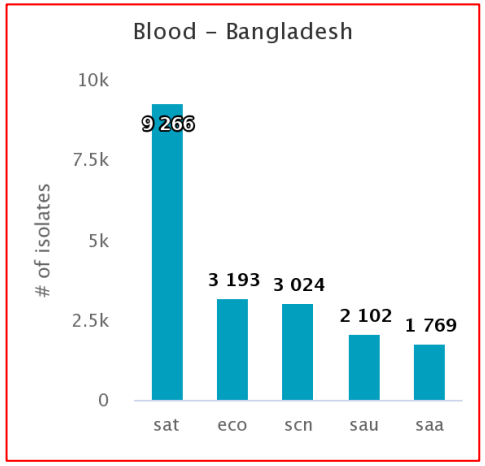
Organism by specimen – Urine and Blood

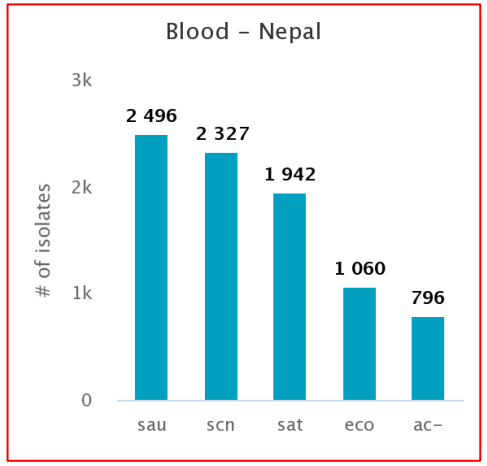


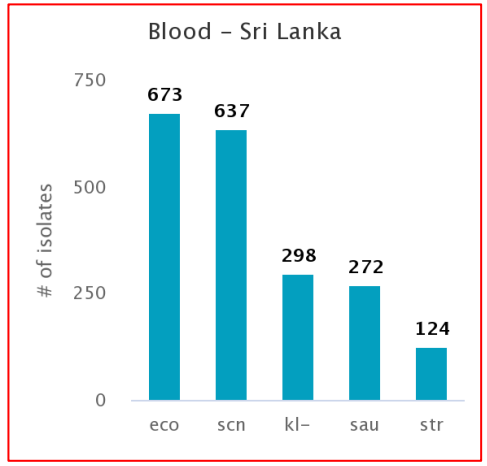


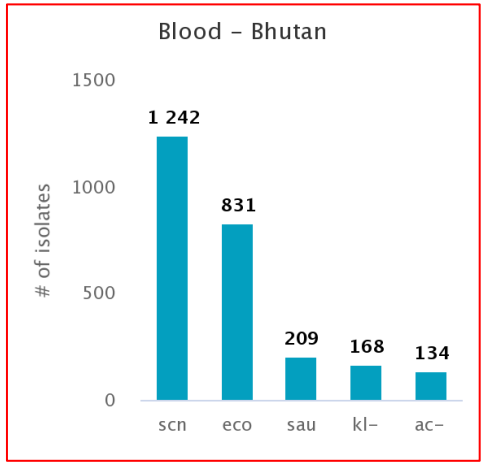
eco	Escherichia coli	ent	Enterococcus sp.
kl-	Klebsiella sp.	scn	Staphylococcus, coagulase negative
sau	Staphylococcus aureus	sat	Salmonella Typhi

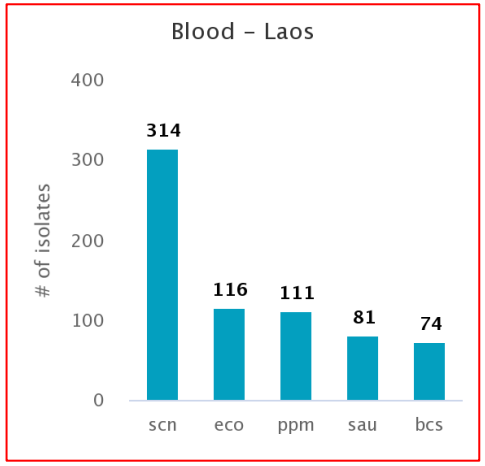
Top 5 isolates from blood: All countries

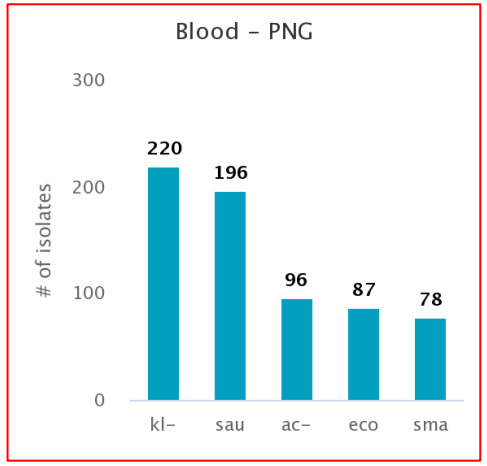


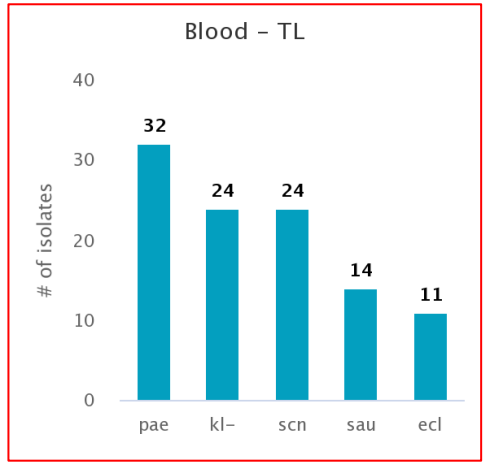






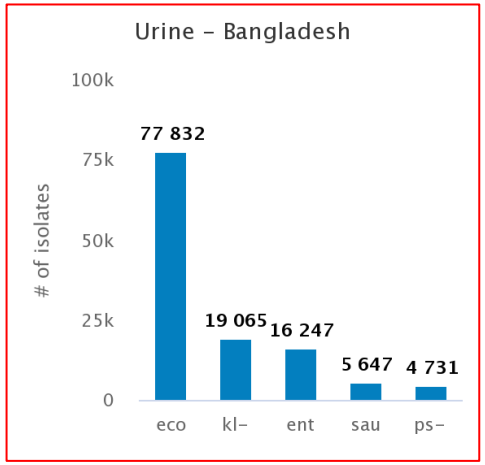


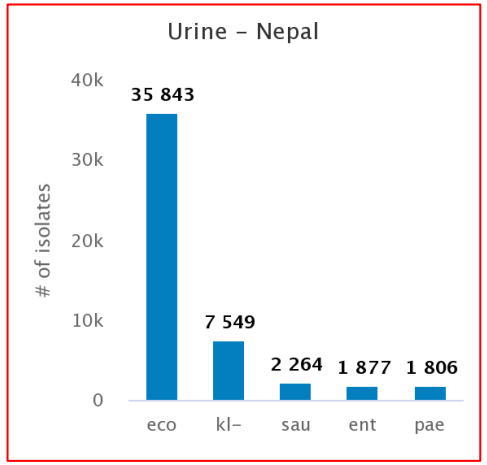


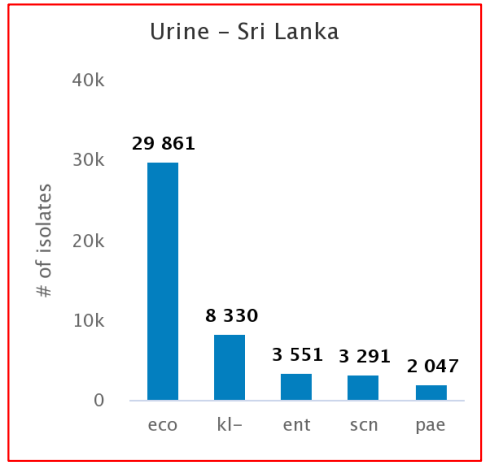


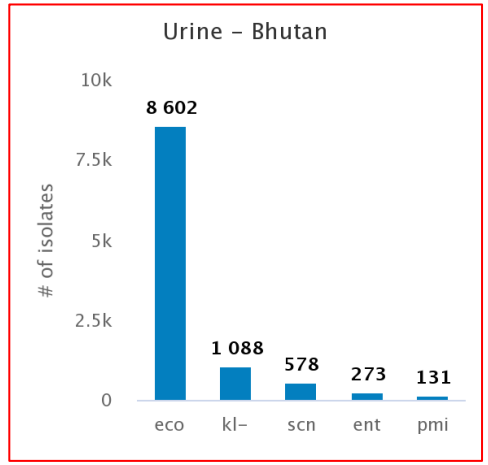
eco	Escherichia coli
sau	Staphylococcus aureus
kl-	Klebsiella sp.
ps-	Pseudomonas sp.
ent	Enterococcus sp.
bcs	Bacillus sp.
ac-	Acinetobacter sp.
saa	Salmonella Paratyphi A
scn	Staphylococcus, coagulase negative
sal	Salmonella sp.
ppm	Burkholderia pseudomallei
sma	Serratia marcescens
Str	Streptococcus spp.
sat	Salmonella Typhi
pae	Pseudomonas aeruginosa
ecl	Enterobacter cloacae

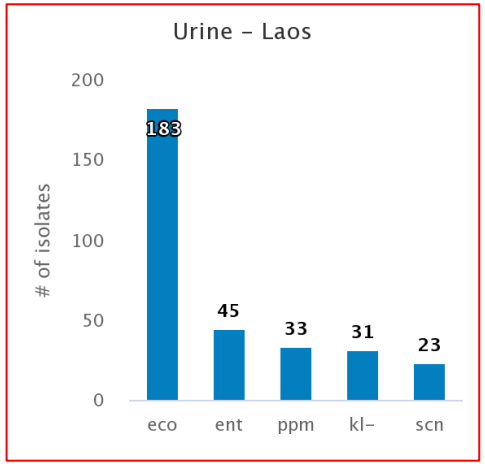
Top 5 isolates from urine: All countries

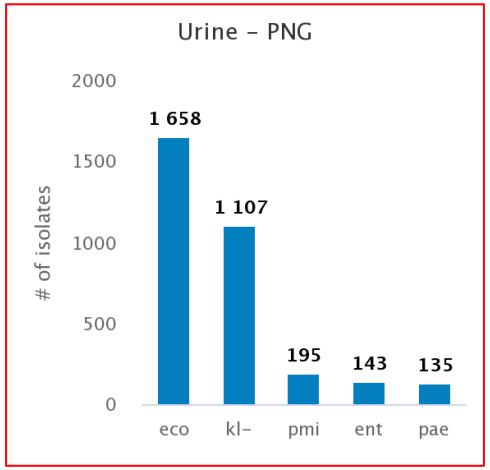


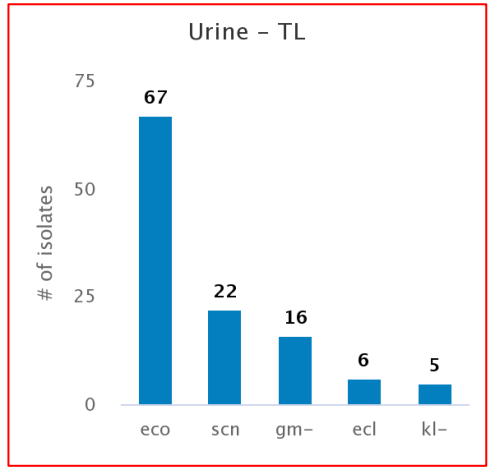






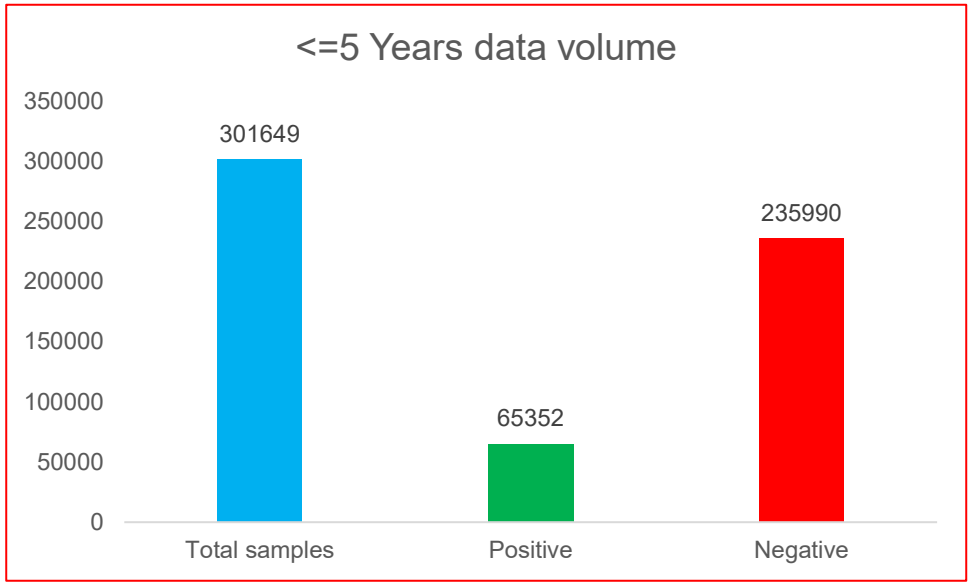


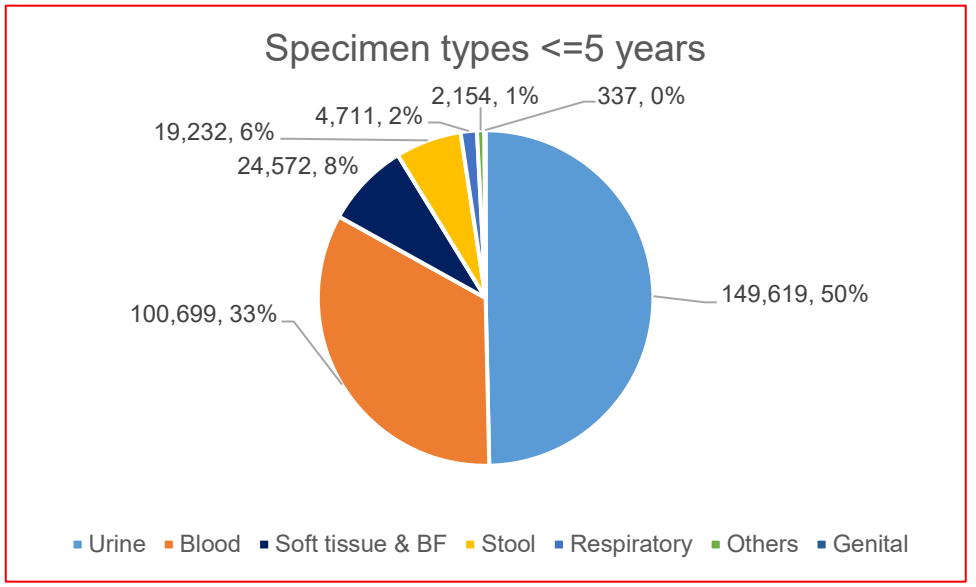


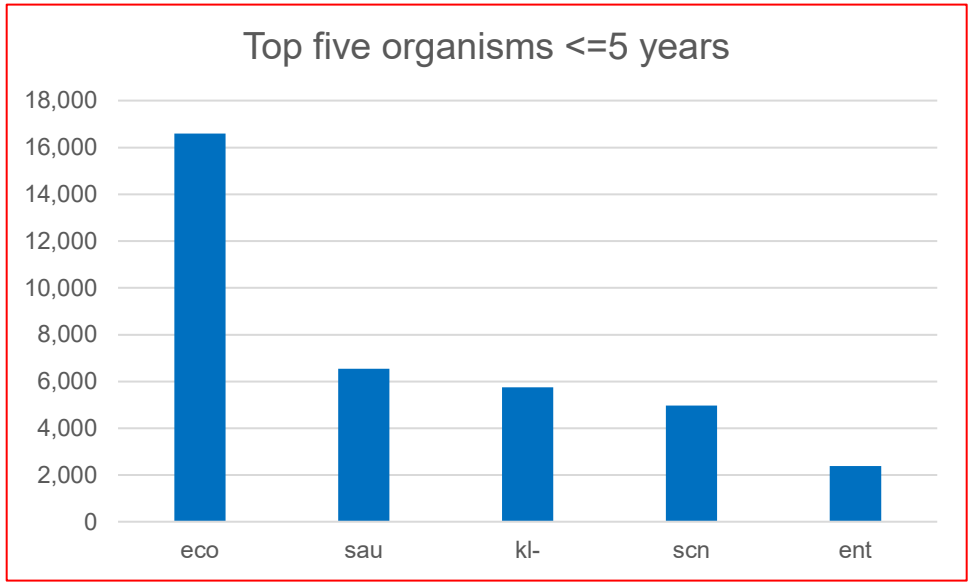


eco	Escherichia coli
sau	Staphylococcus aureus
kl-	Klebsiella sp.
ps-	Pseudomonas sp.
ent	Enterococcus sp.
scn	Staphylococcus, coagulase negative
ppm	Burkholderia pseudomallei
pmi	Proteus miribilis
gm-	Gram negative bacteria
pae	Pseudomonas aeruginosa
ecl	Enterobacter cloacae

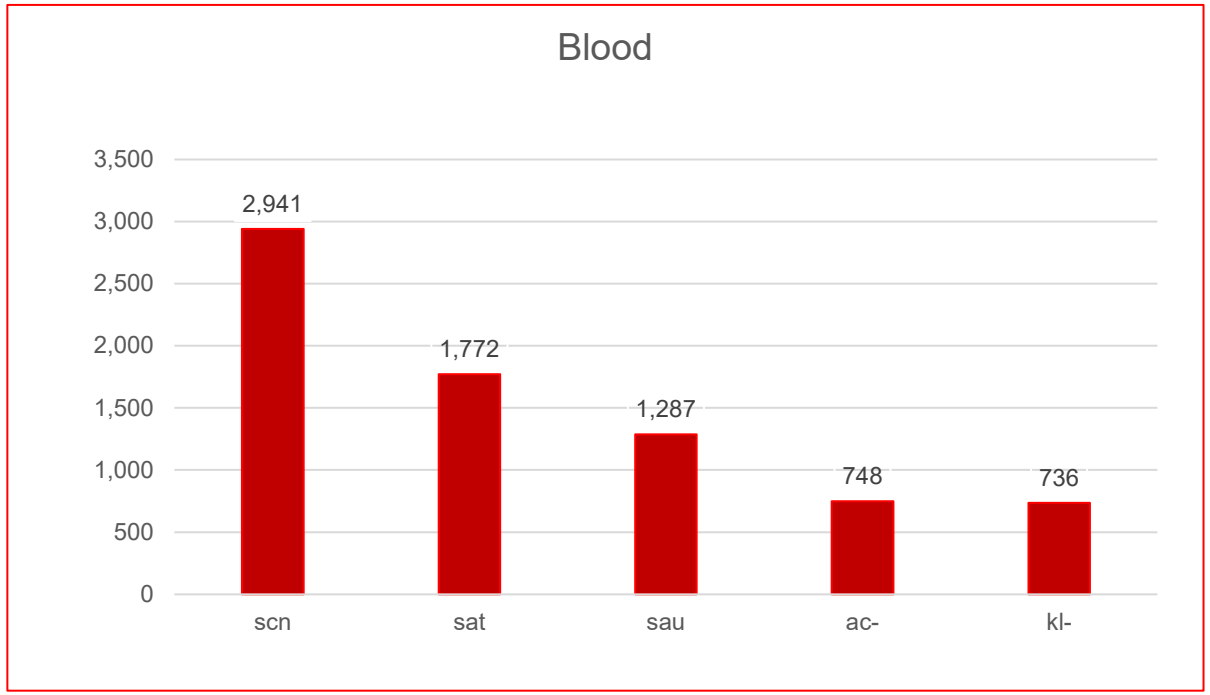
<5 Years samples and top five organisms

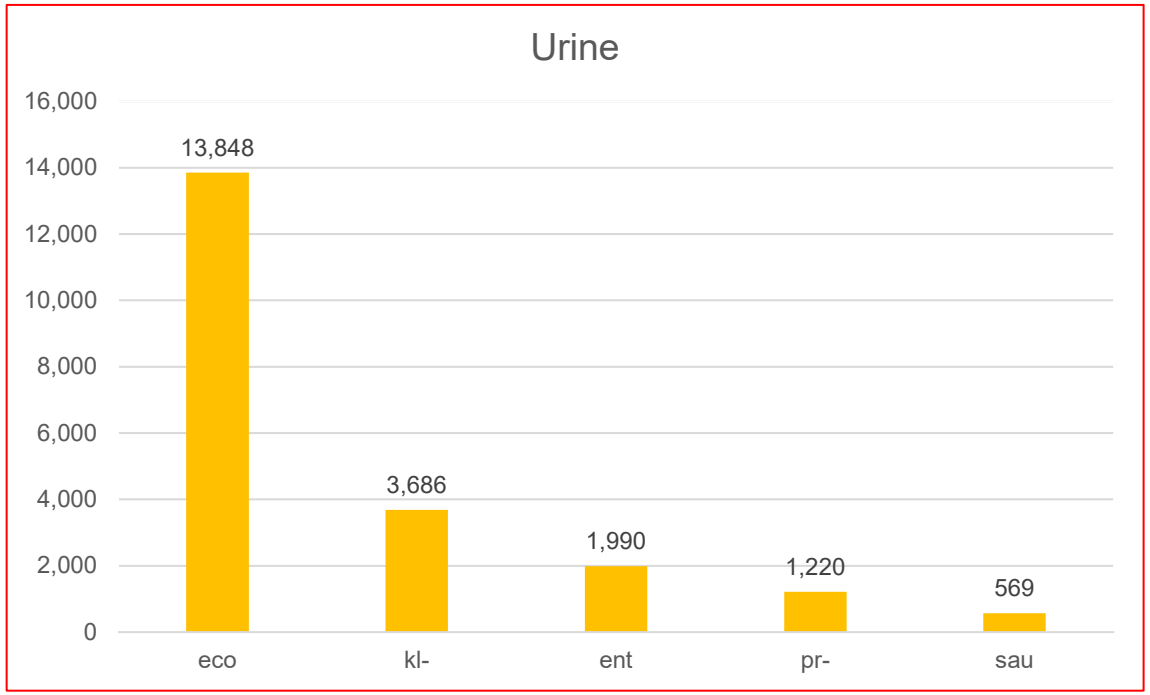






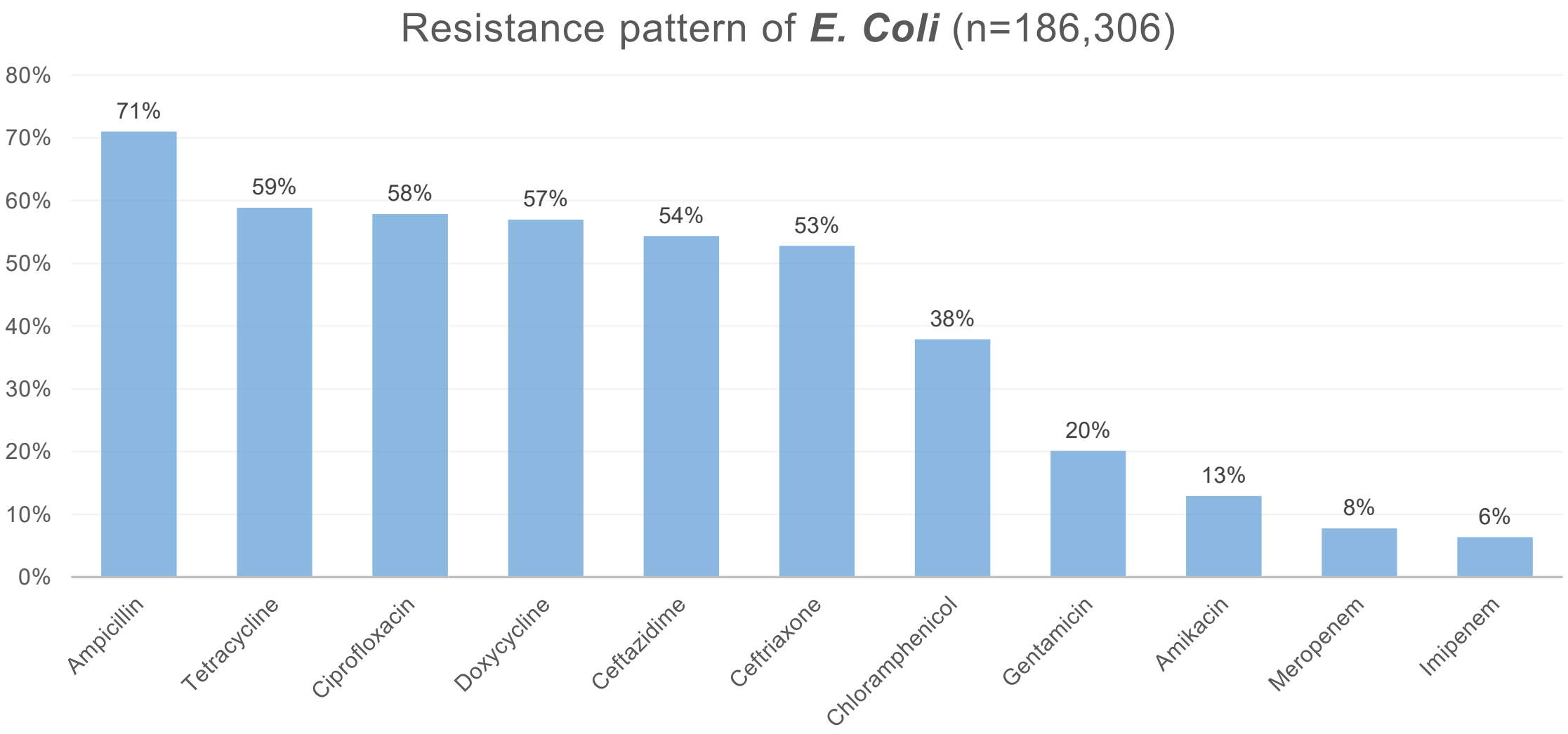
<5 Years samples and top five organisms



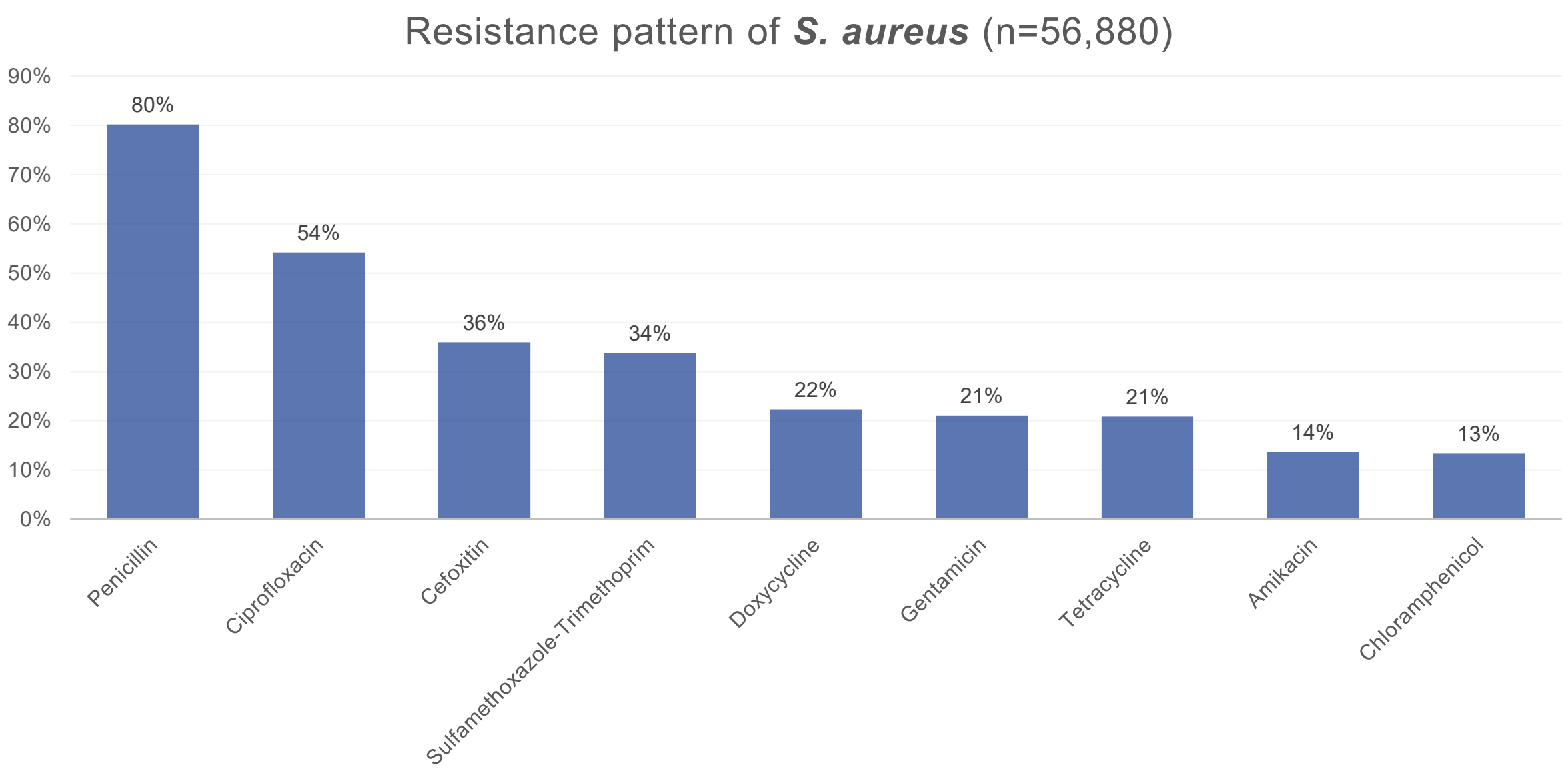


scn	Staphylococcus, coagulase negative
sat	Salmonella Typhi
sau	Staphylococcus aureus
ac-	Acinetobacter sp.
eco	Escherichia coli
kl-	Klebsiella sp.
ent	Enterococcus sp.
pr-	Proteus sp.

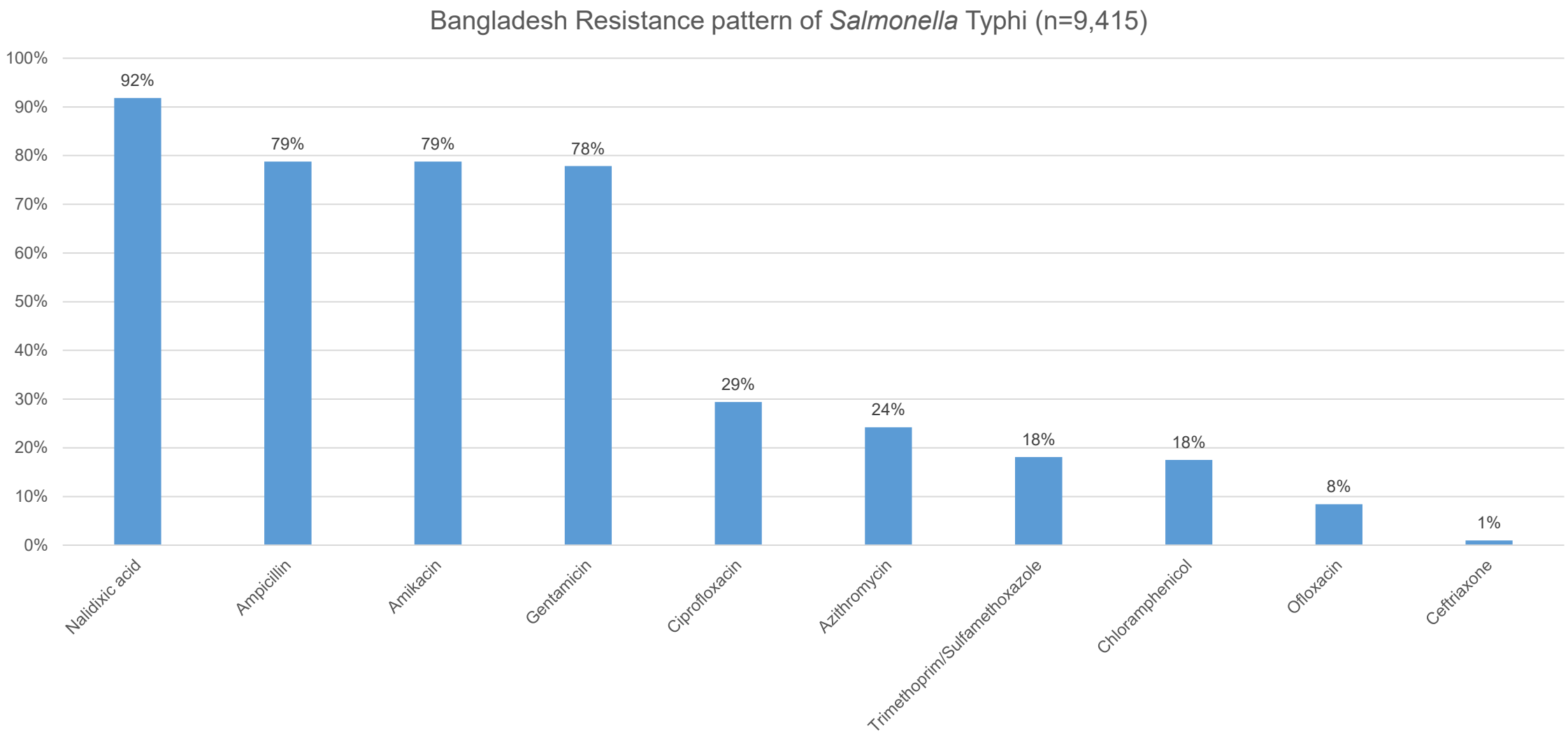
Escherichia coli: Resistance Pattern



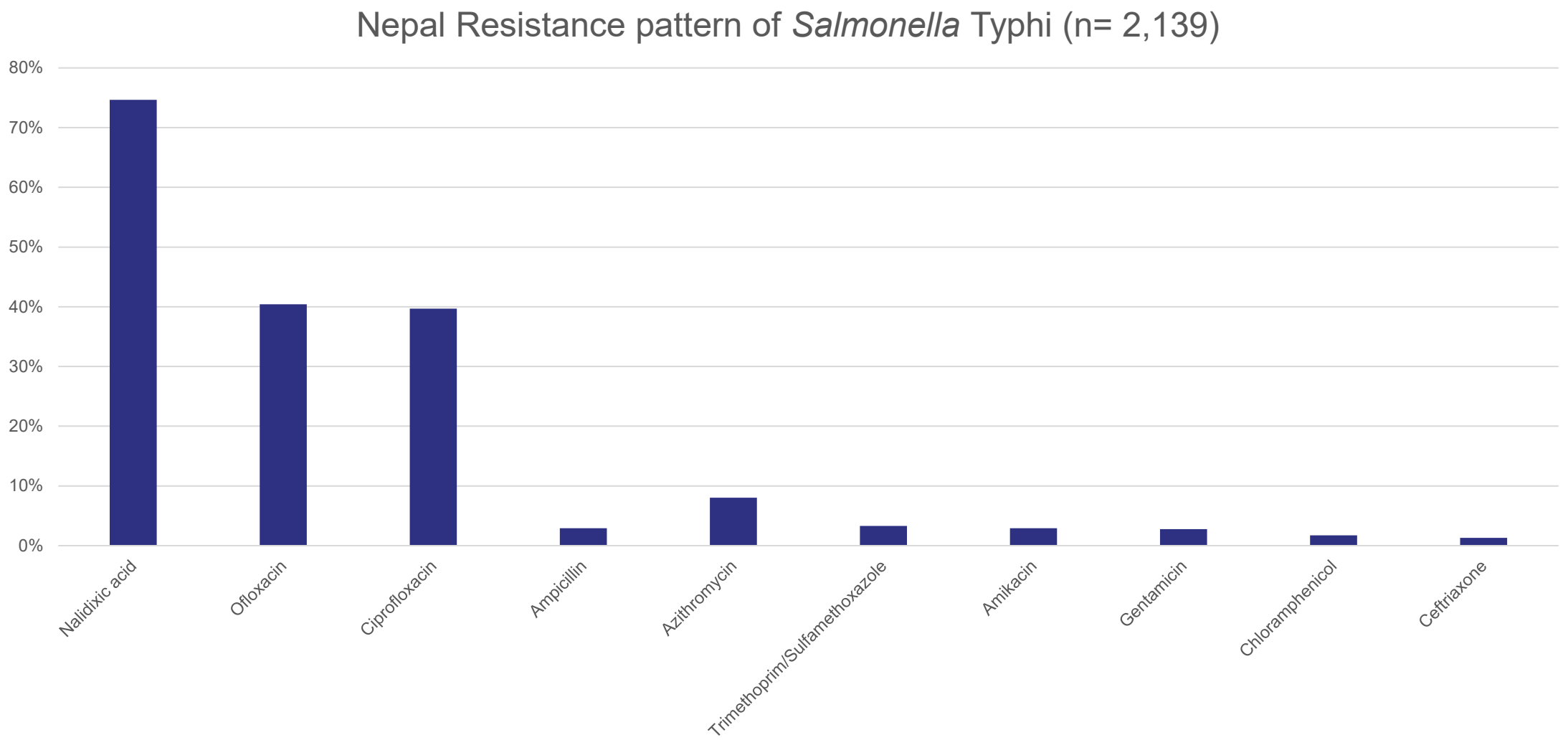
Staphylococcus aureus: Resistance Pattern



Bangladesh – Resistance Pattern of Salmonella Typhi

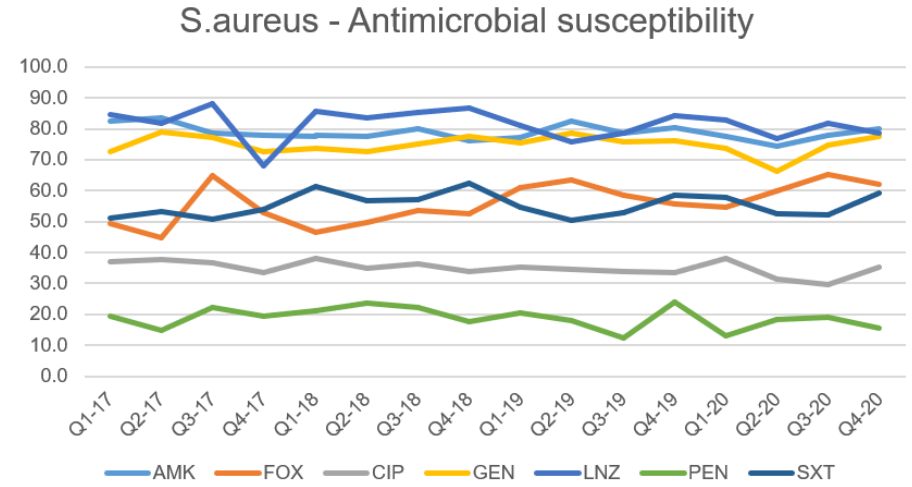


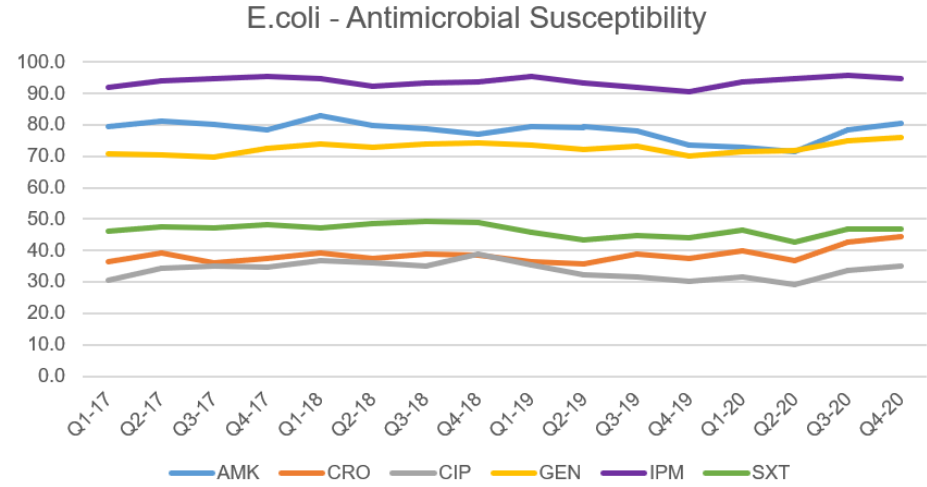
Nepal – Resistance Pattern of Salmonella Typhi



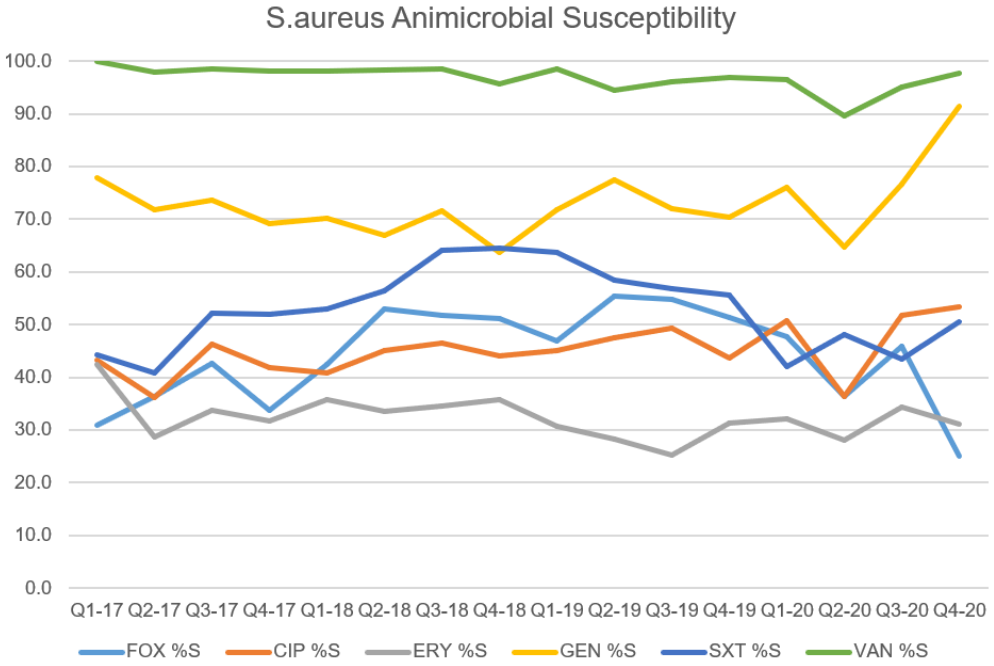
Antimicrobial trends

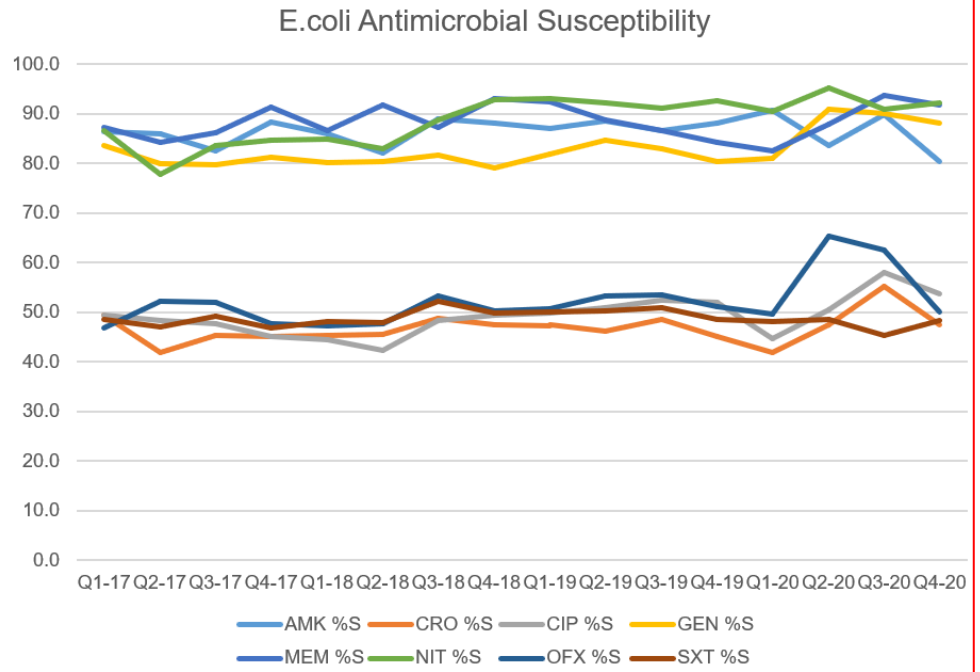
Country A



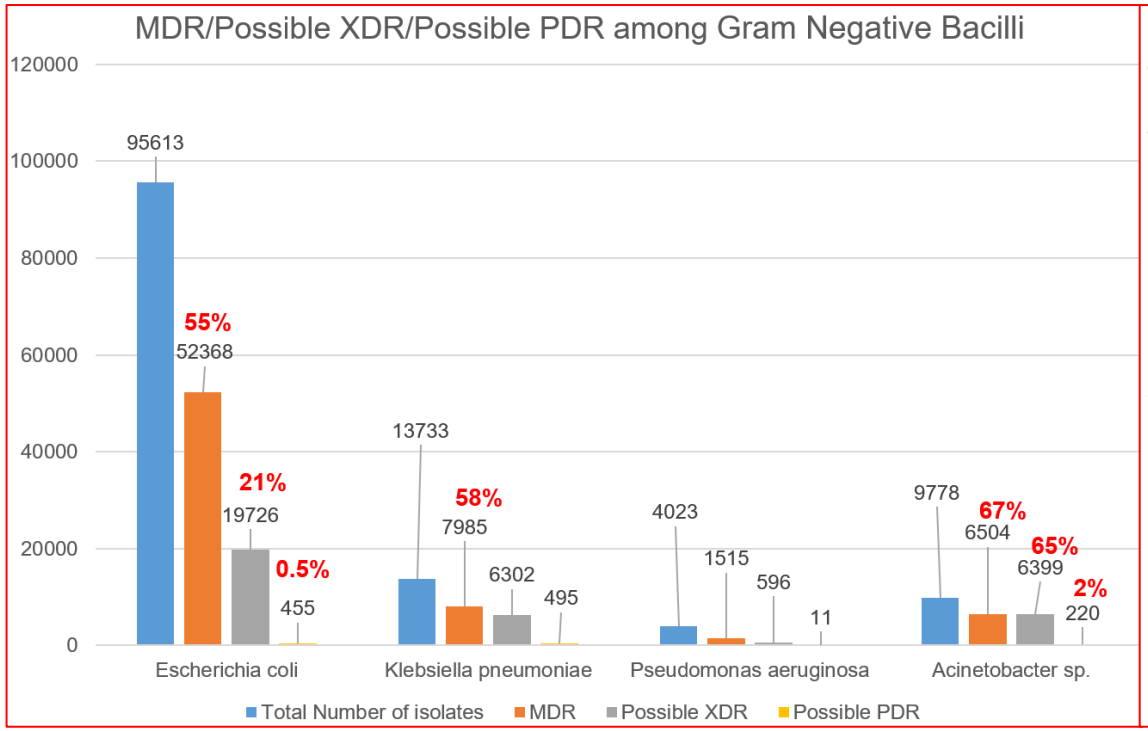


Country B

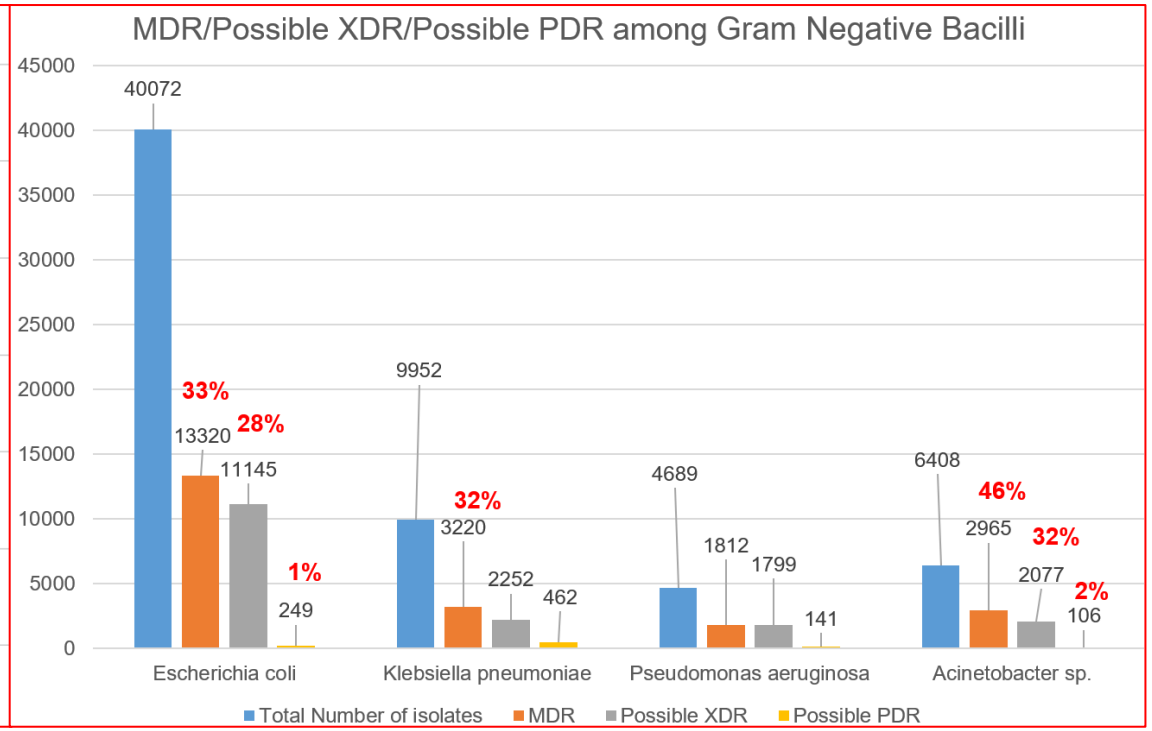




Multidrug resistance (MDR/XDR/PDR)

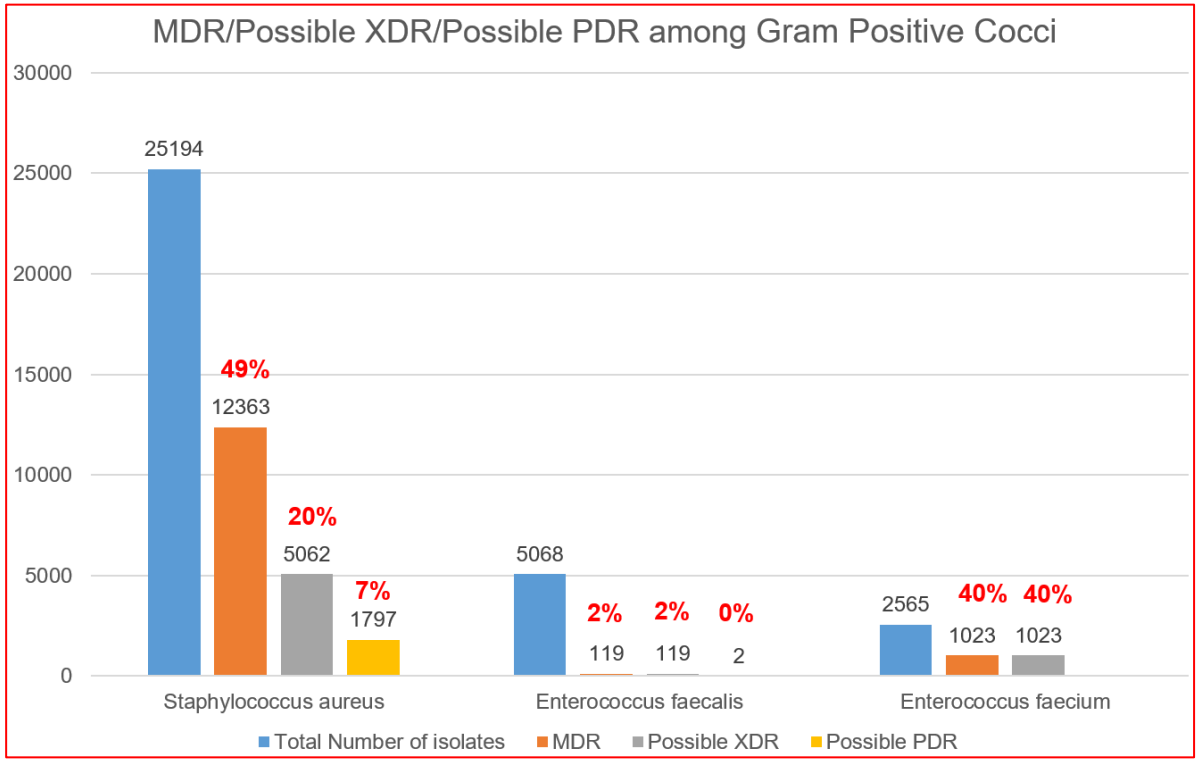


Country A

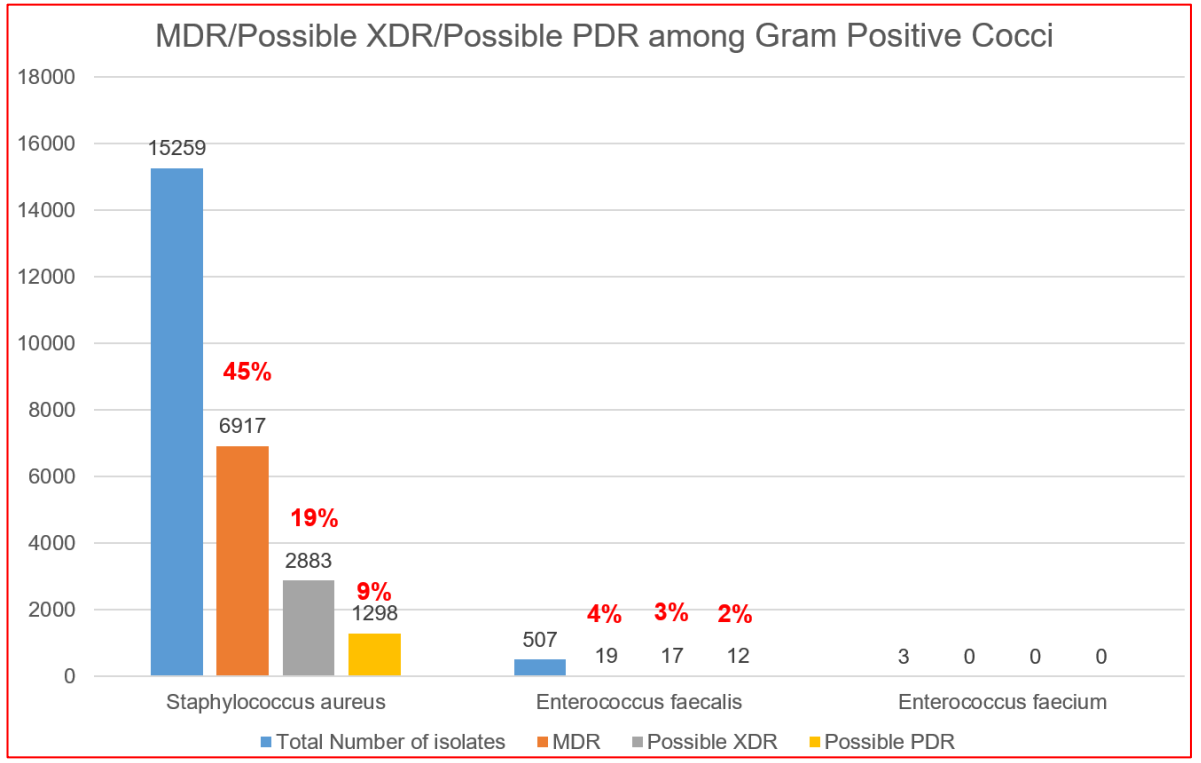


Country B

Multidrug resistance (MDR/XDR/PDR)



Country A



Country B

Key Observations

General Observation

- Huge information resources identified; baseline data foundation created
- Awareness and willingness to share data but hesitancy to some extent
- Potential opportunity for regional data sharing
- Mechanism needs to be ensured for long term sustainability of data collection and sharing mechanism

Technical Observations and areas for improvement

- High level of MDR among frequently identified bacteria and isolation of possible XDR/PDR bacteria warrants validation of the report and close monitoring to prevent the spread of these bugs
- Inconsistencies in recording
    - No record of zone diameter/ treatment and clinical details
- Record Keeping practices
    - No systematic way: storage of paper-based data
    - Device generated electronic data deleted
    - Custom build LIMS fit for clinical reporting not analysis
- Issues with data extraction
- Quality Issues
    - Missing QC records
    - Wrong drug-bug combination
    - Testing antibiotics

Utilizing the data findings going forward

Moving from CAPTURA to next phase

- Many stakeholders, activities, potential data contributors, huge data
- Opportunities and barriers
  - Commitment at government level, willingness to share data
  - Data quality, standardization, data exchange

- CAPTURA: Historical data collection
  - Moving from retrospective one time to prospective real-time sustainable
- Data into action
  - Evidence based policies

Thank you