Wastewater Research at KCRI

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KEMRI

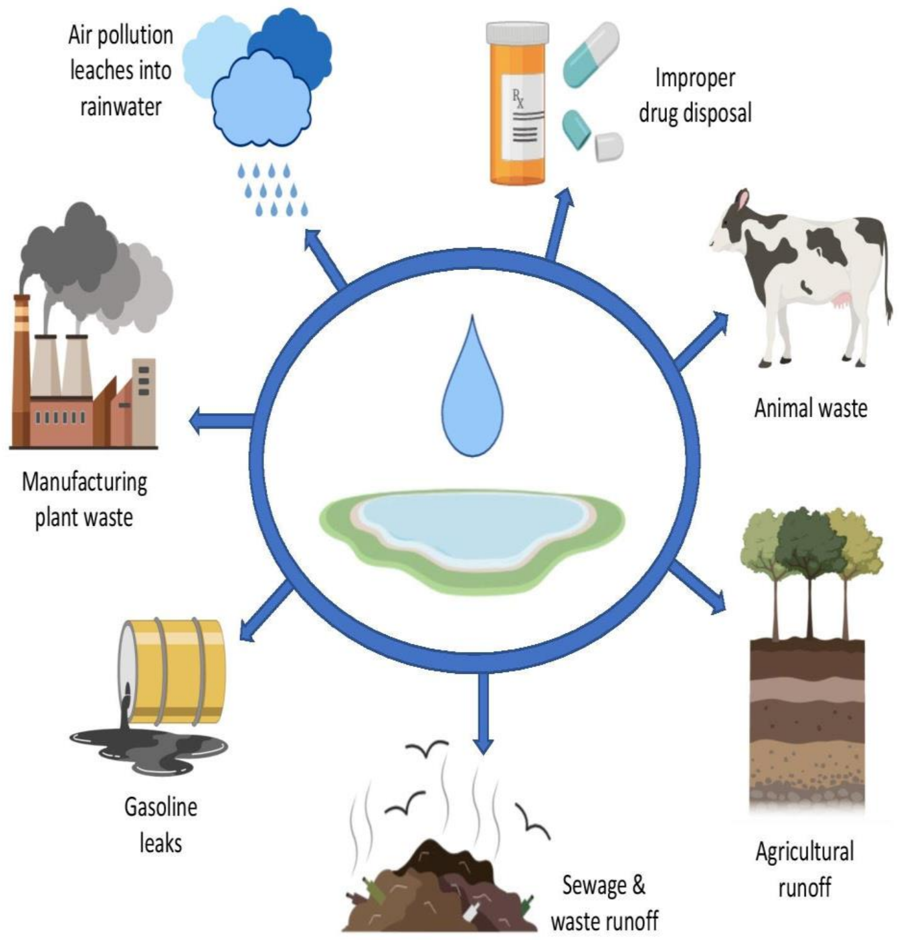
March, 2024.

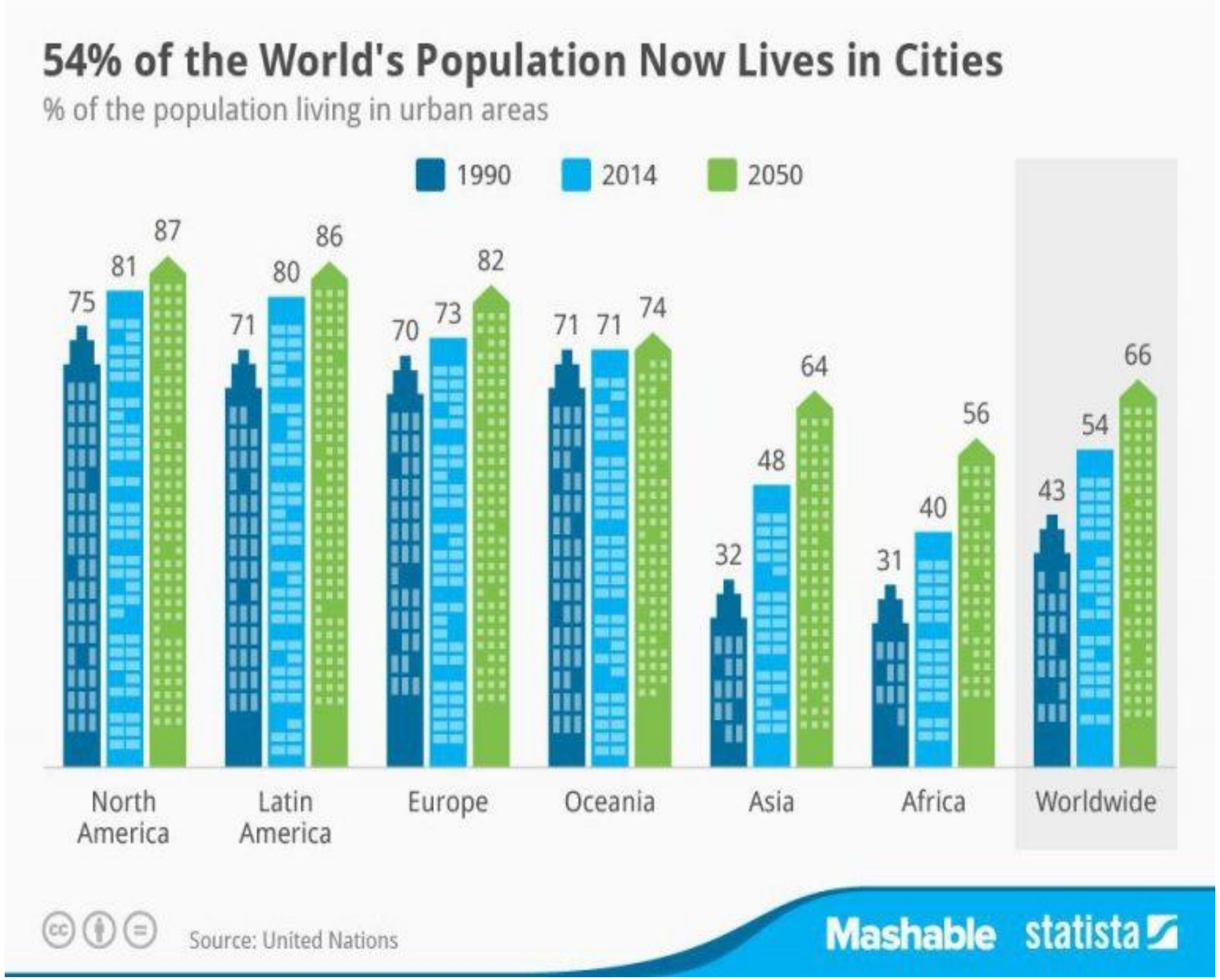
Background

- Wastewater research involves the study of
    - Wastewater which includes domestic,
    - Industrial, and
    - Agricultural runoff that flows into treatment facilities

- Aim to understand various aspects of wastewater, e.g. composition, contaminants, treatment processes, and environmental impact.

- WW-Research investigates
    - ways to improve WW treatment methods,
    - WW for wastewater management technologies,
    - potential risks associated with WW discharge into the environment.



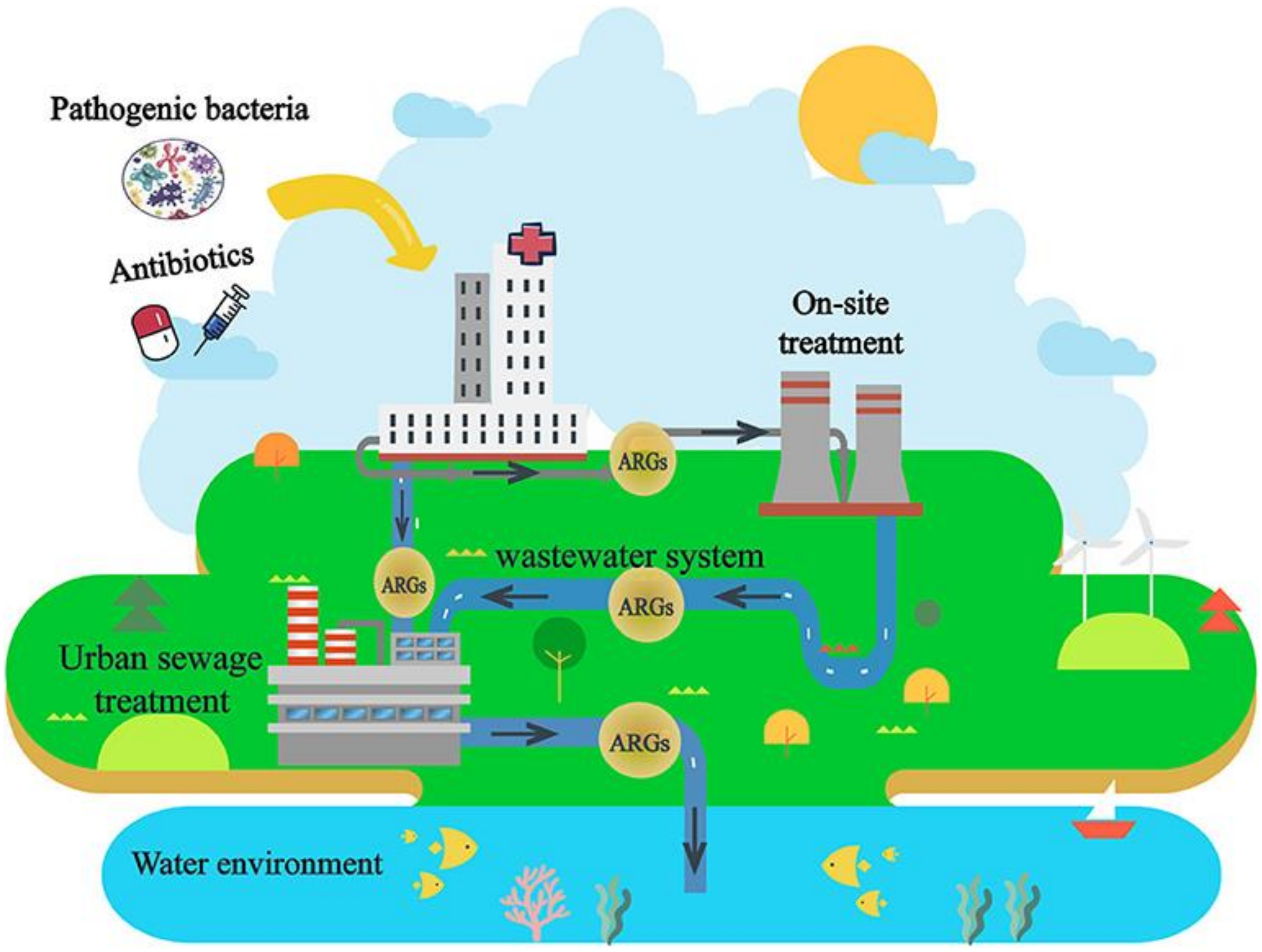


- Rapid population growth in LMICs leads to abrupt expansion of unplanned and informal urban settlements.

    - This leads to overwhelming waste management systems in the cities, resulting in no clear demarcation between human settlements and areas for waste disposal e.g. wastewater treatment plants (WWTPs).

- WasteWaterTreatment Plants have been reported to congregate bacteria of human, animal, and environmental provenance that host antibiotic resistance genes (ARGs).

- They provide an ideal breeding environment for indigenous bacteria, increase the occurrence of ARGs

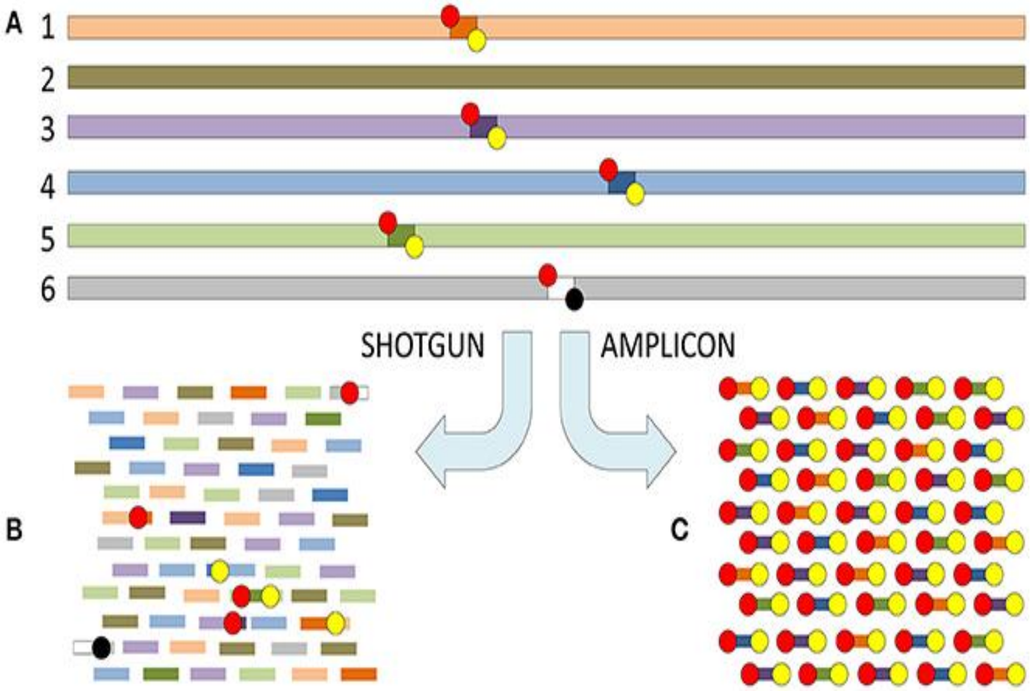


Metagenomics approaches in wastewater surveillance

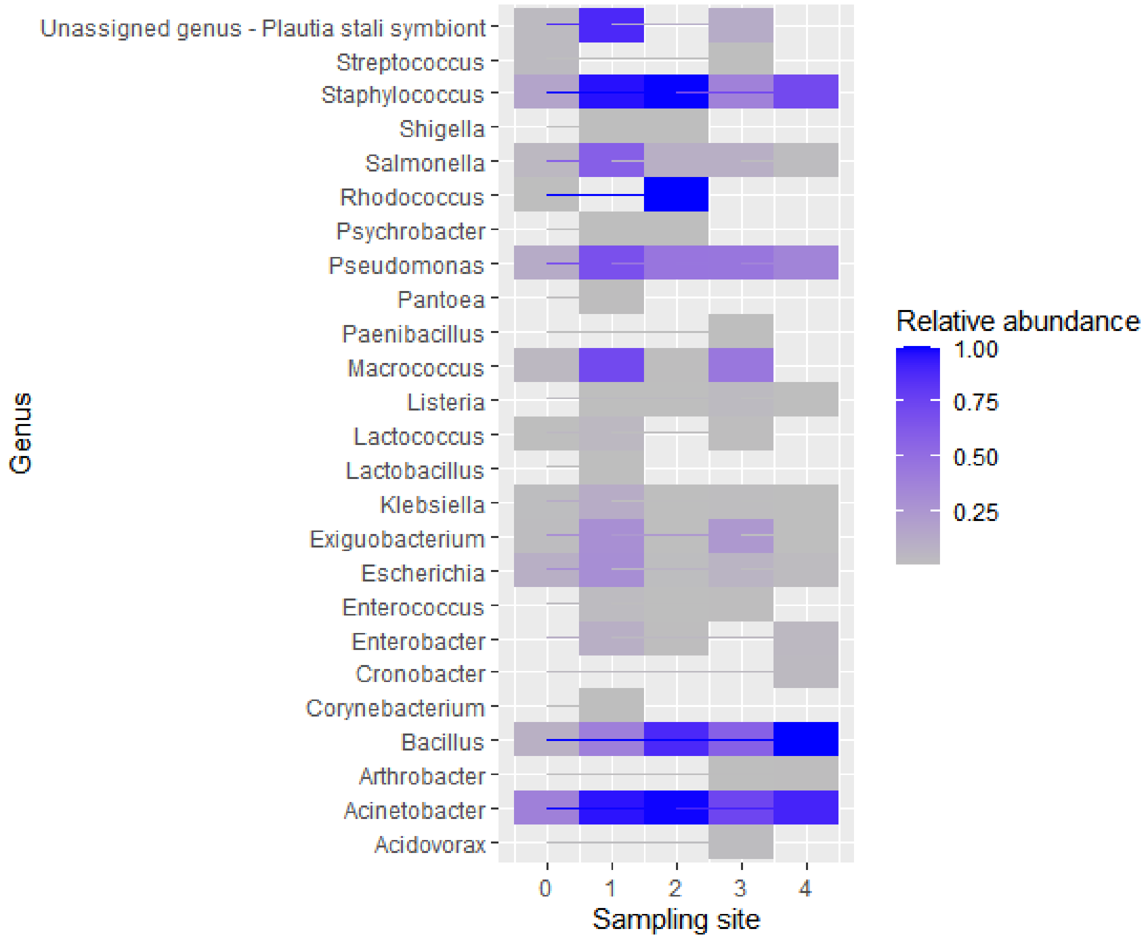
- Metagenomics-study of genetic material recovered directly from environmental samples,

- It has emerged as a powerful tool in wastewater surveillance.

- Metagenomics approaches offer a comprehensive view of microbial communities in wastewater, allowing for the detection of pathogens, monitoring of microbial diversity and dynamics, assessment of environmental health, and development of strategies for wastewater treatment and public health management.

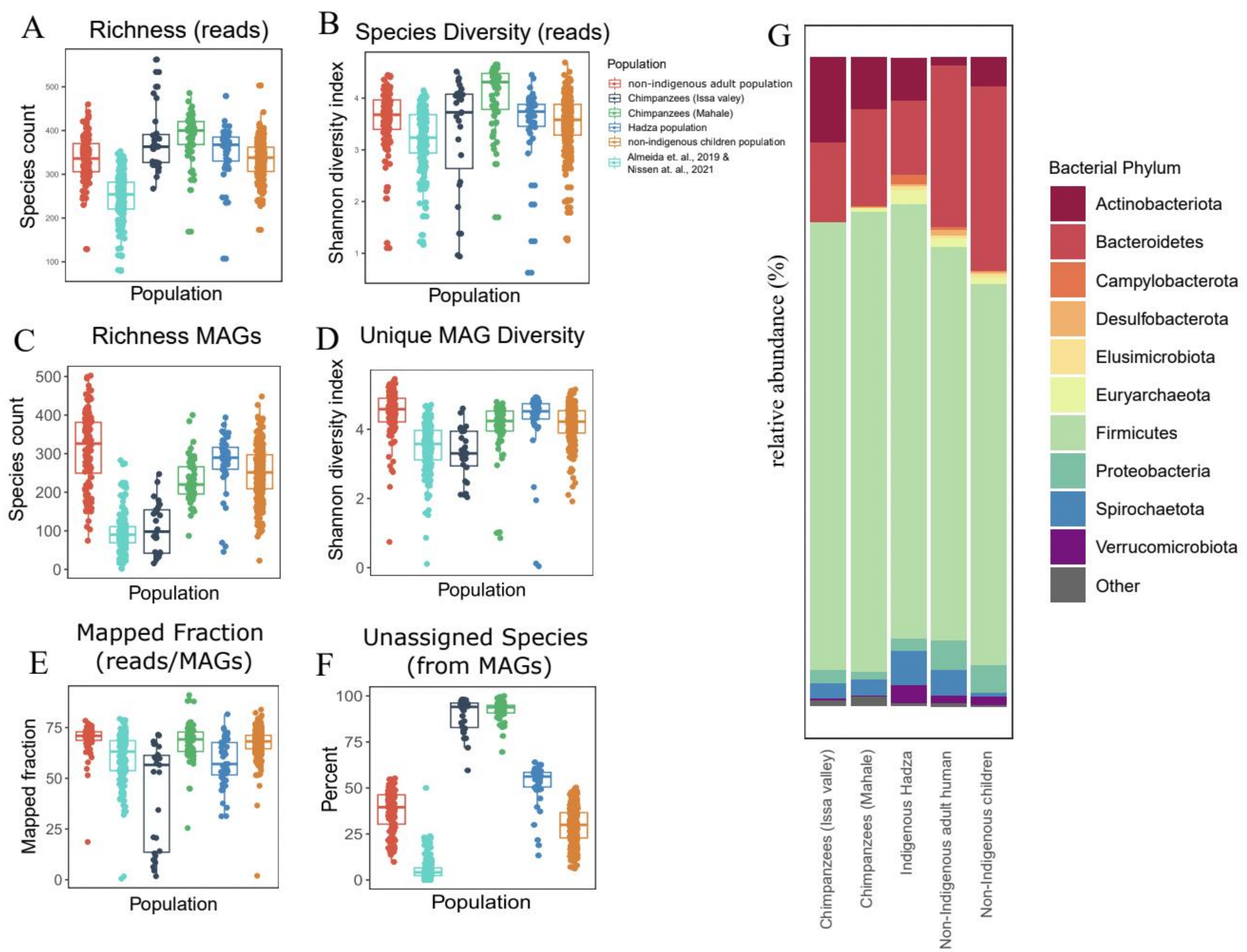


Shotgun Metagenomics



Bus metagenomics-Study conducted at KCRI

- **“whole-genome shotgun sequencing”,**
  - ✓ sequencing all DNA fragments from a complex environmental sample
  - ✓ Not prior target-specific amplification.
- Provides a comprehensive view of the genetic diversity and functional potential of microbial communities within the sample.

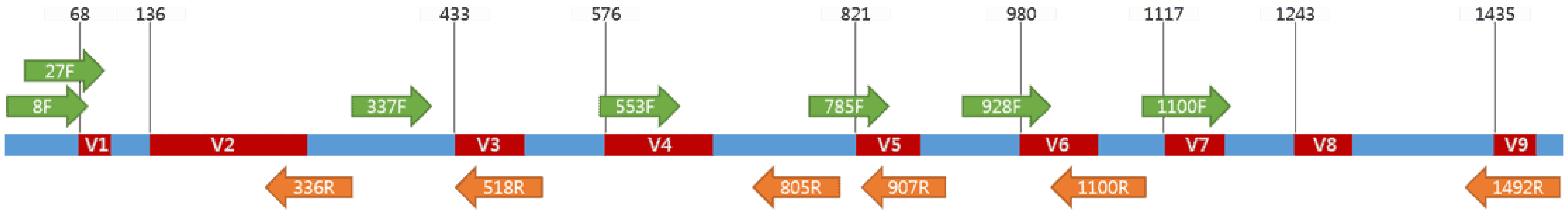


“Genomic and functional co-diversification imprint African Hominidae microbiomes to signal dietary and lifestyle adaptations"

16S rRNA Gene Sequencing

- Targets the 16S ribosomal RNA (rRNA) gene, a highly conserved region present in the genomes of bacteria and archaea.

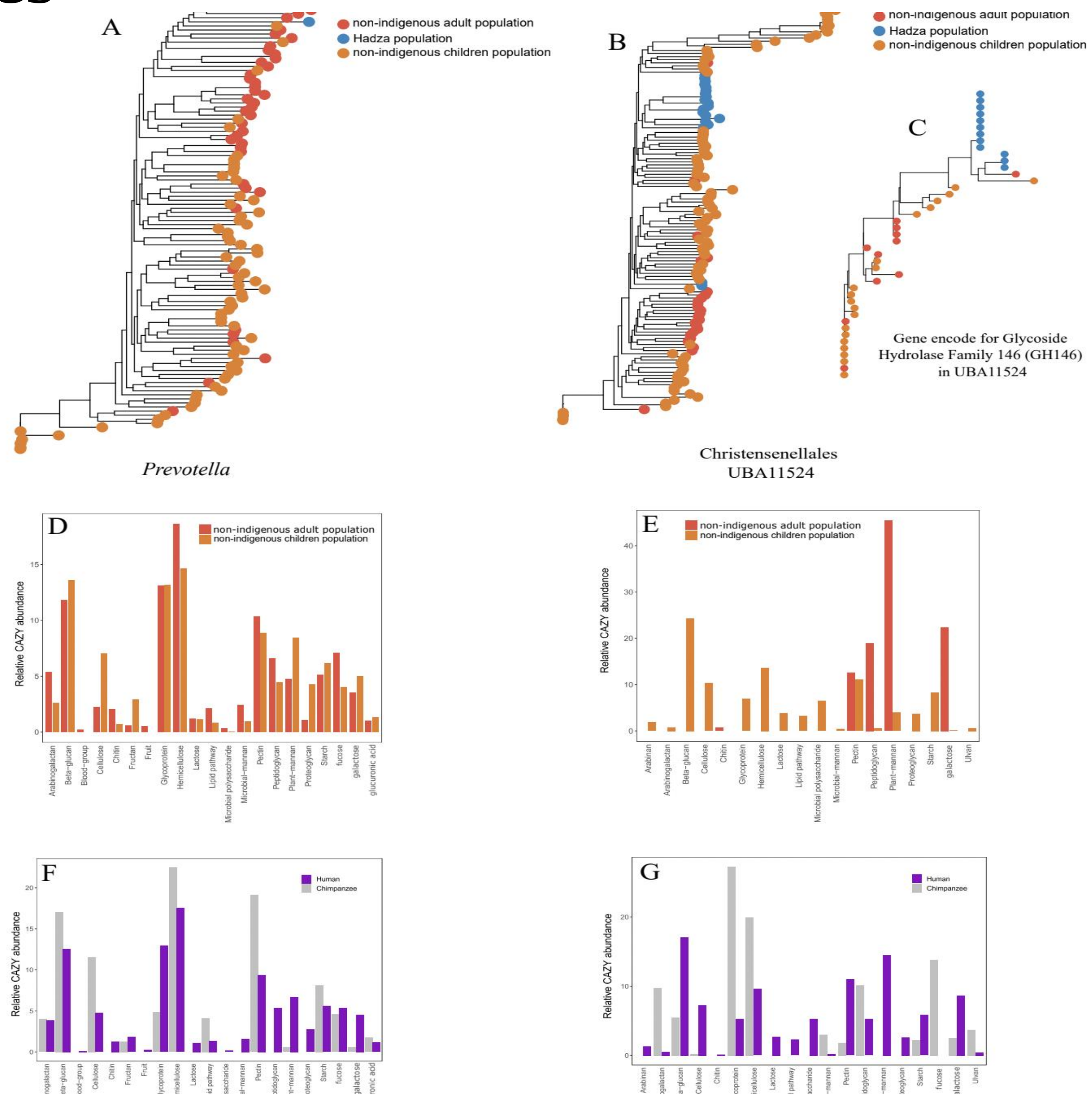
- By sequencing the variable regions of the 16S rRNA gene, researchers can assess microbial diversity and taxonomy within a sample, without requiring whole-genome sequencing.

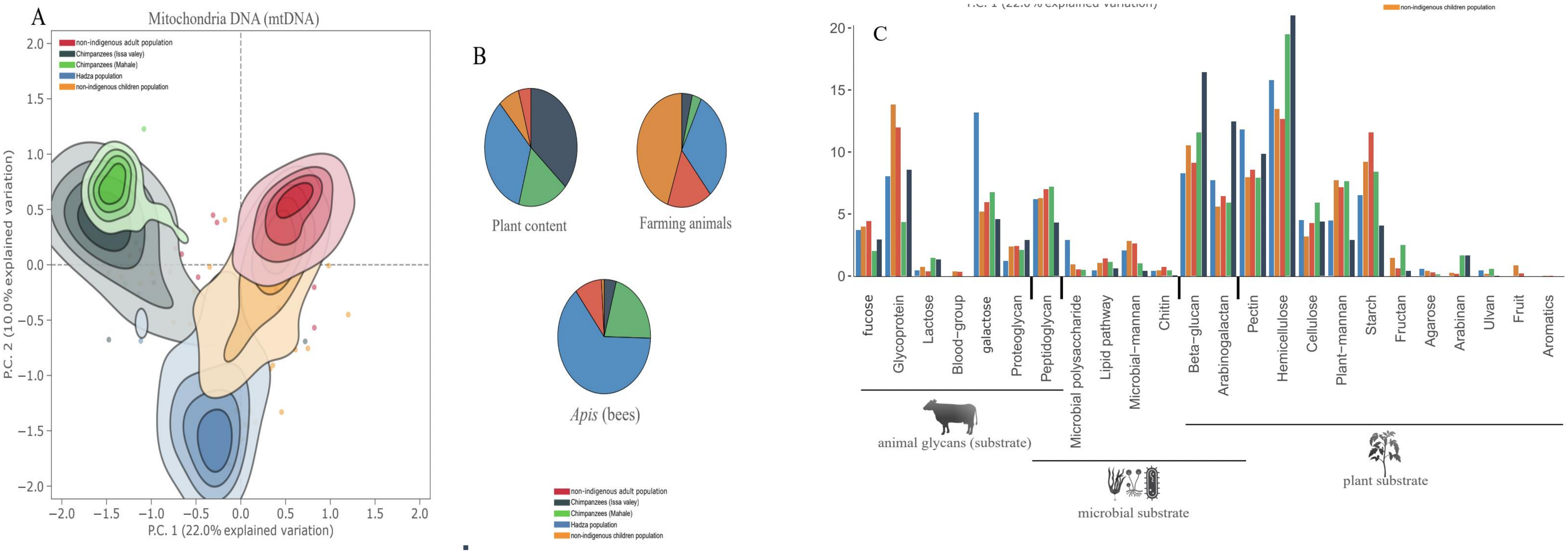


Functional Metagenomics

- Focuses on cloning and heterologous expression of genes from environmental DNA to study the functional properties and activities of microbial enzymes and proteins.

- It allows for the discovery of novel biocatalysts, antibiotic-resistance genes, and other biotechnologically relevant traits.





A
Mitochondria DNA (mtDNA)
non-indigenous adult population
Chimpanzees (Issa valley)
Chimpanzees (Mahale)
Hadza population
non-indigenous children population
P.C. 2 (10.0% explained variation)
P.C. 1 (22.0% explained variation)
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−2.0
B
Plant content
Farming animals
Apis (bees)
non-indigenous adult population
Chimpanzees (Issa valley)
Chimpanzees (Mahale)
Hadza population
non-indigenous children population
C
non-indigenous children population
20
15
10
5
0
fucose
Glycoprotein
Lactose
Blood−group
galactose
Proteoglycan
Peptidoglycan
Microbial polysaccharide
Lipid pathway
Microbial−mannan
Chitin
Beta−glucan
Arabinogalactan
Pectin
Hemicellulose
Cellulose
Plant−mannan
Starch
Fructan
Agarose
Arabinan
Ulvan
Fruit
Aromatics
animal glycans (substrate)
microbial substrate
plant substrate

More metagenomics appraches

Metatranscriptomics

- Involves the sequencing and analysis of RNA transcripts (mRNA) present in a microbial community.
- It provides insights into gene expression patterns, metabolic activities, and functional responses of microorganisms within a specific environment

- **Virome Analysis**: Involves the study of viral communities (viromes) present in environmental samples, biological samples, or microbiomes.
- It aims to characterize viral diversity, identify novel viruses, and investigate viral-host interactions.

Metaproteomics

- Focuses on the identification and quantification of proteins expressed by microbial communities in a given sample.
- It provides information about the functional activities, metabolic pathways, and interactions occurring within the microbial community.

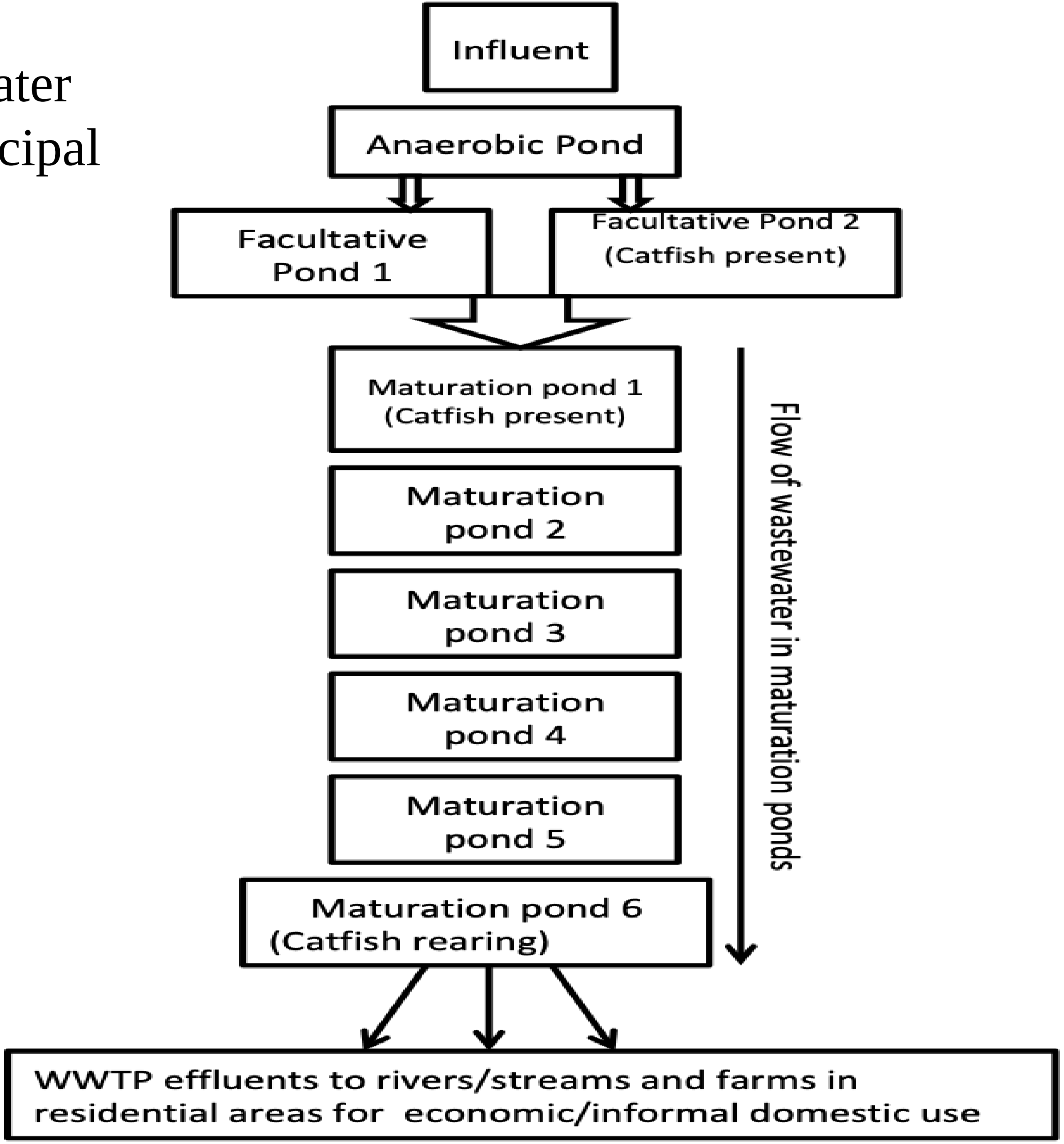
Each type of metagenomics offers unique insights into microbial communities, their diversity, functions, and interactions within different ecosystems. Researchers often combine multiple metagenomic approaches to comprehensively characterize microbial communities and understand their roles in various biological and environmental processes.

Global sewage project-Tanzania through KCRI contributed wastewater samples

- KCRI participated in a global sewage study in 2016 that involved 79 sites from 60 countries around the world.

- The project aimed at characterizing bacterial resistome from untreated sewage water.

Basic Structure of Most Wastewater Treatment Plants in Moshi Municipal



Sample collection at moshi-urban WWTP

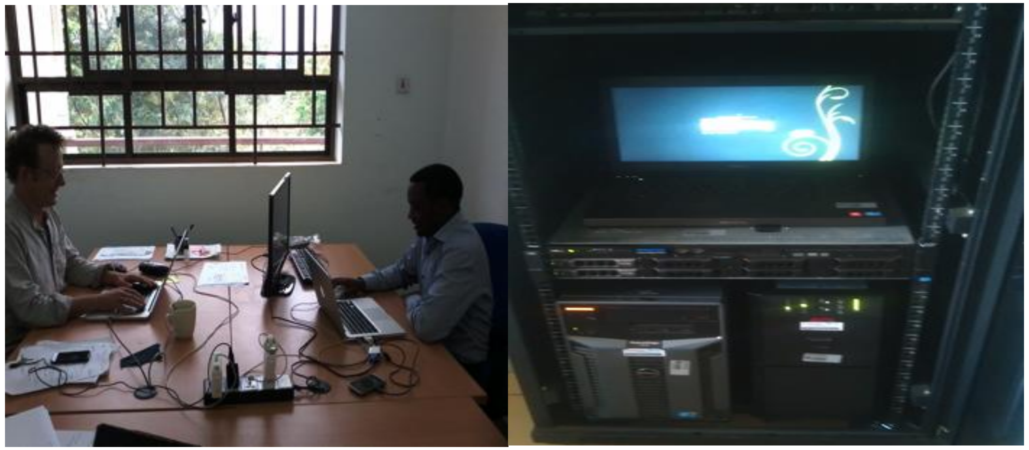
WWTP in Moshi

Collection of WW from WWTP in Mabogini Moshi
For Global Sewage Project 2016

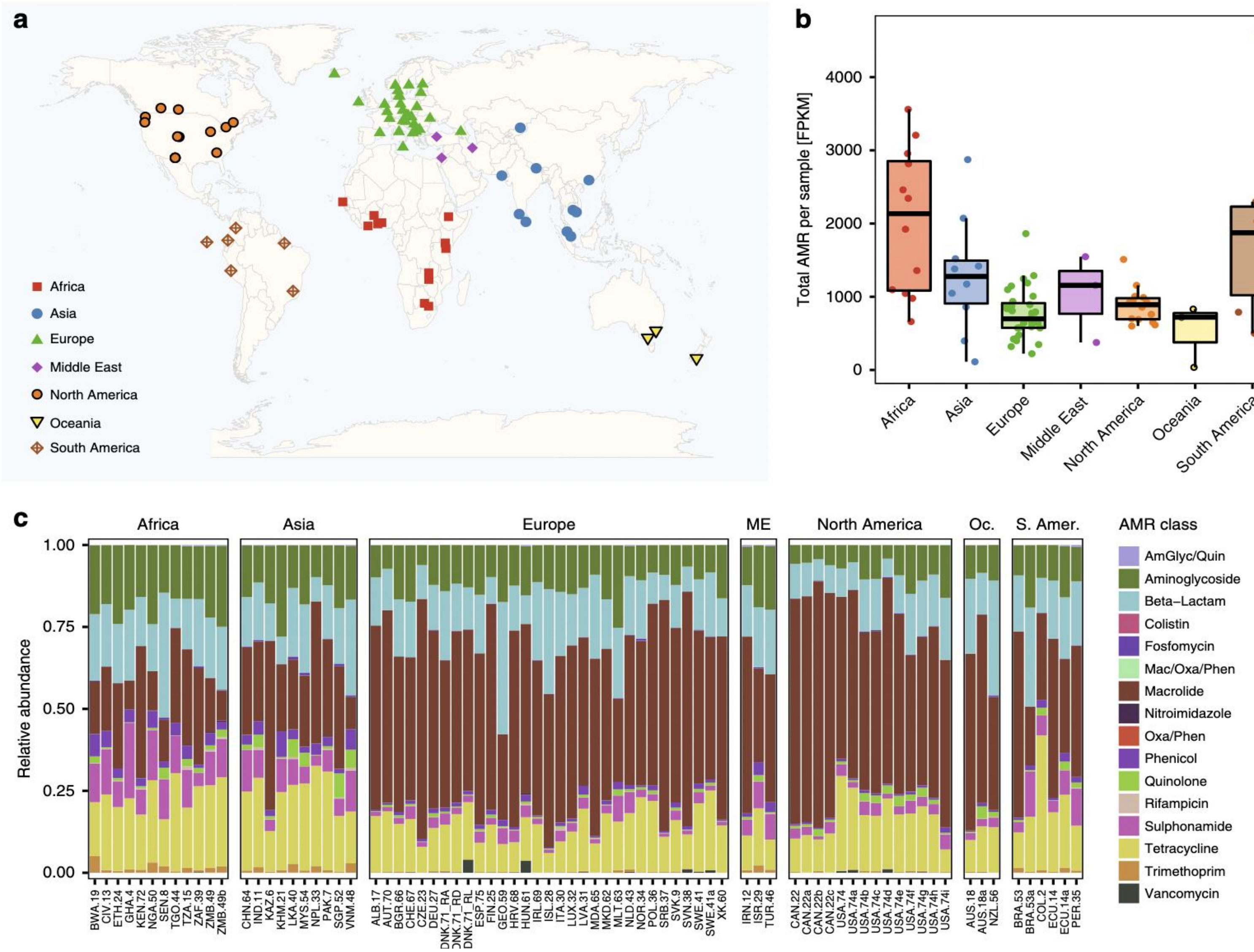
Analysis Approach –Metagenomics sequencing

Illumina technology

Oxford nanopore technology



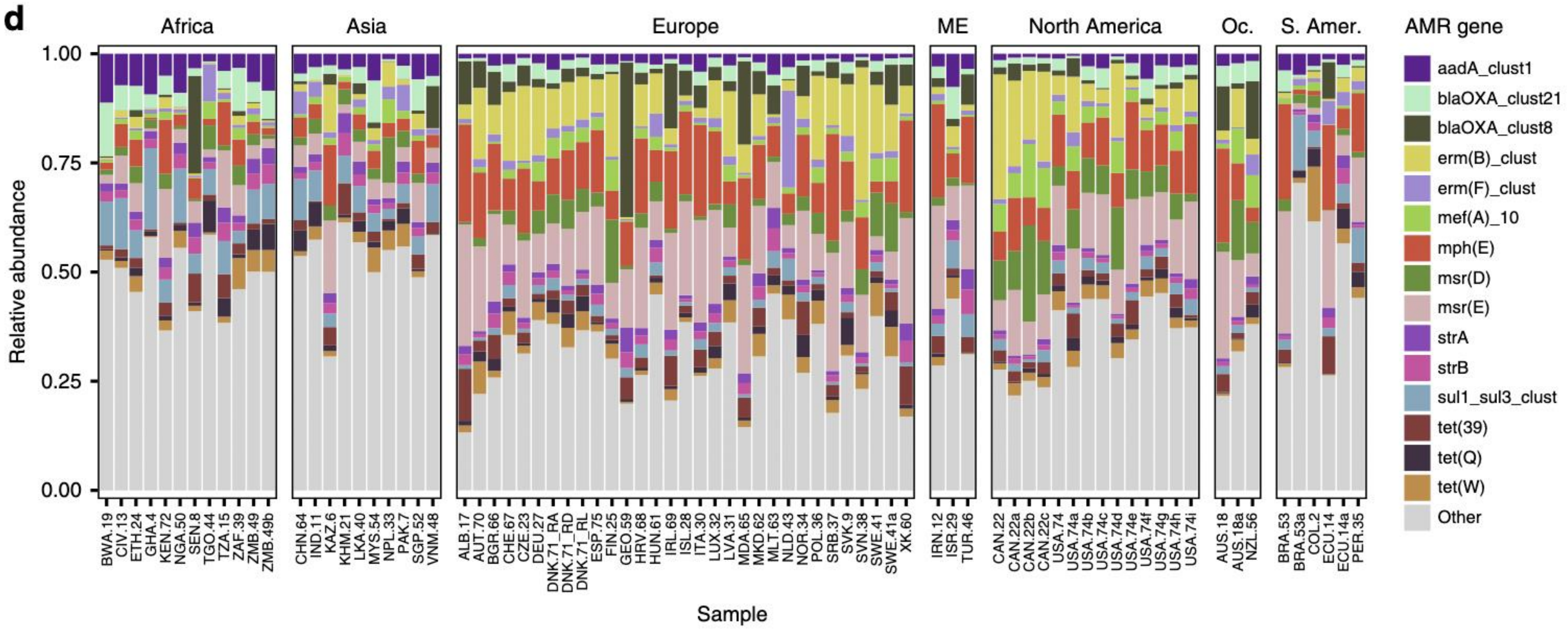
Bioinformatics capacity



a . Map of the sampling sites

b. Boxplots of the total AMR fragments per kilobase per million fragments per sample, stratified by region

c. Relative AMR abundance per antimicrobial class (AmGlycaminoglycoside, Mac macrolide, Oxa oxazolidinone, Phen phenicol, Quin quinolone



d. Relative abundance of the 15 most common AMR genes (mef(A)_10: mef(A)_10_AF376746)

This data suggested that …

- African data on relative AMR abundance per antimicrobial class suggests tetracycline to be amongst the antibiotic class of which drugs under this group are highly resisted.

- Maybe this is due to Tetracycline used in both humans and animals in Tanzania for:

    - treat bacterial infections, such as cholera, typhoid fever, urinary tract infections, and respiratory as well as skin infections.
    - In animals used to treat various bacterial infections, including respiratory infections, skin infections, and gastrointestinal infections.
    - to prevent bacterial infection in food-producing animals, such as cows, pigs, and chickens.

Thank You