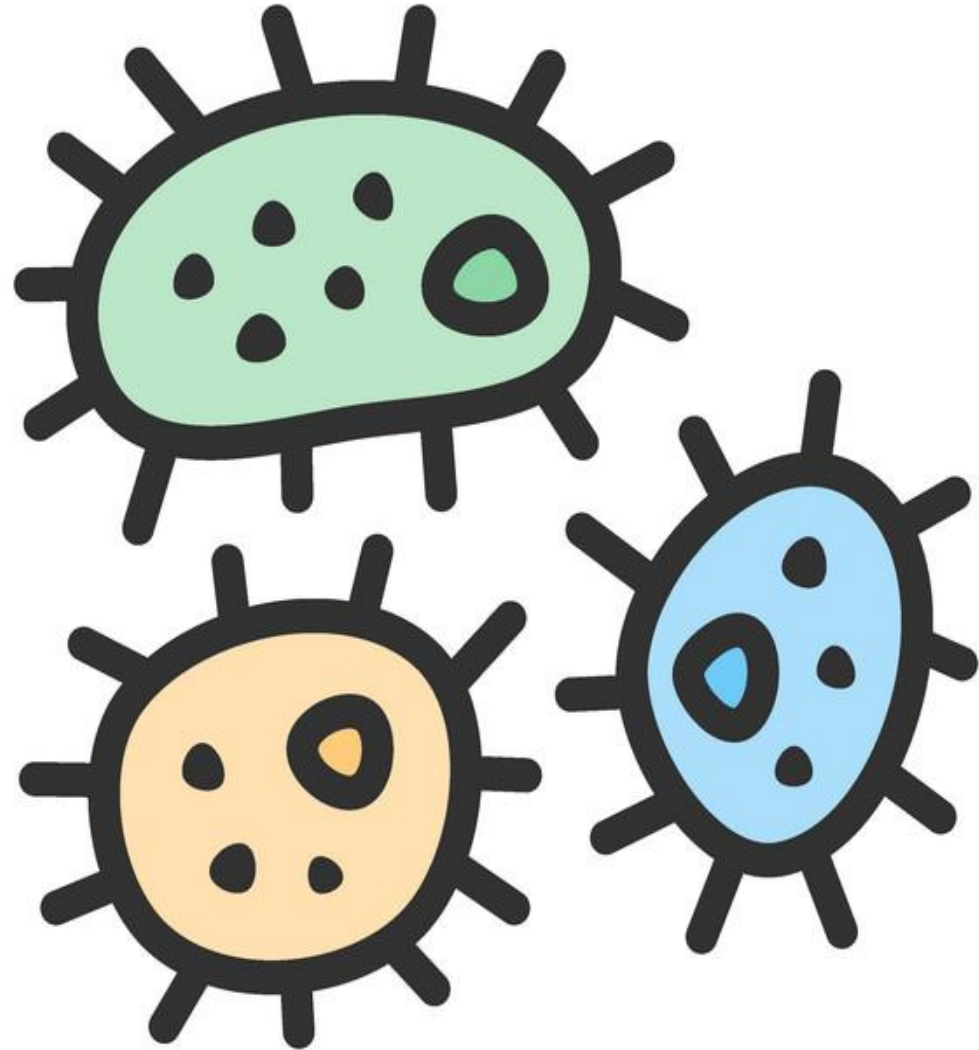
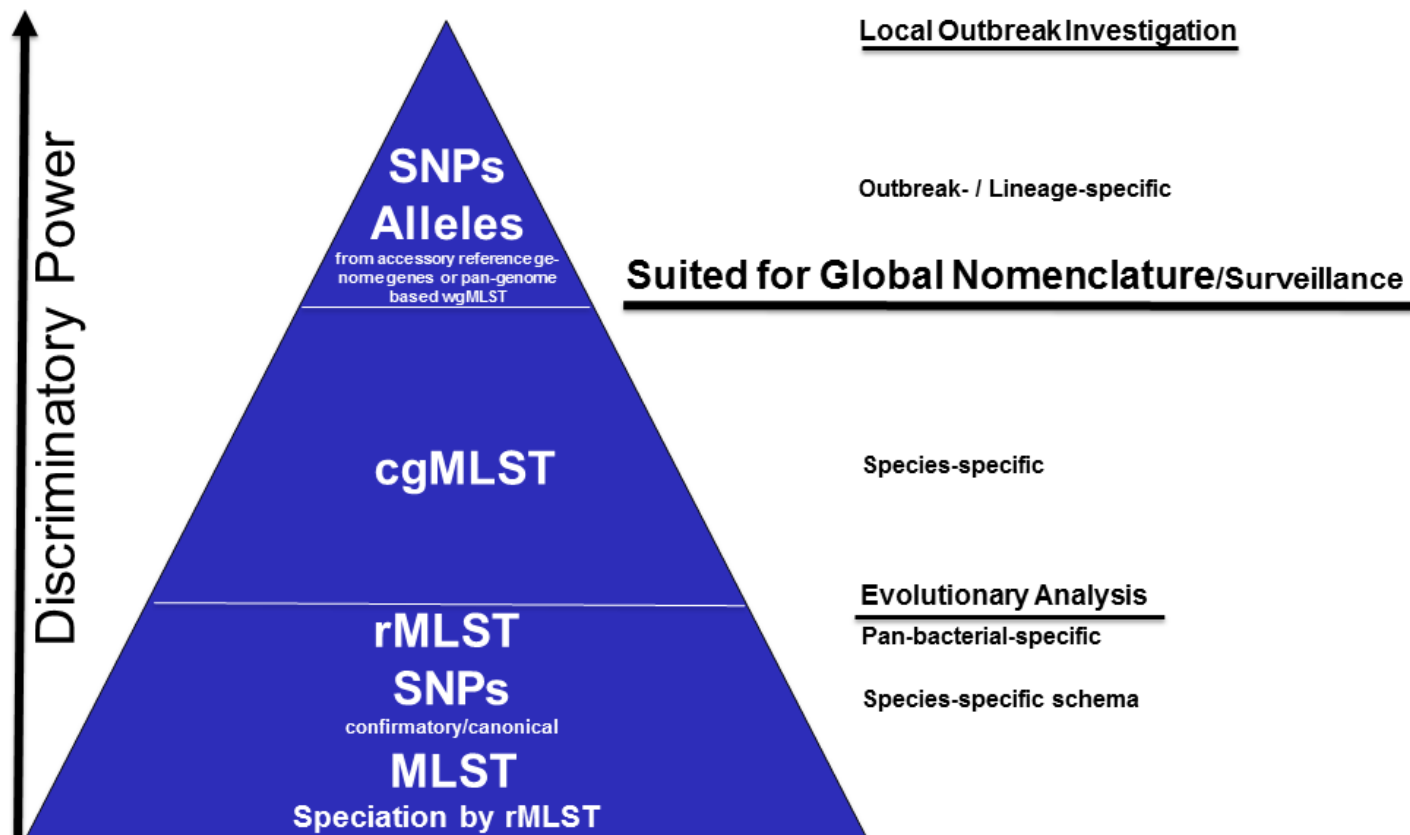


Bacterial Typing

Collins Kigen
18-July-2025



Discriminatory Power of genotyping



Clonal Complex

- ❖ Clonal Complex (CC): Group of closely related isolates with high genetic similarity
- ❖ Defined by MLST: Central Sequence Type (ST) + related STs (differ by 1–2 alleles)
- ❖ Applications:
 - Track outbreaks
 - Study bacterial evolution
 - Understand strain spread

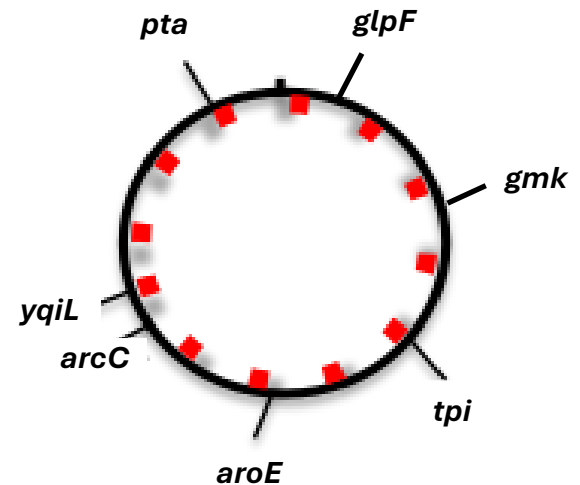
Tool: PubMLST

Clonal Complex	Sequence Type	<i>spa</i> Type
CC1 (n = 2)	ST8511 *	t127
	ST6 ^	t304/t648
CC5 (n = 8)	ST5	t13150
	ST4166 ^	t442/t6100
	ST7895	t002
	ST789	t091
CC8 (n = 82)	ST2416	t1476
	ST4803 ^	t008, t024, t064, t104, t121, t211, t1476
	ST4705	t2029
	ST6610	t293
	ST7635 ^	t030/t037
	ST7894	t037/t11766
	ST8 ^	t1476/t104
	ST239 **	t037
	ST241 **	t037/t2029
	ST7460	t1476

Nyasinga et.al., 2024

MLST

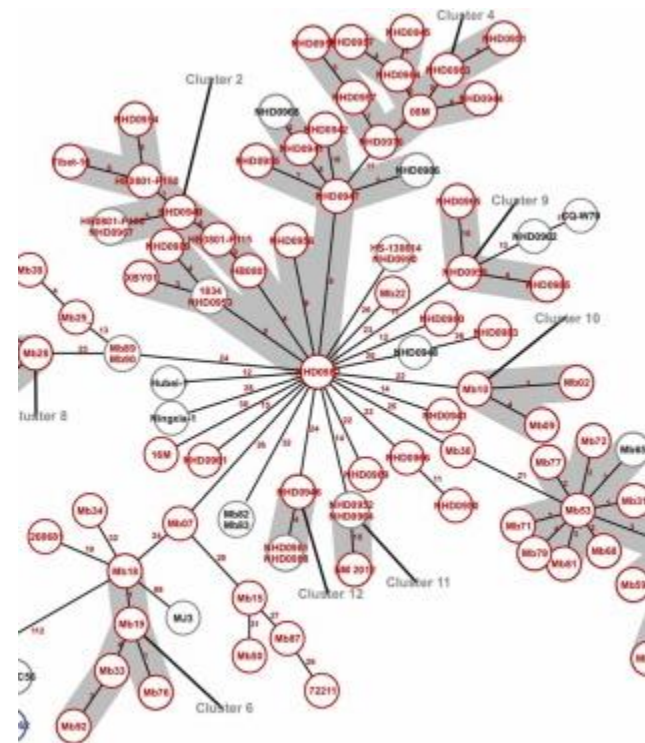
- ❖ MLST (Multilocus Sequence Typing)
- ❖ Characterizes isolates using sequences of 7 housekeeping genes
- ❖ Assigns a Sequence Type (ST) based on allelic profile
- ❖ Related STs form Clonal Complexes (CCs)
- ❖ Applications:
 - Global surveillance and epidemiology
 - Track evolution and outbreaks



Tool: mlst

cgMLST

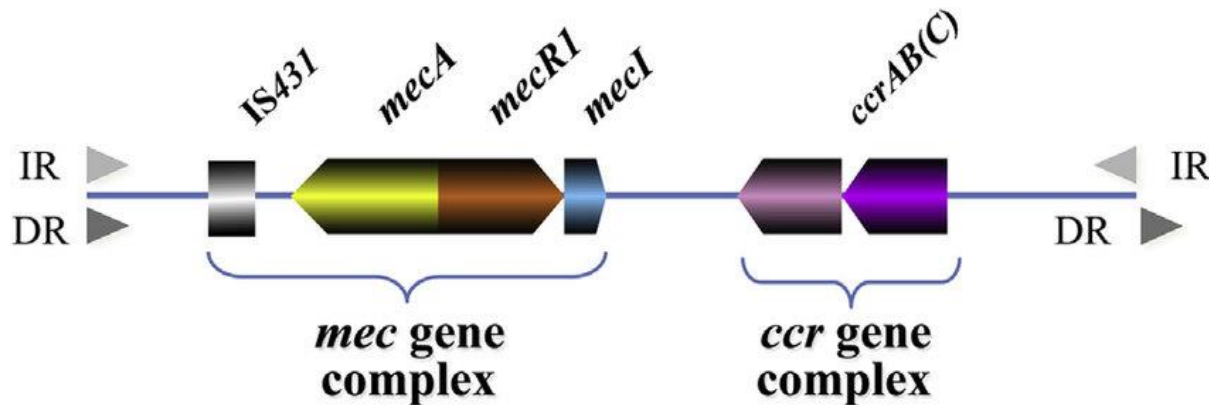
- ❖ cgMLST (Core Genome MLST)
- ❖ Targets ~1,500–3,000 core genes instead of 7 housekeeping genes
- ❖ Provides greater discriminatory power for closely related strains
- ❖ Advantages:
 - ❖ High-resolution typing for outbreak investigations
 - ❖ Reproducible and standardized across labs
- ❖ Applications:
 - ❖ Detailed epidemiology and cluster analysis
 - ❖ Tracing transmission chains



Tool: chewbbaca

SCCmec typing

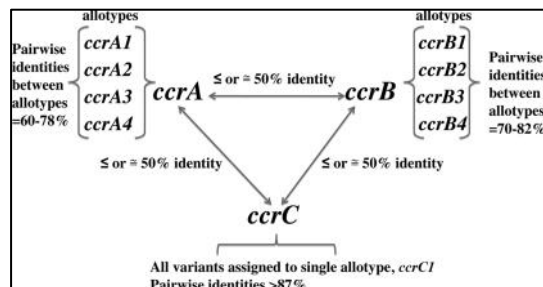
Staphylococcal cassette chromosome



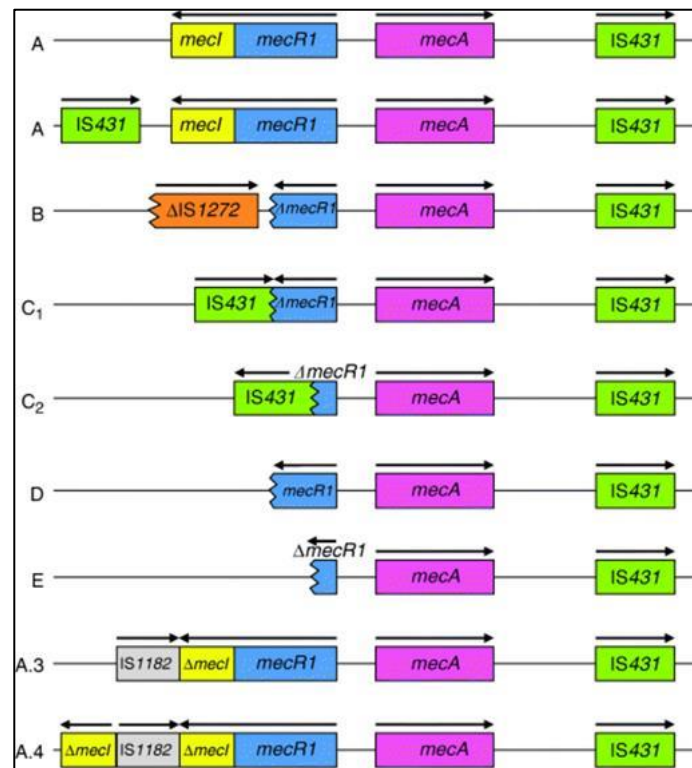
Tool: sccmec

SCCmec types

ccr complex types



mec complex types

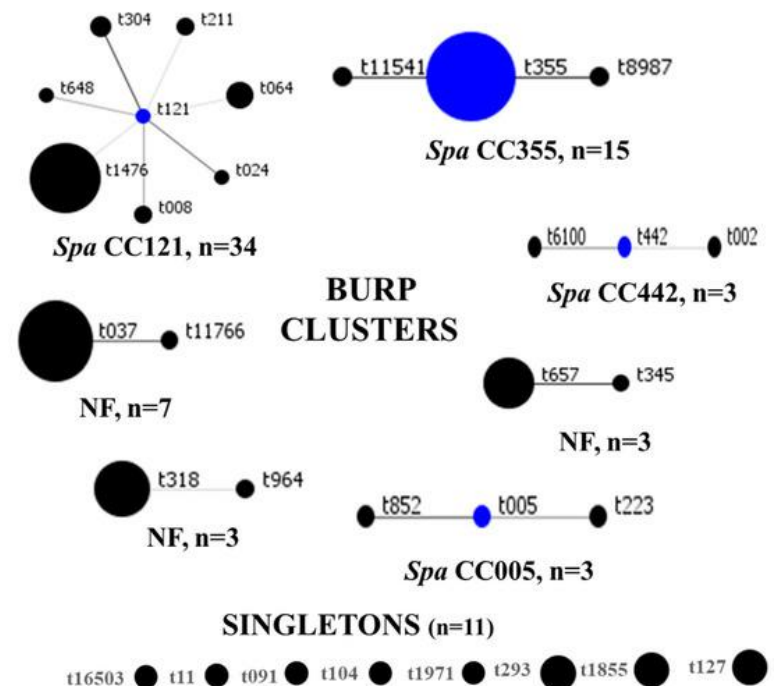


SCCmec types

SCCmec Type	Ccr Complex Type	mec Complex Class
I (1B)	1 (A1B1)	B
II (2A)	2 (A2B2)	A
III (3A)	3 (A3B3)	A
IV (2B)	2 (A2B2)	B
V (5C2)	5 (C1)	C2
VI (4B)	4 (A4B4)	B
VII (5C1)	5 (C1)	C1
VIII (4A)	4 (A4B4)	A
IX (1C2)	1 (A1B1)	C2
X (7C1)	7 (A1B6)	C1
XI (8E)	8 (A1B3)	E
XII (9C2)	9 (C2)	C2
XIII (9A)	9 (C2)	A
XIV (5A)	5 (C1)	A

Spa typing

- spa Typing (Staphylococcal Protein A typing):
- Based on sequence variation in the X region of the spa gene (tandem repeats)
- Assigns isolates a spa type (e.g., t008, t037)



Nyasinga et.al., 2024

Tool: spatyper

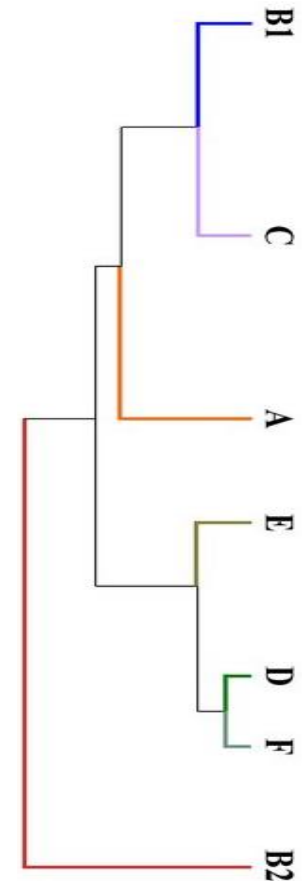
E. coli pathotyping

Pathotype	Key Marker Genes
EPEC	eae (intimin), bfpA
ETEC	lt (LT), st (ST)
EHEC/STEC	stx1, stx2, eae
EIEC	ipaH
EAEC	aggR, aafA
DAEC	daaE
UPEC	pap, hlyA, cnf1

Tool: abricate/VFDB

E. coli phylogroups

Phylogroup	Description/Pathotype
A	Commensal strains
B1	Commensal strains
B2	Extraintestinal pathogenic strain
C	Closely related but distinct from B1
D	Diffusely adherent
F	Enteroinvasive strains
G	Intermediate of B2 and F
E	Enteropathogenic strains
U/cryptic	Monophyletic cryptic clade



Tool: ezclermont



Typing Method

Capsular typing (K-locus)

O-locus typing

Pilus/Adhesin typing

Plasmid typing

Phage typing (in silico)

CRISPR typing

Sequence-based ribotyping

PorA/B typing (*Neisseria*)

fimH typing (*E. coli*)

emm typing (*Streptococcus pyogenes*)

PorA/PorB typing (*Neisseria*)

Toxin gene typing

VNTR/MIRU typing (*M. tuberculosis*)

Tools

Kaptive, Kleborate (*Klebsiella*)

Kaptive (*Klebsiella*, *Acinetobacter*)

Kleborate, custom BLAST

PlasmidFinder, mob-suite, mlplasmids

PHASTER, PHAST, phage_finder

CRISPRCasFinder, CRISPRDetect

RiboTree, custom rRNA BLAST

PubMLST *Neisseria*

FimTyper

emmTyper, SRST2

PubMLST schema

ToxFinder, VFDB (via ABRicate)

MIRU-VNTRplus, TB-Profiler

