

MHK Training on Bacterial Genomics and Bioinformatics

Bacterial Genomics

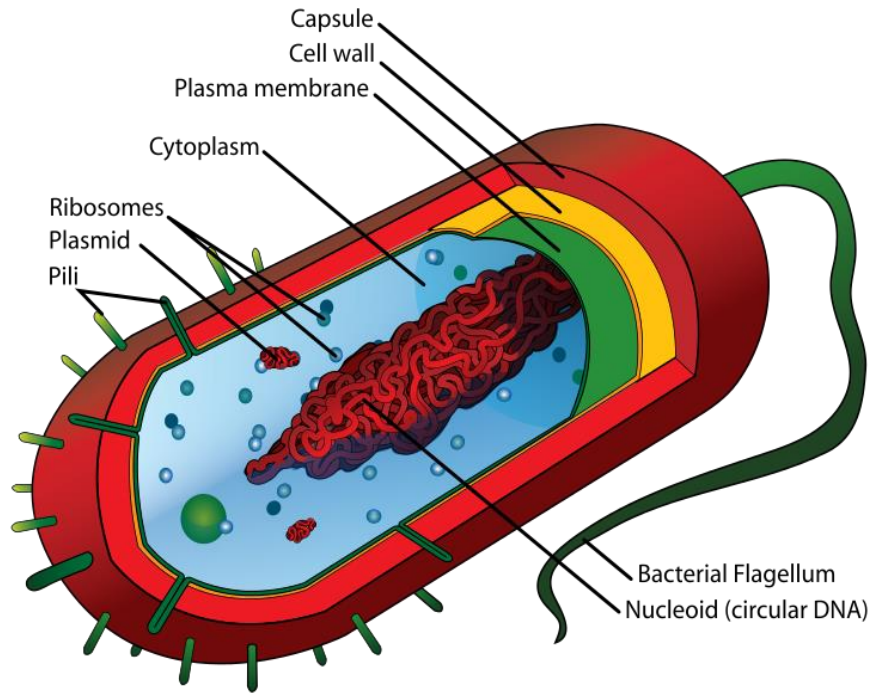
Justin Nyasinga

17.07.2025

Outline

- Recap the previous sessions (Nucleic acid extraction and Genome sequencing)
- Introduction to structure and organization of prokaryotic genomes
- Technologies for studying bacterial genomes
- Applications of bacterial genomics
- Emerging trends in bacterial genomics
- Q&A, Discussions

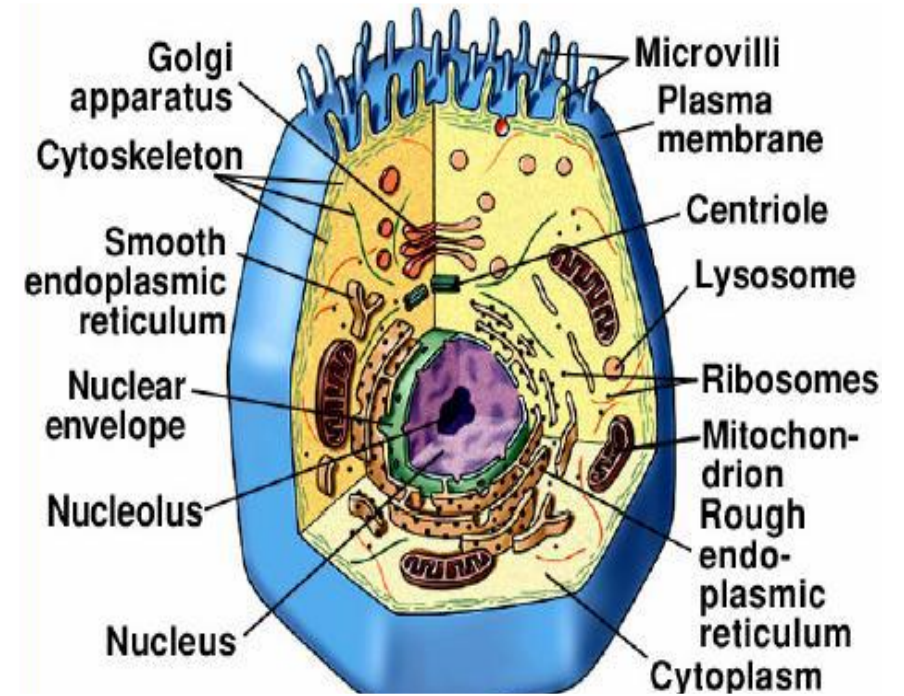
Prokaryotic cell



Gammoudi, 2012

Small, fewer organelles, no nucleus, 70S ribosomes, single circular chromosomes etc.

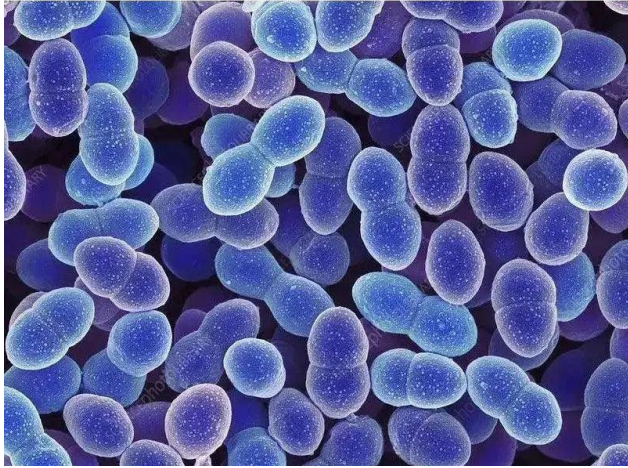
Eukaryotic cell



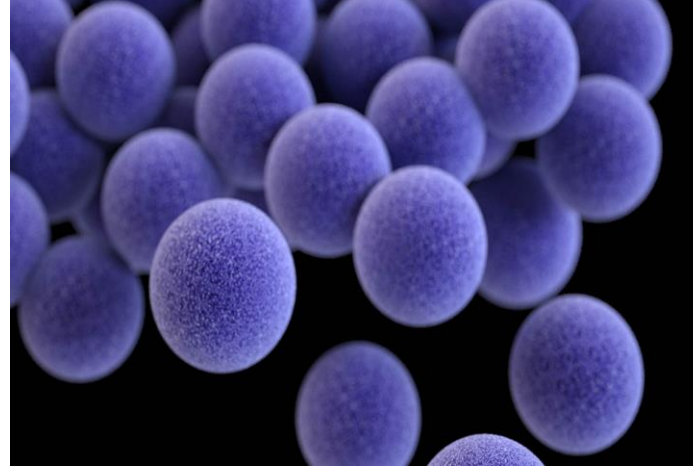
<https://quizlet.com/>

Larger, more organelles, defined nucleus, 80S ribosomes, multiple linear chromosomes etc.

ESKAPE bacterial pathogens



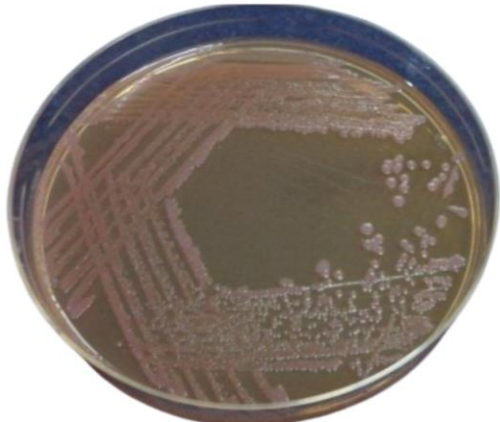
E. faecium



S. aureus



K. pneumoniae



A. baumannii



P. aeruginosa



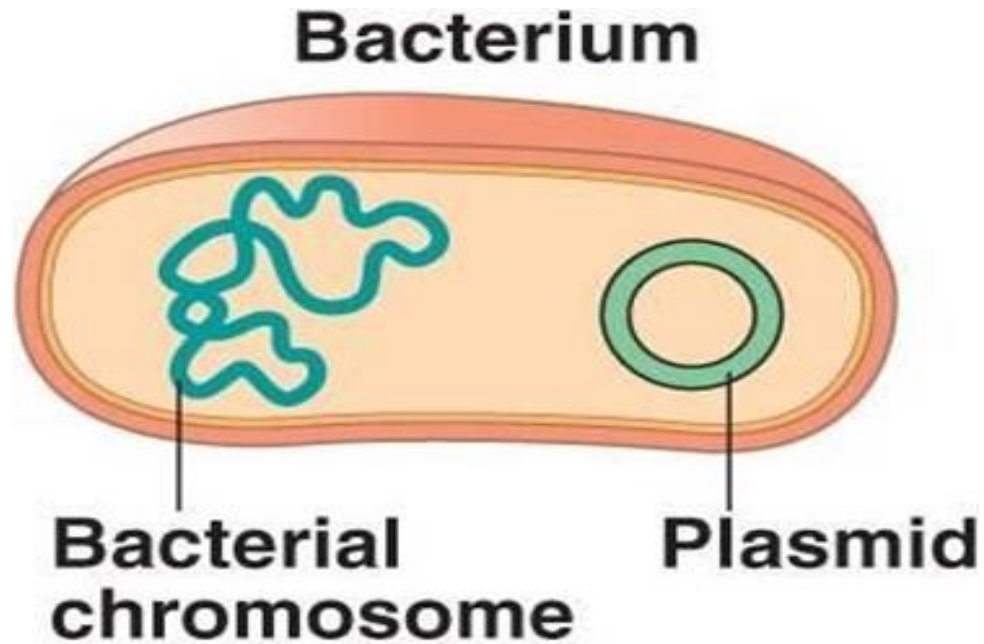
Enterobacter spp.



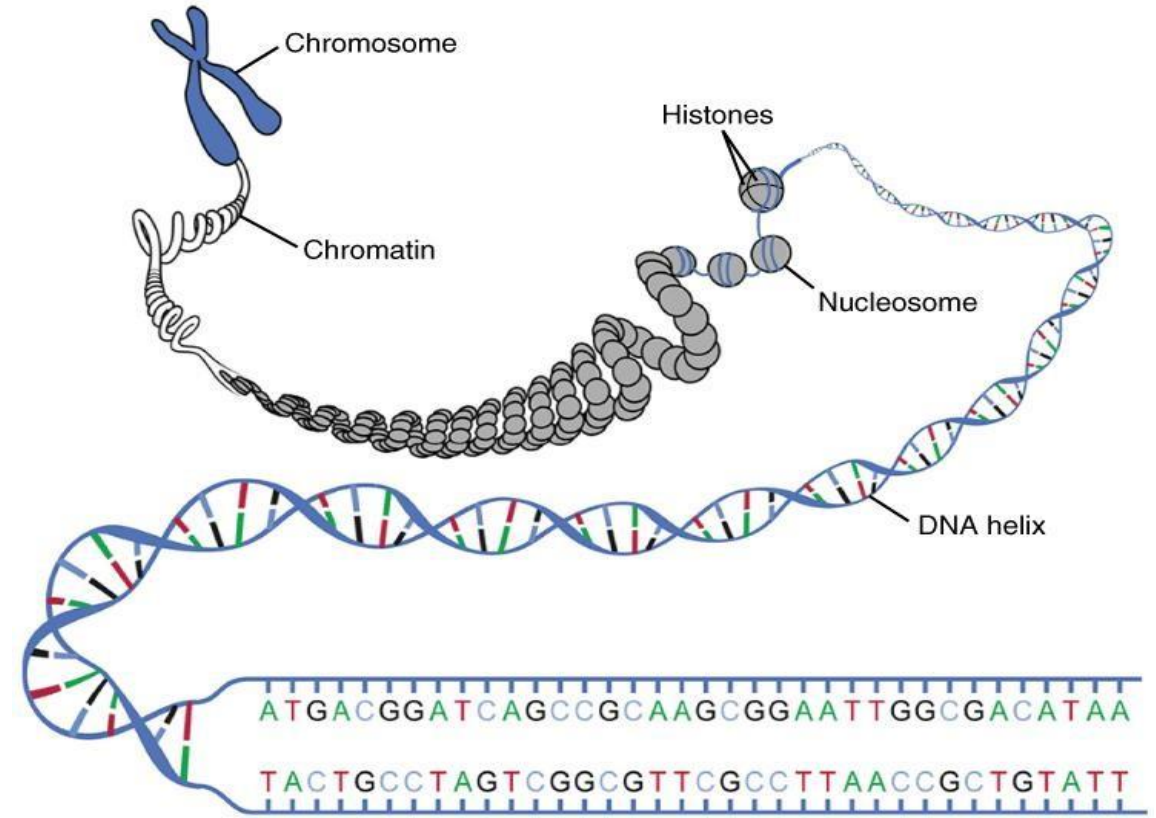
E. coli

ESKAPE pathogens are a challenge esp. in healthcare settings because they can persist in the environment, resist antiseptics & antimicrobials, and can cause death.

Prokaryotic and eukaryotic genome organization

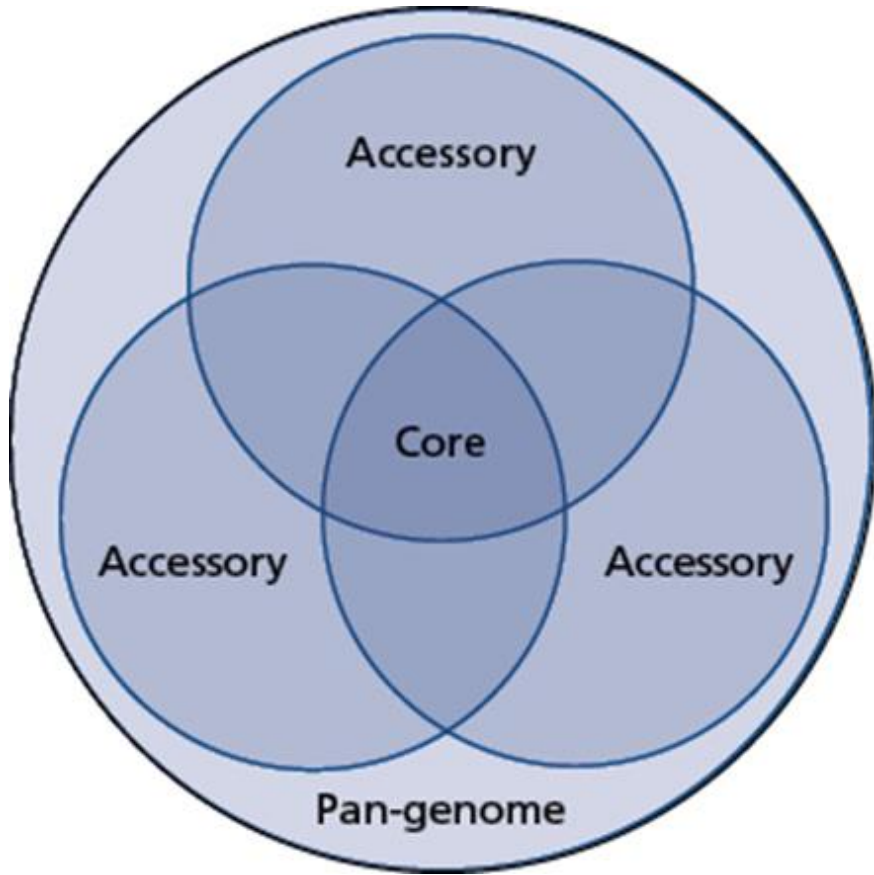


Small, haploid, circular chromosomes, packaging by supercoiling, extrachromosomal DNA in plasmids



Large, diploid (mostly), linear chromosomes, packaging by histone proteins, Limited extrachromosomal DNA

Features of prokaryotic genomes



Core genome: Genes found in all members of a given microbial group; essential for basic metabolism and survival.

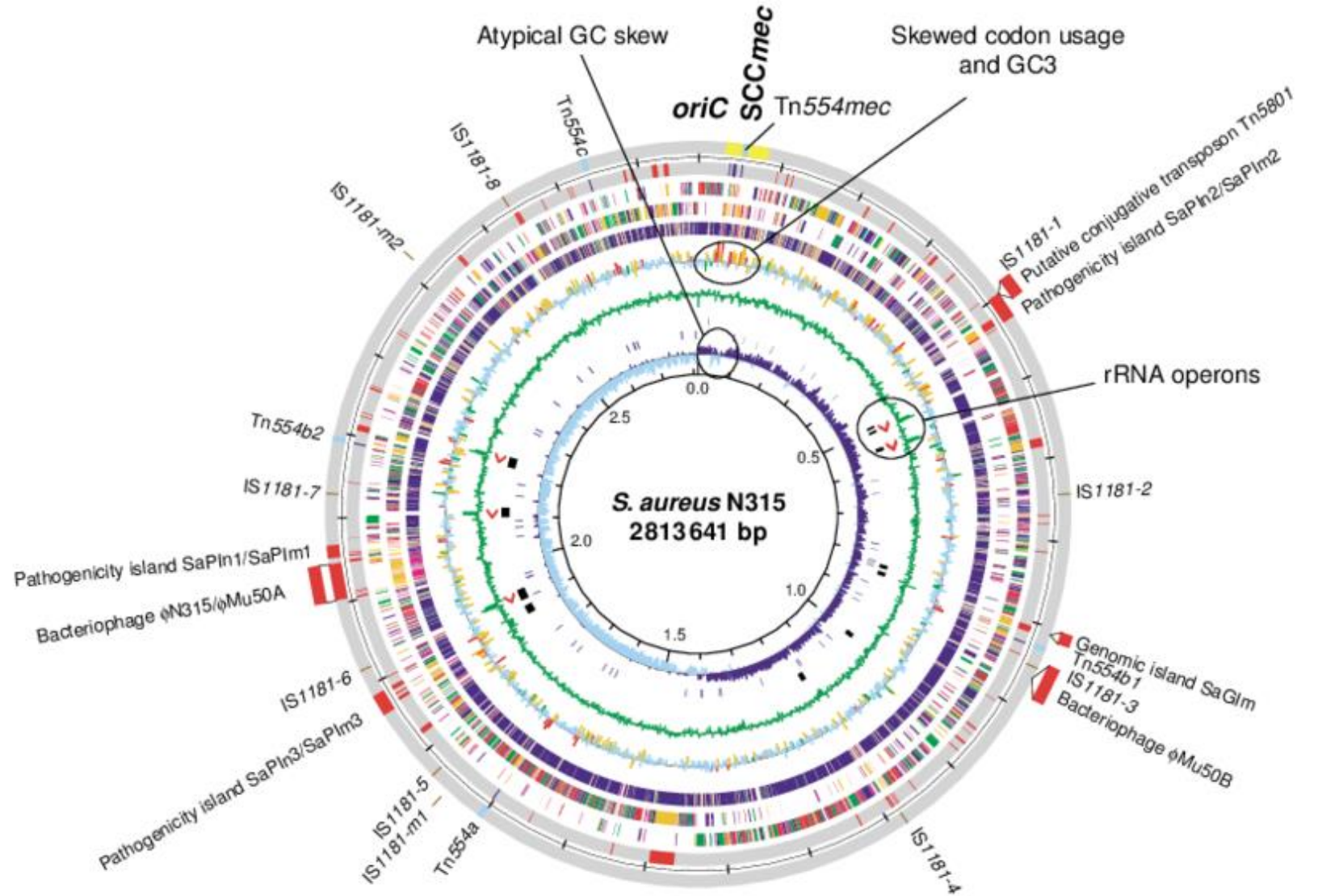
Accessory genome: Genes found in some but not all; may confer competitive advantage to hosts.

Pangenome: Total genetic diversity within a microbial group.

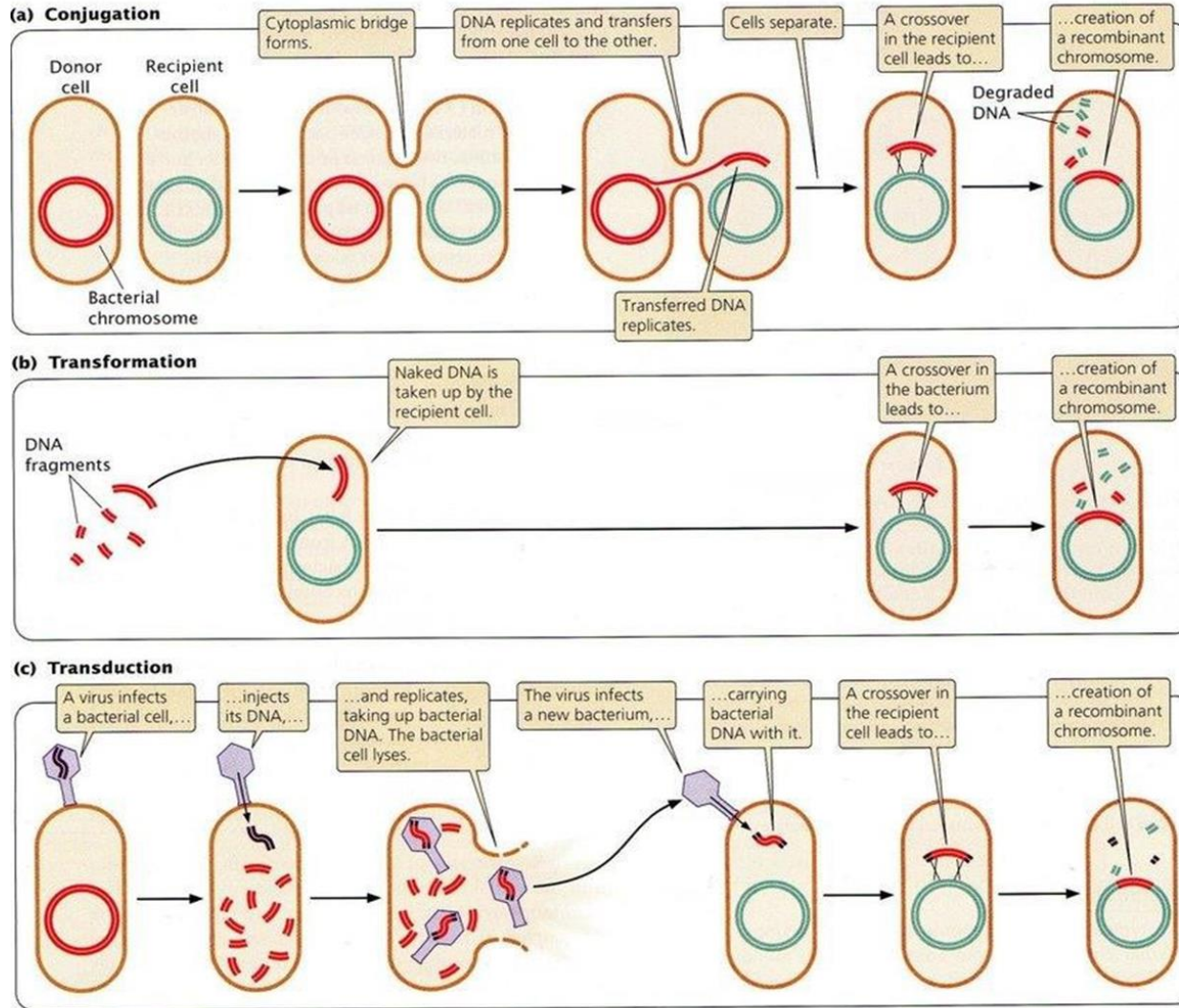
Accessory genome is driven by mobile genetic elements (MGEs) through horizontal gene transfer (HGT)

MGEs include Plasmids (p); Pathogenicity islands (PI); Transposons (Tn); Insertion sequences (IS), Bacteriophages etc.

Features of prokaryotic genomes



Sources of variation in prokaryotic genomes



- Chromosomal mutations (deleterious and advantageous)
- Cell-to-cell horizontal gene transfer (Conjugation, Transformation & Transduction).
- Intrachromosomal transfer of MGEs such as transposons.

Introduction to “omics”

- Employment of high throughput technologies for holistic study of biological systems.
- **Genomics:** Study of the structure, function, organization and evolution of the entire DNA of an organism.
- **Transcriptomics:** Study of the entire population of transcribed RNA in a cell/ tissue/organism.
- **Proteomics:** Focus on entire population of expressed proteins in a cell/ tissue/organism.
- **Other omics:** Lipidomics, Metabolomics; Metagenomics Epigenomics.

Tools for genomic analysis genomes

First generation

Second generation
(next generation sequencing)

Third generation



Sanger sequencing
Maxam and Gilbert
Sanger chain termination



454, Solexa,
Ion Torrent,
Illumina



PacBio
Oxford Nanopore

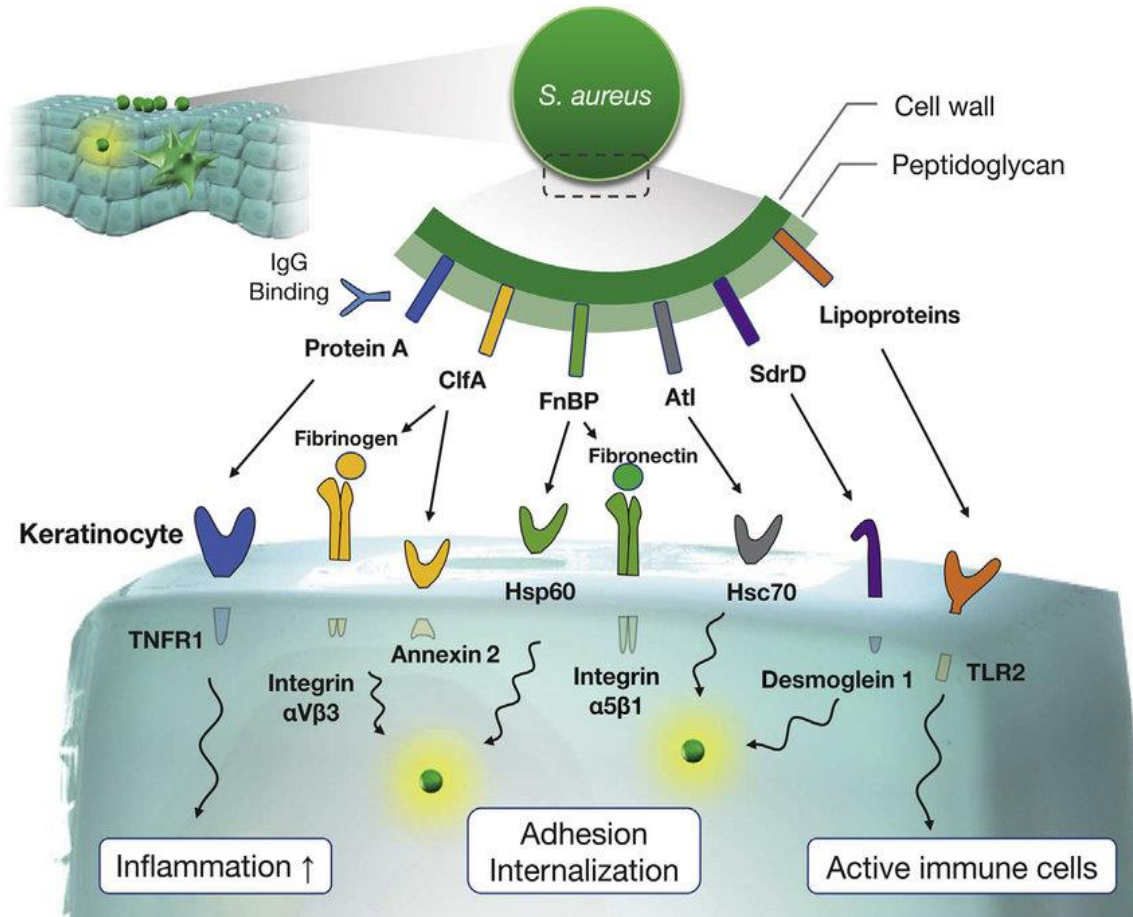
<https://www.pacb.com/>

- Sequencing technologies have shown significant improvements in read accuracy, throughput, read sizes, input material, analysis pipelines, costs, turnaround times etc.

Applications of bacterial genomics

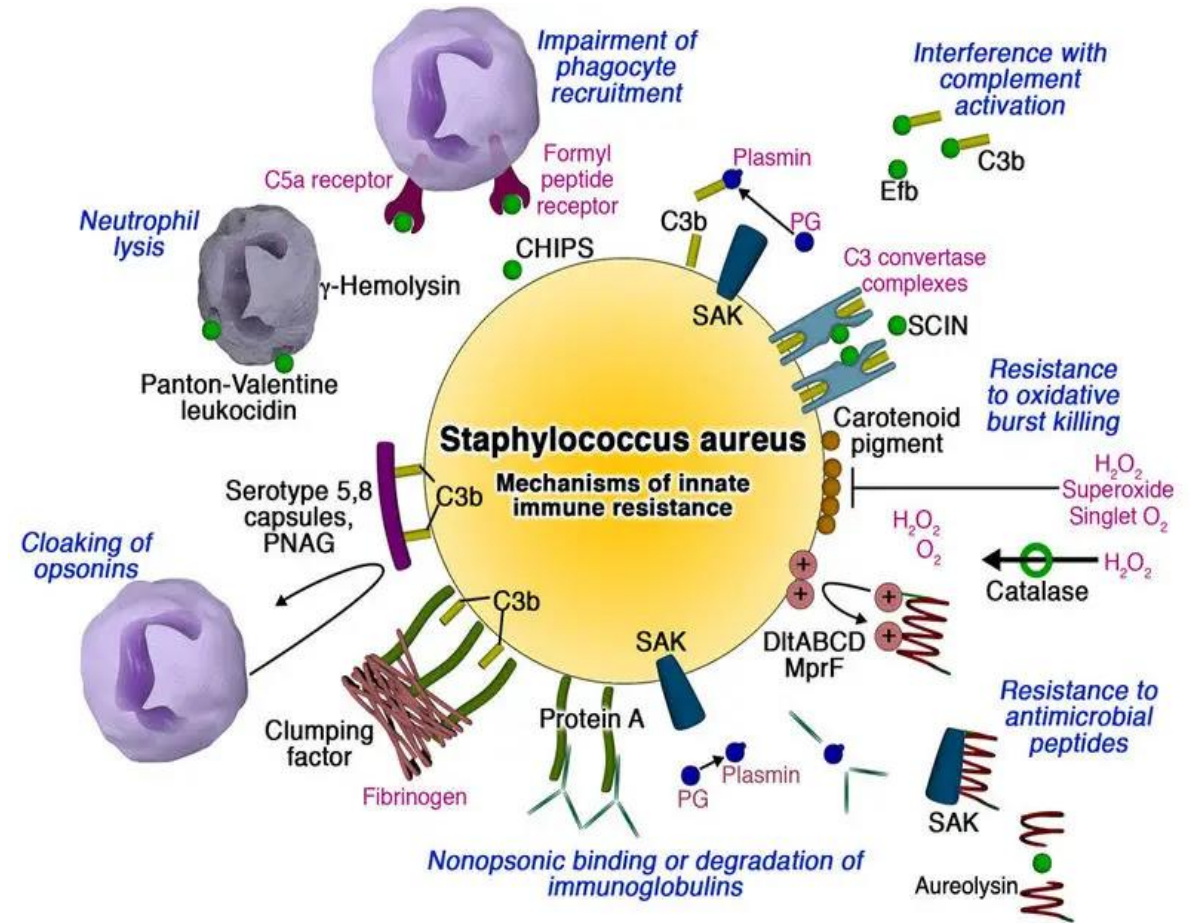
- **Understand microbial disease pathogenesis** (Adhesins, toxins, immune evasion etc.)
- **Antimicrobial resistance surveillance** (mechanisms of AMR, emergence, transmission, reservoirs, etc.)
- **Public health** (Outbreak detection, Outbreak spread and outbreak threats).
- **Microbial diagnostics** (rapid and accurate detection pathogens and associated AMR)
- **Drug and vaccine discovery**
- **Evolutionary biology** and microbial ecology (Microbiomes, biofilms, evolutionary relatedness etc).

***Staphylococcus aureus* pathogenicity/virulence**



Michihiro et al., 2019

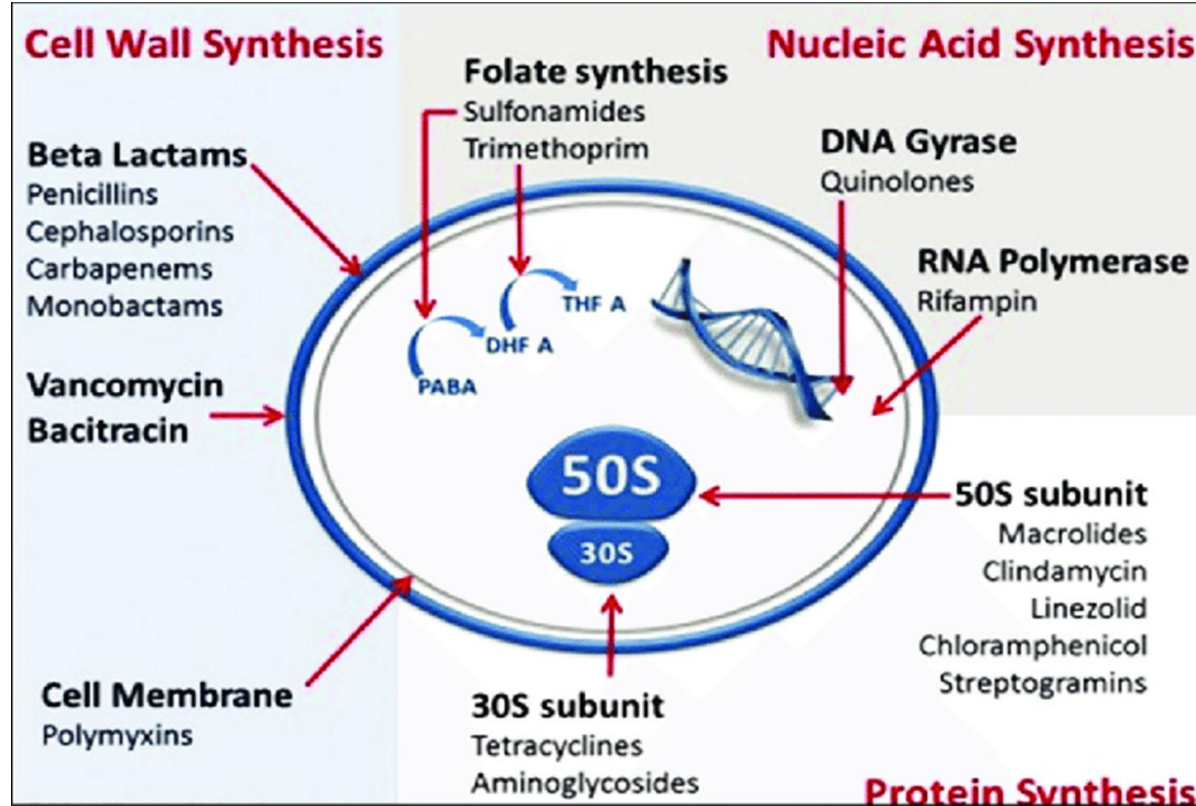
***S. aureus* adhesins and MSCRAMMs**



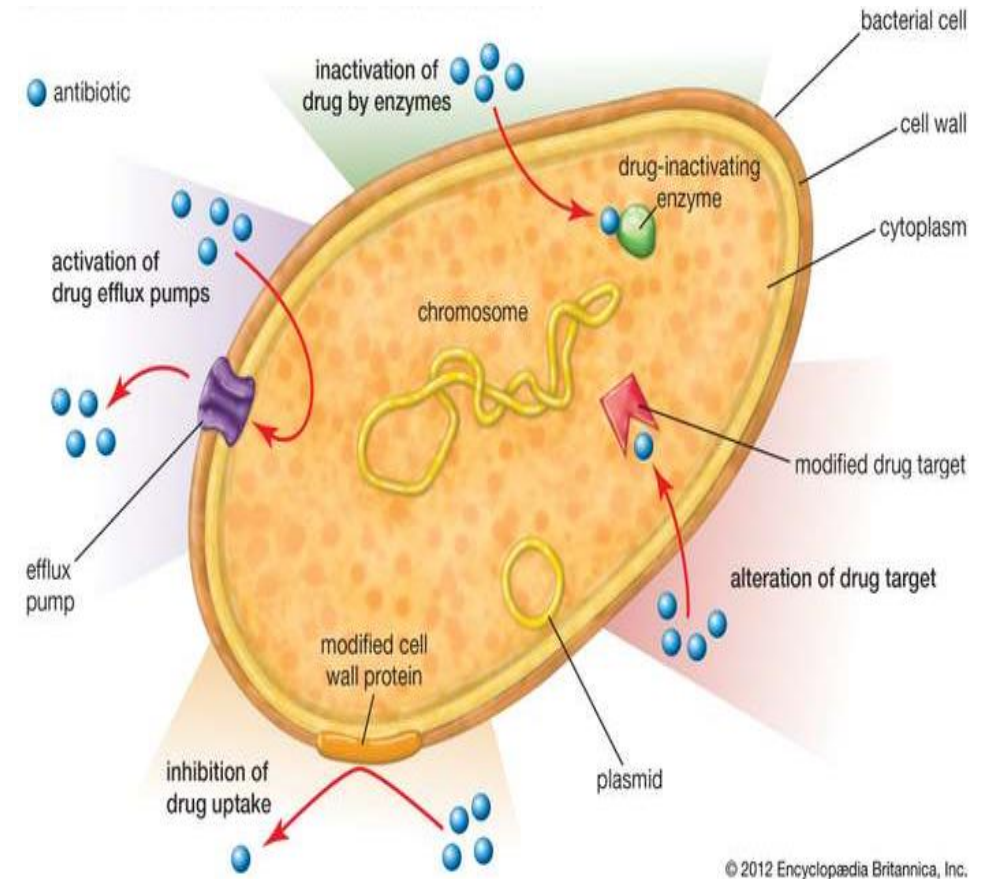
<https://microbeonline.com/>

***S. aureus* toxins and immune evasion**

Mechanisms of antimicrobial resistance



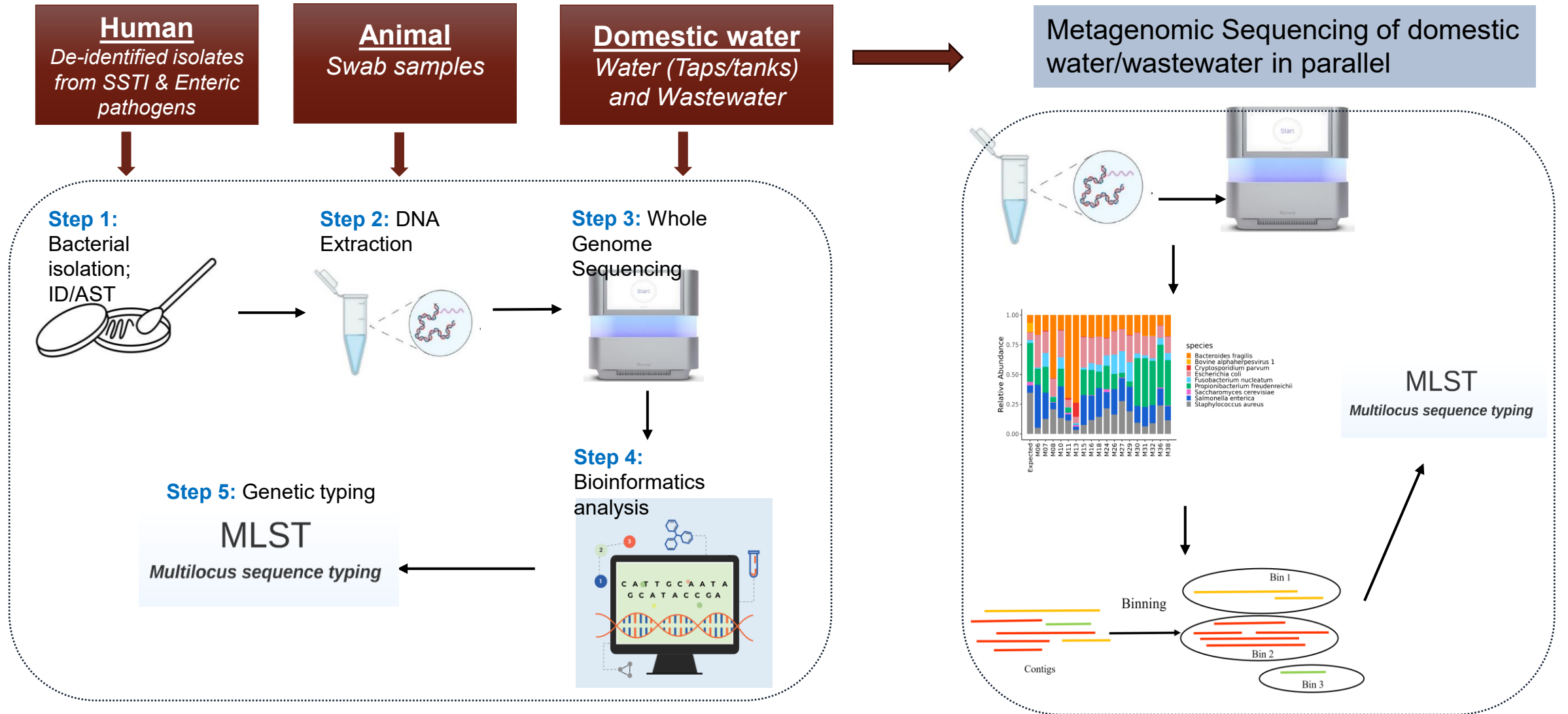
<https://britannica.com/>



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- Some resistance mechanisms are **gene-driven**, others **mutation-driven**
- Some resistance mechanisms are **chromosomal**, others are **plasmid-mediated**
- Some resistance mechanisms may be **known**, others **novel**.

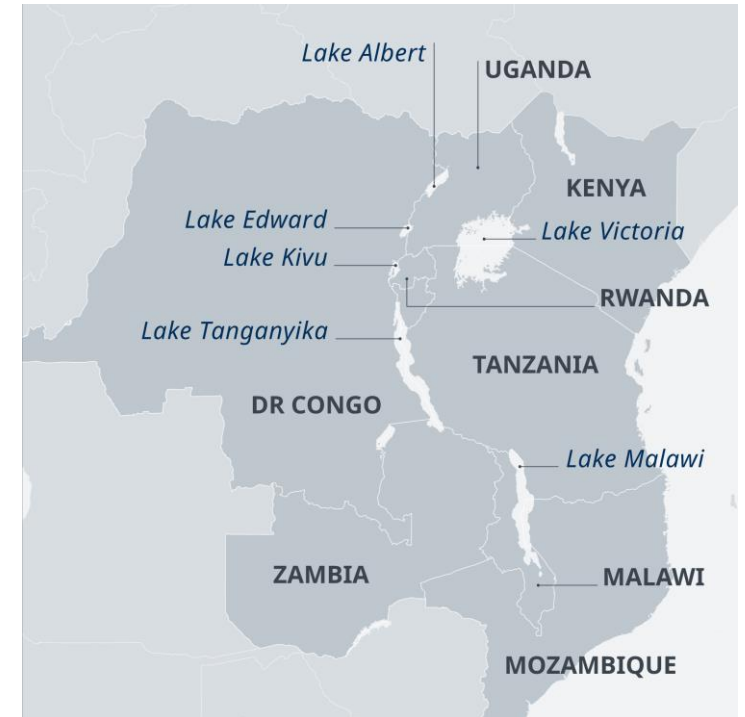
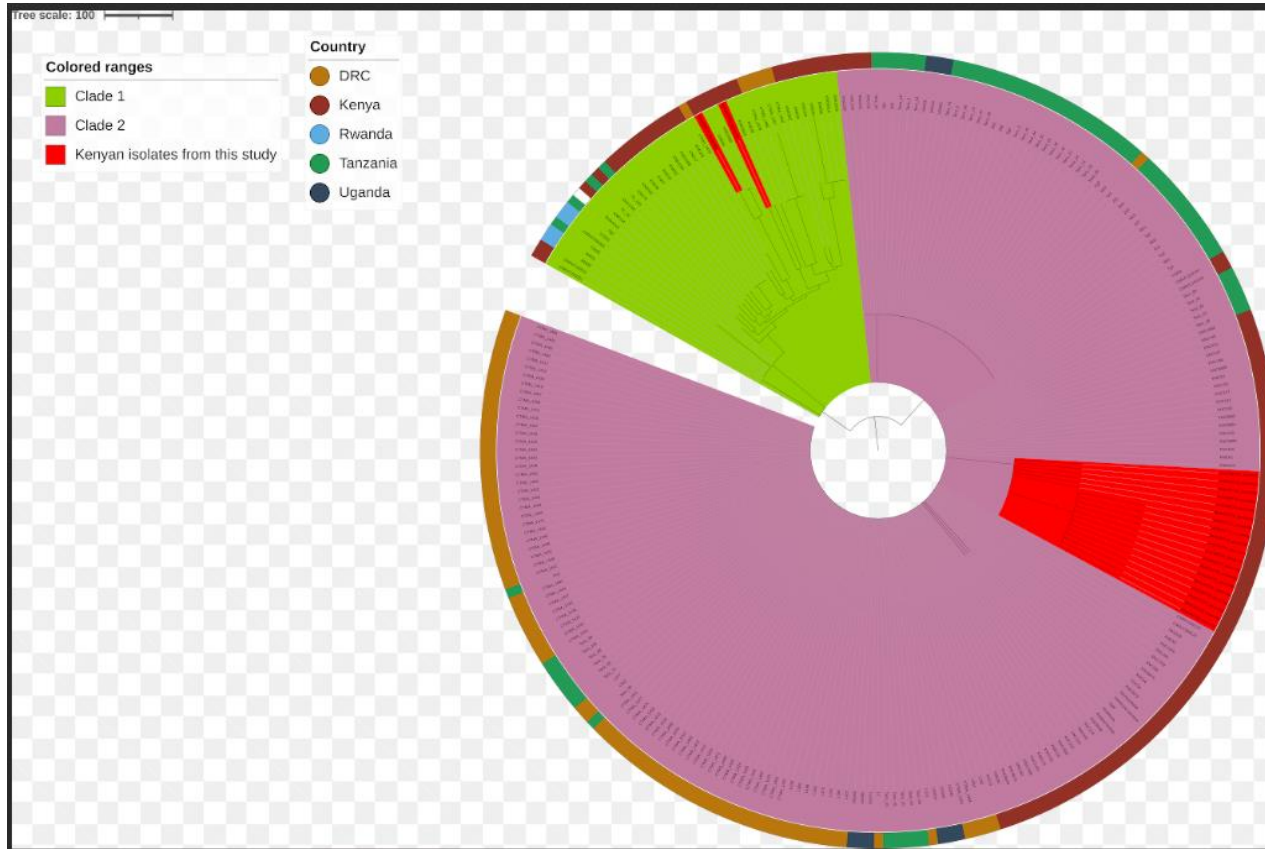
ONE HEALTH AMR Surveillance in Kenya



Credits: Collins Kigen

Proposed investigations in various parts of Kenya by Musila et al.,

Evolutionary relationships in space and time

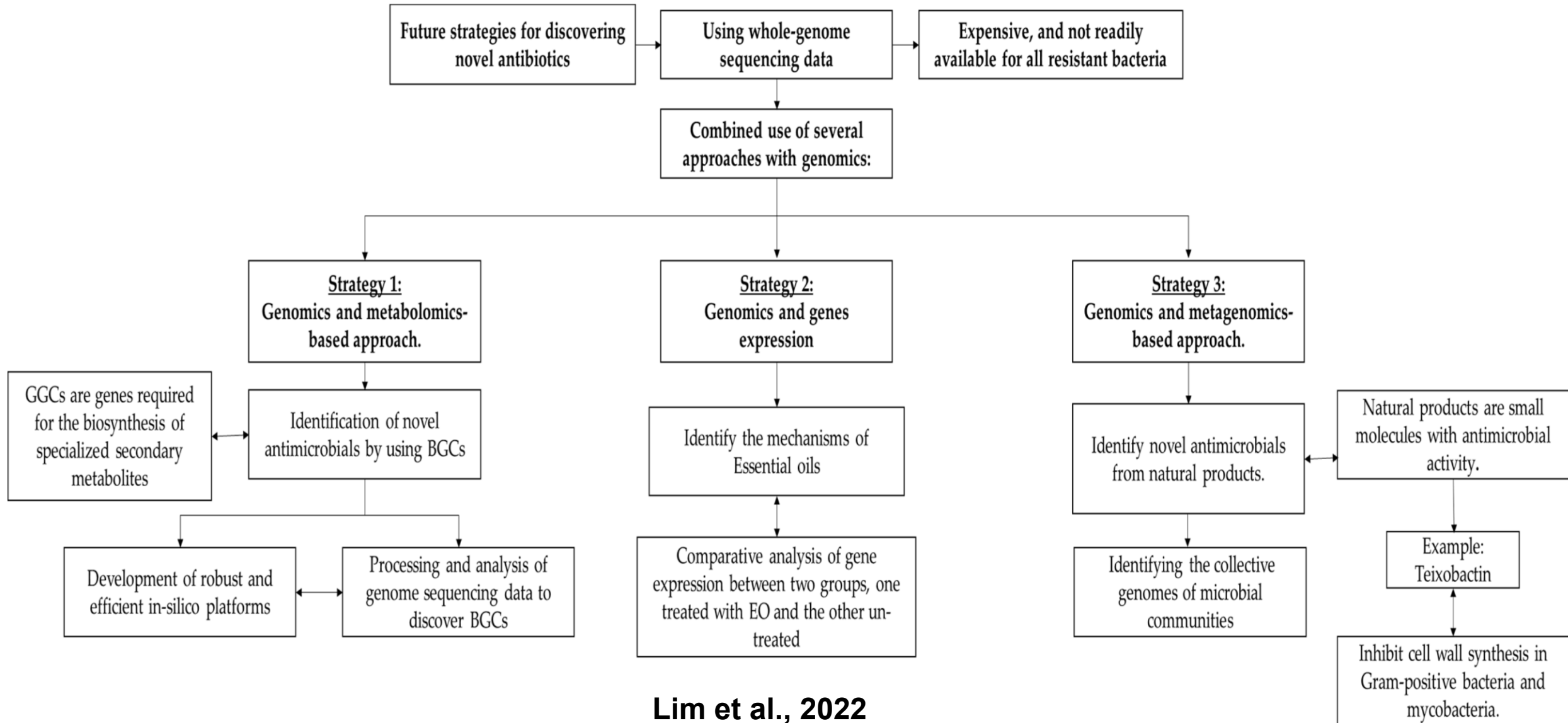


<https://mg.co.za/>

A phylogenetic analysis of *V. cholerae* genomes from the Great Lakes region. **Credits: Vanessa Natasha**

- Genomic analysis allows for serotype identification, single gene phylogeny (***spa* typing**), multi-gene phylogeny (**MLST**), core genome phylogeny (**cgMLST**), whole genome phylogeny (**wgMLST**).
- Various tree construction methods (and tools) are available.


Genomics for antibiotic discovery



Lim et al., 2022

Genomics for shigella vaccine discovery

The identification of novel immunogenic antigens as potential *Shigella* vaccine components


[Ruklanthi de Alwis](#)^{1,2}, [Li Liang](#)³, [Omid Taghavian](#)³, [Emma Werner](#)⁴, [Hao Chung The](#)⁵, [Trang Nguyen Hoang Thu](#)⁵, [Vu Thuy Duong](#)⁵, [D Huw Davies](#)³, [Philip L Felgner](#)³, [Stephen Baker](#)⁶,

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PMCID: PMC7809897 PMID: [33451348](#)

Article | [Open access](#) | Published: 31 January 2022

Pathogenomic analyses of *Shigella* isolates inform factors limiting shigellosis prevention and control across LMICs

[Rebecca J. Bengtsson](#), [Adam J. Simpkin](#), [Caisey V. Pulford](#), [Ross Low](#), [David A. Rasko](#), [Daniel J. Rigden](#), [Neil Hall](#), [Eileen M. Barry](#), [Sharon M. Tennant](#) & [Kate S. Baker](#)

[Nature Microbiology](#) **7**, 251–261 (2022) | [Cite this article](#)

Review Article | Published: 29 February 2016

The genomic signatures of *Shigella* evolution, adaptation and geographical spread

[Hao Chung The](#), [Duy Pham Thanh](#), [Kathryn E. Holt](#), [Nicholas R. Thomson](#) & [Stephen Baker](#)

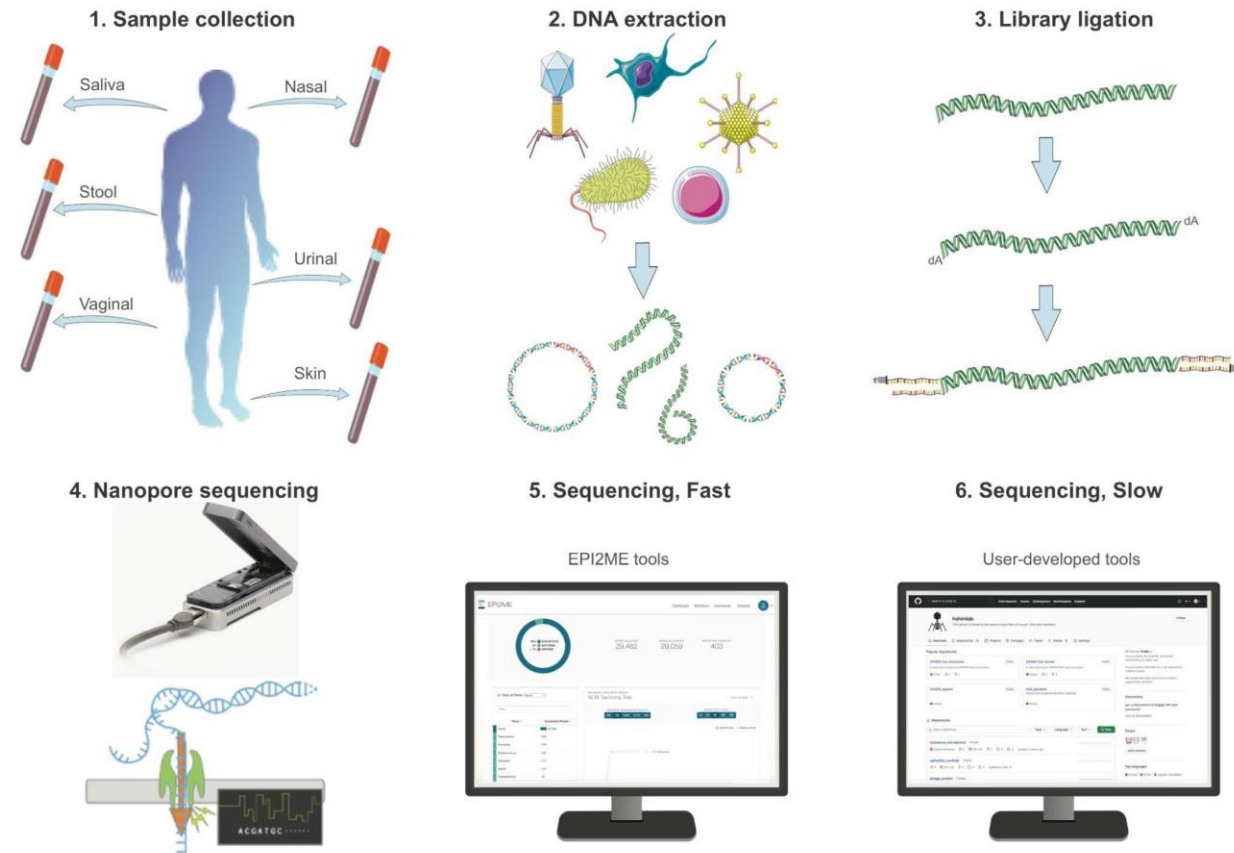
[Nature Reviews Microbiology](#) **14**, 235–250 (2016) | [Cite this article](#)

17k Accesses | **176** Citations | **18** Altmetric | [Metrics](#)

- Identify potential and conserved vaccine candidate targets
- Identify strain variation and changes over time
- Identify vaccine escape variants

Metagenomics for outbreak/Disease X detection

- The Great Lakes region is prone to various outbreaks (Mpox, Marburg, Cholera etc.)
- Outbreak response is often centralized and slow leading to greater casualties.
- ONT+ Bioinformatics show promise as a rapid, real-time, field-deployable diagnostic option for outbreak response especially in rural settings



Shim et al., 2023

The Great-Life project is testing the utility of ONT metagenomics for rapid detection of diarrheal pathogens in the Great Lakes region

Genomics for outbreak/Disease X detection in the Great Lakes

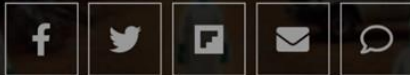
Mpox Outbreak in Uganda Situation Update - 14 March 2025

The total confirmed cases of mpox in Uganda are 4,342 with 31 cumulative deaths.

Kisumu Confirms Cholera Outbreak After 3 People Died



By OJWANG JOE
Published 6 days ago



Global health

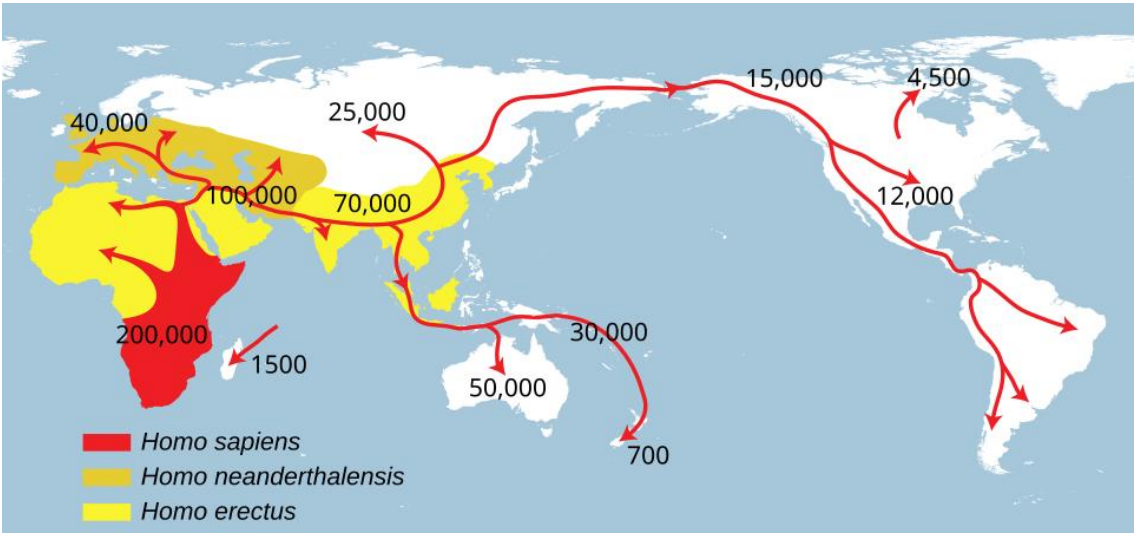
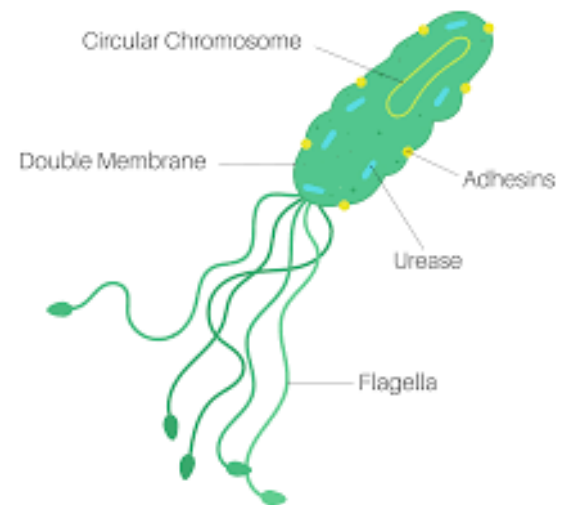
This article is more than 2 months old

Suspected outbreak of deadly Marburg virus disease kills eight in Tanzania

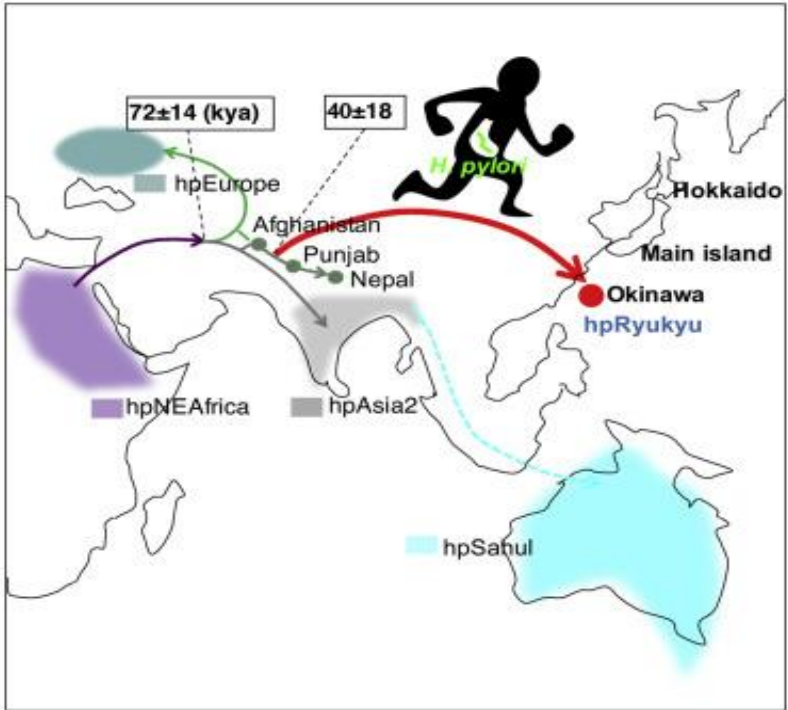
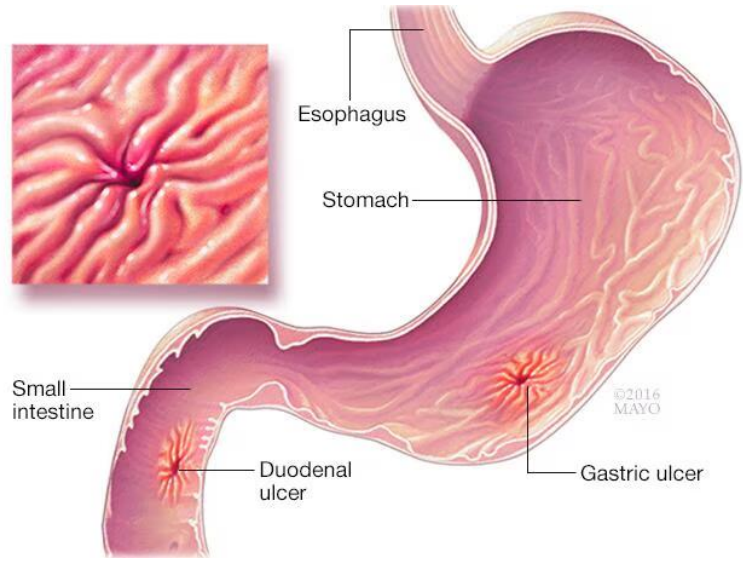


Mystery illness triggers panic in South Mugirango, Kisii

H. pylori predicts the evolutionary migration route of man




<https://en.wikipedia.org/>



Post-genomic applications

Article | [Open access](#) | Published: 23 September 2024

Core and accessory genomic traits of *Vibrio cholerae* O1 drive lineage transmission and disease severity

[Alexandre Maciel-Guerra](#), [Kubra Babaarslan](#), [Michelle Baker](#), [Aura Rahman](#), [Maqsud Hossain](#), [Abdus Sadique](#), [Jahidul Alam](#), [Salim Uzzaman](#), [Mohammad Ferdous Rahman Sarker](#), [Nasrin Sultana](#), [Ashraful Islam Khan](#), [Yasmin Ara Begum](#), [Mokibul Hassan Afrad](#), [Nicola Senin](#), [Zakir Hossain Habib](#), [Tahmina Shirin](#), [Firdausi Qadri](#) & [Tania Dottorini](#) 

Machine learning on the Core Genome and Mobilome of *Vibrio cholera* for outbreak prediction and source attribution – **Latifah Mukanga MSc. Dissertation**

Interactive discussion

THANK YOU