How NSSLRL (Ireland) has implemented WGS-based AMR Surveillance

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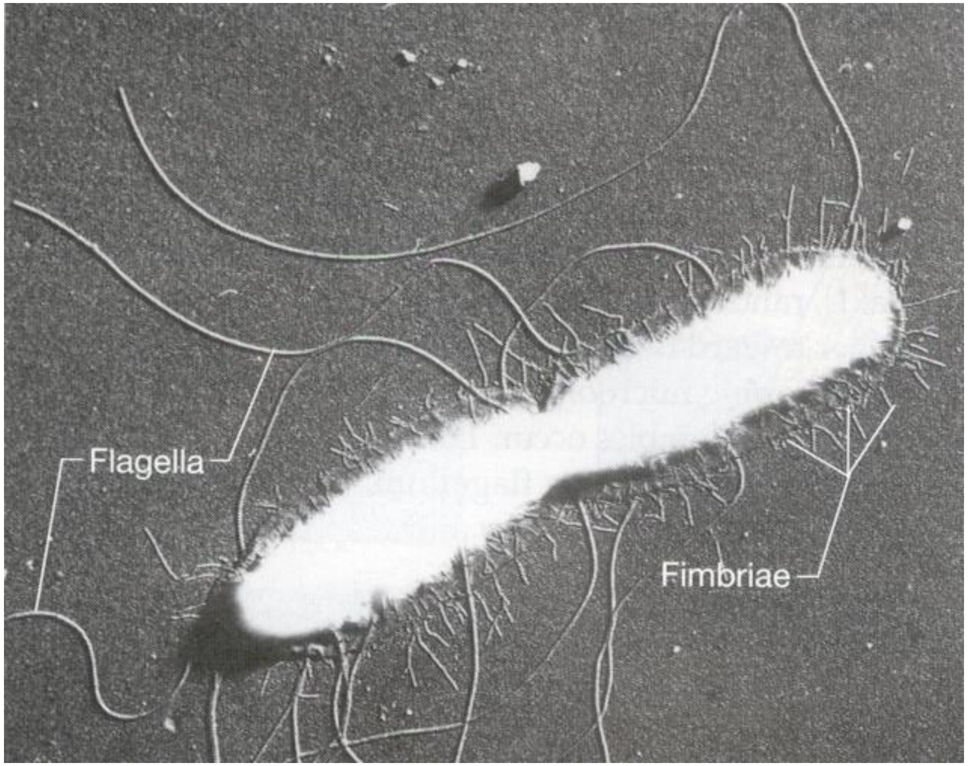
Galway Microbiology Reference Laboratory Services

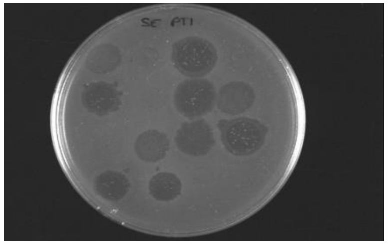
National *Salmonella*, *Shigella* & *Listeria* Reference Laboratory

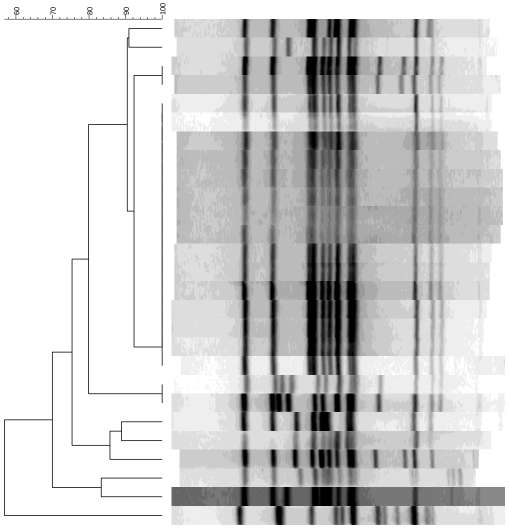
National Carbapenamase Producing Enterobacterales Reference Laboratory
(+ COVID)



Techniques

- Serotyping
- Phage Typing
- PFGE
- MLVA
- AST
  - Disk Diffusion
  - Broth Microdilution with TREK Sensititre
  - EUCAST Guidelines



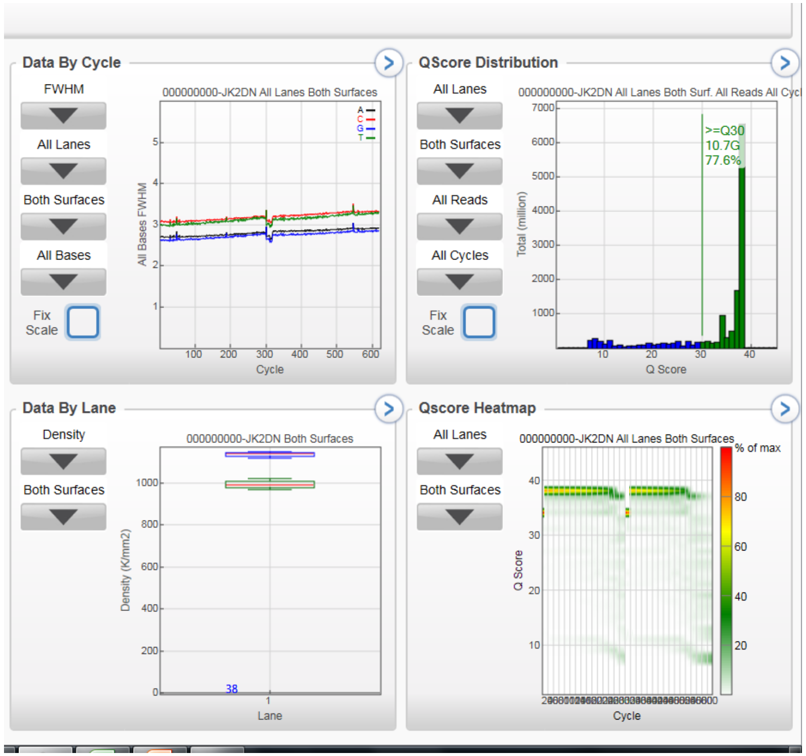


2010

WGS The Beginning

- End of 2015
- Extracted DNA and sent to PHE
- FileZilla software
- Downloaded fastq files
- Analysed

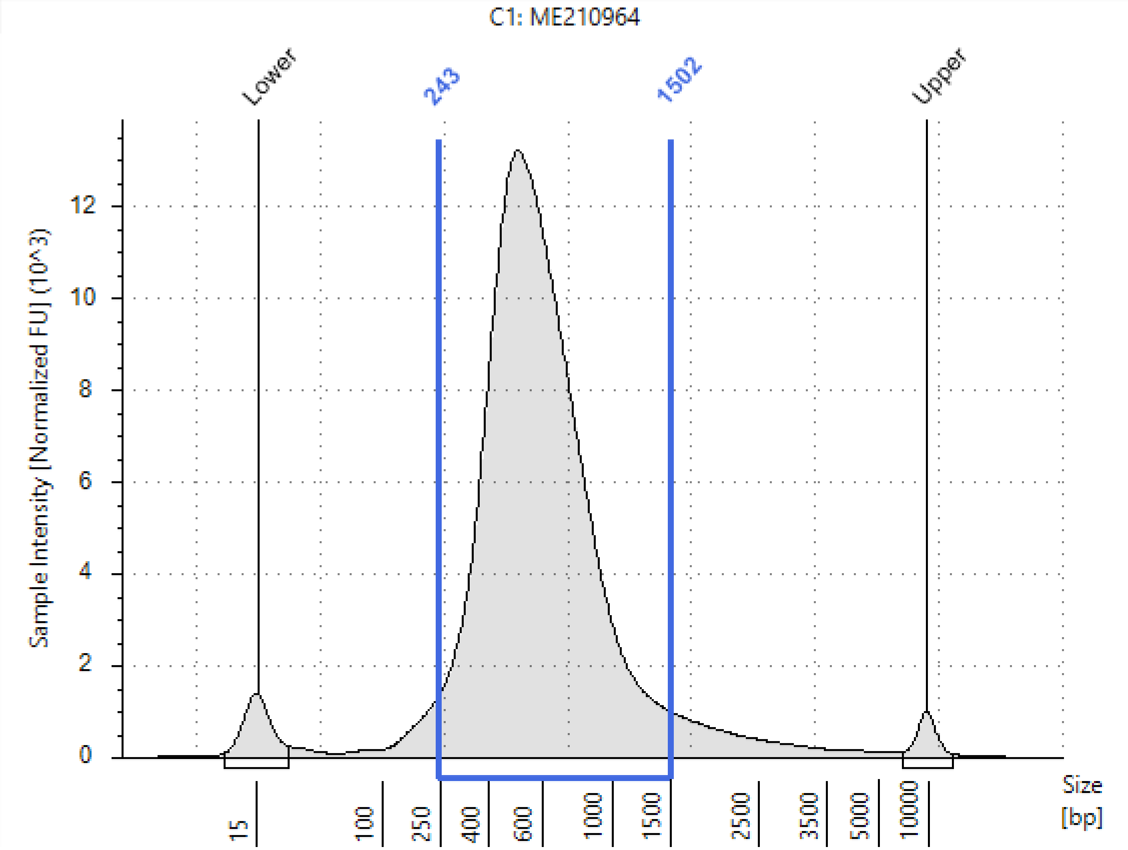
2018



- Qiagen EZ1
- MiSeq
- Illumina Nextera XT
  - Changed to Flex/DNA Prep (July 2019)
- MiSeq V3 kit
  - 300bp reads

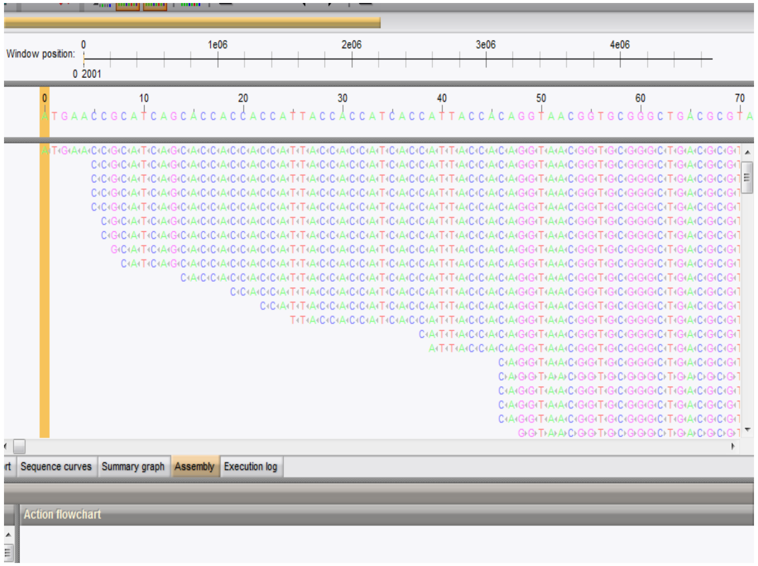
Robotic Liquid Handler

Tapestation



Analysis

- BioNumerics software
  - BioNumerics
  - EnteroBase
  - CGE
  - pubMLST
  - PathogenWatch



- Ran WGS and Conventional Techniques in Tandem until October 2018

AST Contamination

Broth MIC		**Resistance Genes**
ASSuTTmNaCp	v	none
ASuTNaCpAzt	v	ASuT
T	v	none (*E.coli*)
ASu	v	none

On repeat all matched with resistance genes

ASuTTmNaCp

ast Name	Specimen /	Iso.	Organism	Source	Species
	MS180241				
	MS180241	1	Salmonella species	Faeces	Human

Plates Read
○ Show All
● EUVSEC
○ EUVSEC

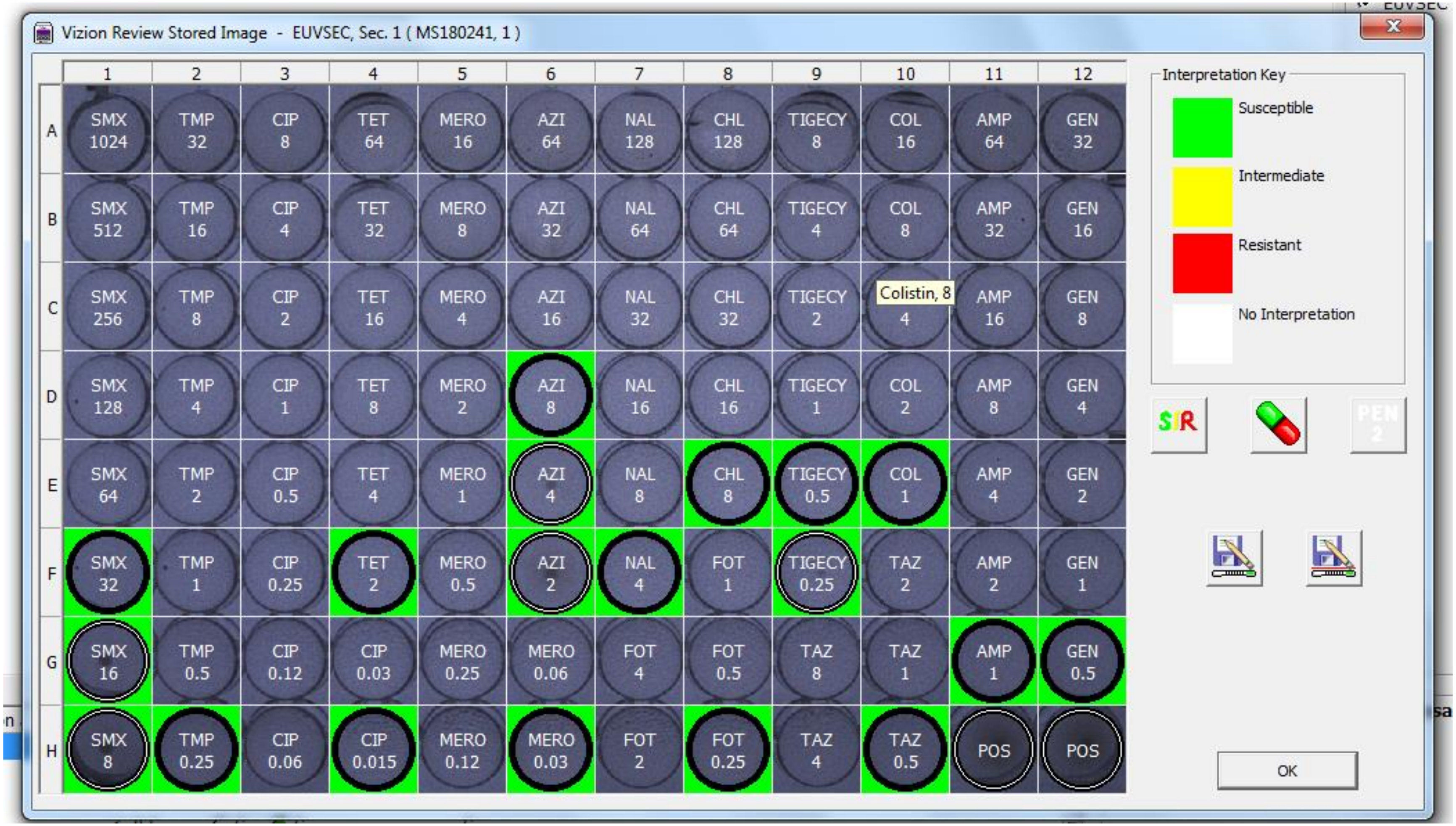
Vizion Review Stored Image - EUVSEC, Sec. 1 (MS180241, 1)

	1	2	3	4	5	6	7	8	9	10	11	12
A	SMX 1024	TMP 32	CIP 8	TET 64	MERO 16	AZI 64	NAL 128	CHL 128	TIGECY 8	COL 16	AMP 64	GEN 32
B	SMX 512	TMP 16	CIP 4	TET 32	MERO 8	AZI 32	NAL 64	CHL 64	TIGECY 4	COL 8	AMP 32	GEN 16
C	SMX 256	TMP 8	CIP 2	TET 16	MERO 4	AZI 16	NAL 32	CHL 32	TIGECY 2	COL 4	AMP 16	GEN 8
D	SMX 128	TMP 4	CIP 1	TET 8	MERO 2	AZI 8	NAL 16	CHL 16	TIGECY 1	COL 2	AMP 8	GEN 4
E	SMX 64	TMP 2	CIP 0.5	TET 4	MERO 1	AZI 4	NAL 8	CHL 8	TIGECY 0.5	COL 1	AMP 4	GEN 2
F	SMX 32	TMP 1	CIP 0.25	TET 2	MERO 0.5	AZI 2	NAL 4	FOT 1	TIGECY 0.25	TAZ 2	AMP 2	GEN 1
G	SMX 16	TMP 0.5	CIP 0.12	CIP 0.03	MERO 0.25	MERO 0.06	FOT 4	FOT 0.5	TAZ 8	TAZ 1	AMP 1	GEN 0.5
H	SMX 8	TMP 0.25	CIP 0.06	CIP 0.015	MERO 0.12	MERO 0.03	FOT 2	FOT 0.25	TAZ 4	TAZ 0.5	POS	POS

Nalidixic Acid, 32

Interpretation Key
🟩 Susceptible
🟨 Intermediate
🟥 Resistant
⬜ No Interpretation

No Resistance



Vizion Review Stored Image - EUVSEC, Sec. 1 (MS180241, 1)

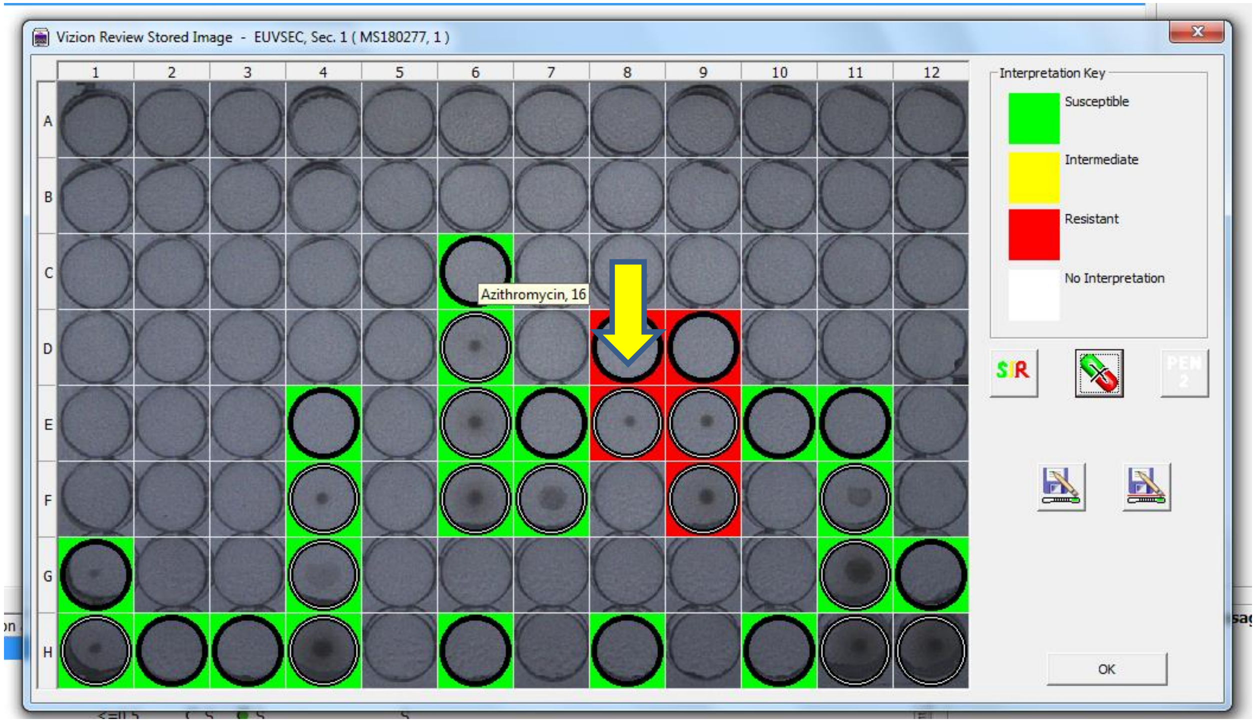
	1	2	3	4	5	6	7	8	9	10	11	12
A	SMX 1024	TMP 32	CIP 8	TET 64	MERO 16	AZI 64	NAL 128	CHL 128	TIGECY 8	COL 16	AMP 64	GEN 32
B	SMX 512	TMP 16	CIP 4	TET 32	MERO 8	AZI 32	NAL 64	CHL 64	TIGECY 4	COL 8	AMP 32	GEN 16
C	SMX 256	TMP 8	CIP 2	TET 16	MERO 4	AZI 16	NAL 32	CHL 32	TIGECY 2	Colistin, 8 4	AMP 16	GEN 8
D	SMX 128	TMP 4	CIP 1	TET 8	MERO 2	🟩 AZI 8	NAL 16	CHL 16	TIGECY 1	COL 2	AMP 8	GEN 4
E	SMX 64	TMP 2	CIP 0.5	TET 4	MERO 1	🟩 AZI 4	NAL 8	🟩 CHL 8	🟩 TIGECY 0.5	🟩 COL 1	AMP 4	GEN 2
F	🟩 SMX 32	TMP 1	CIP 0.25	🟩 TET 2	MERO 0.5	🟩 AZI 2	🟩 NAL 4	FOT 1	🟩 TIGECY 0.25	TAZ 2	AMP 2	GEN 1
G	🟩 SMX 16	TMP 0.5	CIP 0.12	CIP 0.03	MERO 0.25	MERO 0.06	FOT 4	FOT 0.5	TAZ 8	TAZ 1	🟩 AMP 1	🟩 GEN 0.5
H	🟩 SMX 8	🟩 TMP 0.25	CIP 0.06	🟩 CIP 0.015	MERO 0.12	🟩 MERO 0.03	FOT 2	🟩 FOT 0.25	TAZ 4	🟩 TAZ 0.5	POS	POS

Interpretation Key

- 🟩 Susceptible
- 🟨 Intermediate
- 🟥 Resistant
- ⬜ No Interpretation

Validation

- 412/418 isolates correlated (98.6%)
- Resistance to Chloramphenicol (n=3) with no corresponding gene
- MIC=16



Discrepancies

- Azithromycin resistance (n=2) with no corresponding genes
  - MIC=32 & MIC=64
  - ? Variations in Efflux Pumps
  - acrB efflux pump
- *sul*1 gene present & MIC=16 (Susceptible)

Trimethoprim *Salmonella*

- No *dfr*A genes MIC <=2
- *dfr*A1 100% n=8 >32
- *dfr*A5 100% n=1 >32
- dfrA7 100% n=6 >32
- *dfr*A12 100% n=14 >32
- *dfr*A14 99.59-.79 n=12 >32

1. Azithromycin has been used in the treatment of enteric infections, primarily with Salmonella Typhi and Shigella spp. For wild-type isolates of both species, the MICs are ≤16 mg/L and the inhibition zone diameters for the azithromycin 15 µg disk ≥12 mm.

Salmonella

Resistant

mph(A)	n= 4	MIC = 64	
No genes	n=35	MIC = 32	ST65 *S.*Brandenburg

? Efflux pumps

Susceptible

No genes	n=28	MIC = 16
No genes	n=619	MIC <= 8

ESBL in *Salmonella*

- ESBL Phenotype
  - blaCTX-M-15 (2)
  - blaCTX-M-14 (1)
  - blaCTX-M-14b (1)
  - blaSHV-12 (2)
  - blaCMY-2 (1)
  - blaDHA-1 (1)

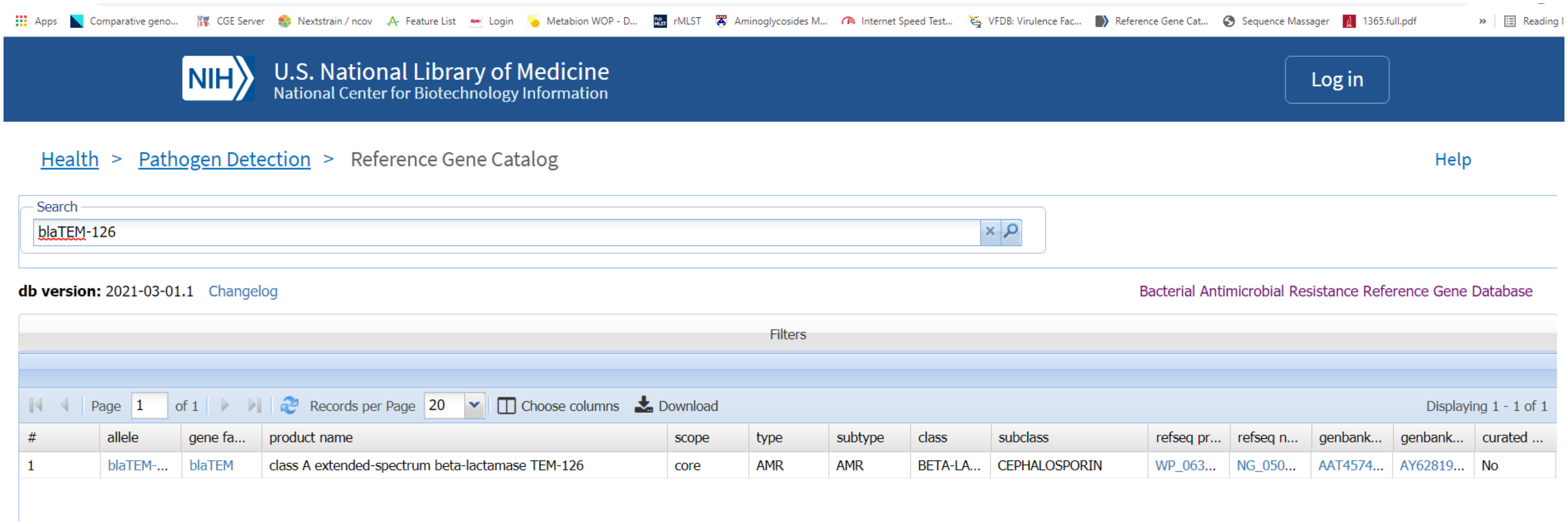
Non-ESBL Phenotype

- *bla*TEM
  - -1A (2), 1B (186), -1C (3), -57 (2), -104 (1), -126 (38), -143 (1), -166 (1)
- *bla*CARB-2 (23)
- *bla*OXA-1 (3), *bla*OXA-10 (1)

*bla*TEM-126 (99.77 & 99.88%)

*bla*TEM-143 (95.55%)

NCBI Reference Gene Catalog
TEM-126



Health > Pathogen Detection > Reference Gene Catalog

Search: blaTEM-126

db version: 2021-03-01.1 Changelog

Bacterial Antimicrobial Resistance Reference Gene Database

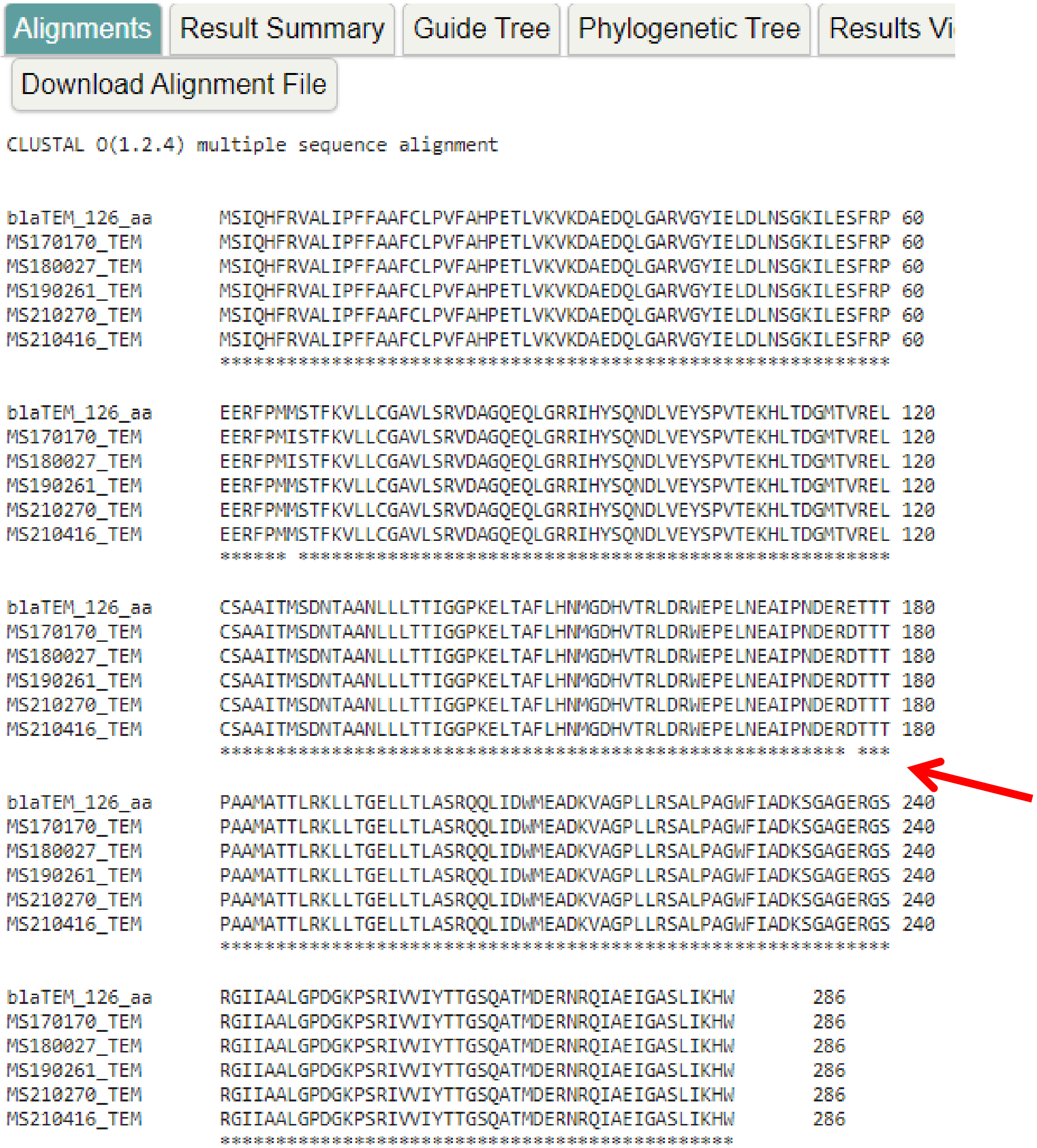
#	allele	gene fa...	product name	scope	type	subtype	class	subclass	refseq pr...	refseq n...	genbank...	genbank...	curated ...
1	blaTEM-...	blaTEM	class A extended-spectrum beta-lactamase TEM-126	core	AMR	AMR	BETA-LA...	CEPHALOSPORIN	WP_063...	NG_050...	AAT4574...	AY62819...	No

*bla*TEM-126

Nucleotide Differences

Some with 2 (99.77% ID) and some with 1 (99.88%) nt differences.

Both resulted in the same 1 Amino Acid Substitution



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CLUSTAL O(1.2.4) multiple sequence alignment


blaTEM_126_aa      MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRP 60
MS170170_TEM       MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRP 60
MS180027_TEM       MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRP 60
MS190261_TEM       MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRP 60
MS210270_TEM       MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRP 60
MS210416_TEM       MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRP 60
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blaTEM_126_aa      EERFPMMSTFKVLLCGAVLSRVDAGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVREL 120
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MS180027_TEM       EERFPMISTFKVLLCGAVLSRVDAGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVREL 120
MS190261_TEM       EERFPMMSTFKVLLCGAVLSRVDAGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVREL 120
MS210270_TEM       EERFPMMSTFKVLLCGAVLSRVDAGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVREL 120
MS210416_TEM       EERFPMMSTFKVLLCGAVLSRVDAGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVREL 120
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blaTEM_126_aa      CSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRLDRWEPELNEAIPNDERETTT 180
MS170170_TEM       CSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTT 180
MS180027_TEM       CSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTT 180
MS190261_TEM       CSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTT 180
MS210270_TEM       CSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTT 180
MS210416_TEM       CSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTT 180
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MS170170_TEM       PAAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGS 240
MS180027_TEM       PAAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGS 240
MS190261_TEM       PAAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGS 240
MS210270_TEM       PAAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGS 240
MS210416_TEM       PAAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGS 240
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MS180027_TEM       RGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIAEIGASLIKHW       286
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MS210270_TEM       RGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIAEIGASLIKHW       286
MS210416_TEM       RGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIAEIGASLIKHW       286
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blaTEM-143

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CLUSTAL O(1.2.4) multiple sequence alignment


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                                 **********************************************

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                   ************************************************************

blaTEM_143_RC      CAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAA 180
MS170063_TEM       cagtgctgcaatgataccgcgagacccacgctcaccggctccagatttatcagcaataaa 166
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blaTEM_143_RC      CCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCA 240
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                   ************************************************************

blaTEM_143_RC      GTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAA 300
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blaTEM_143_RC      CGTTGTTGCCATTGCTGCAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATT 360
MS170063_TEM       cgttgttgccattgctgcaggcatcgtggtgtcacgctcgtnnnttggtatggcttcatt 346
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blaTEM_143_RC      CAGCTCCGGTTCCCAACAATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGC 420
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                   ********                    ********************************

blaTEM_143_RC      GGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCAGCAGTGTTATCACT 480
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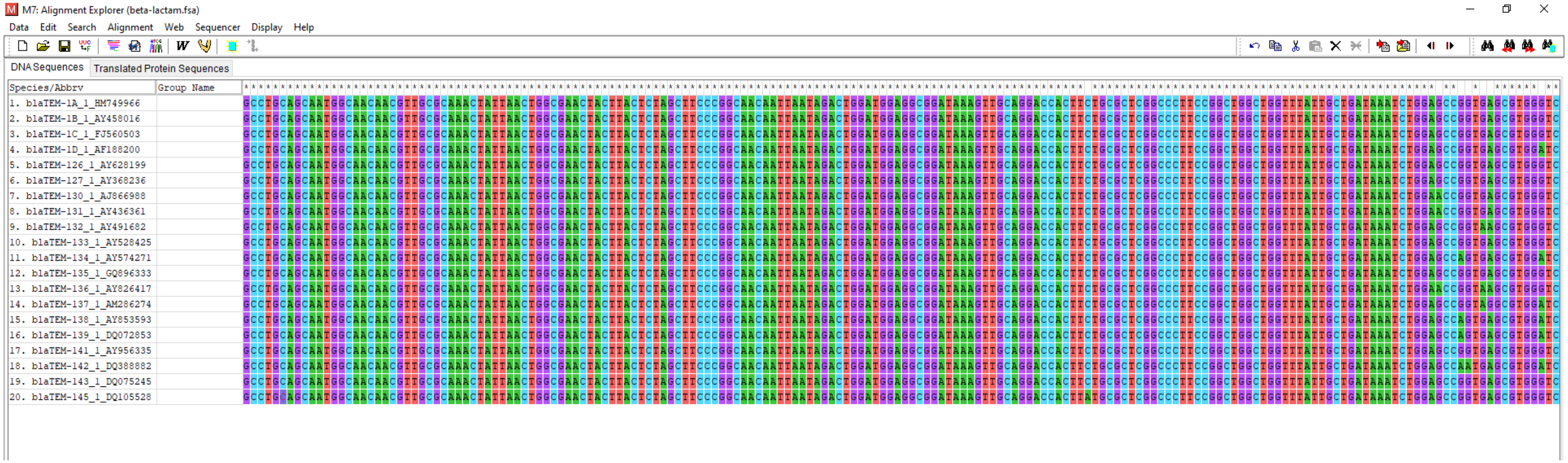
Mega



Species/Abbrv	Group Name
1. blaTEM-1A_1_HM749966	
2. blaTEM-1B_1_AY458016	
3. blaTEM-1C_1_FJ560503	
4. blaTEM-1D_1_AF188200	
5. blaTEM-126_1_AY628199	
6. blaTEM-127_1_AY368236	
7. blaTEM-130_1_AJ866988	
8. blaTEM-131_1_AY436361	
9. blaTEM-132_1_AY491682	
10. blaTEM-133_1_AY528425	
11. blaTEM-134_1_AY574271	
12. blaTEM-135_1_GQ896333	
13. blaTEM-136_1_AY826417	
14. blaTEM-137_1_AM286274	
15. blaTEM-138_1_AY853593	
16. blaTEM-139_1_DQ072853	
17. blaTEM-141_1_AY956335	
18. blaTEM-142_1_DQ388882	
19. blaTEM-143_1_DQ075245	
20. blaTEM-145_1_DQ105528	

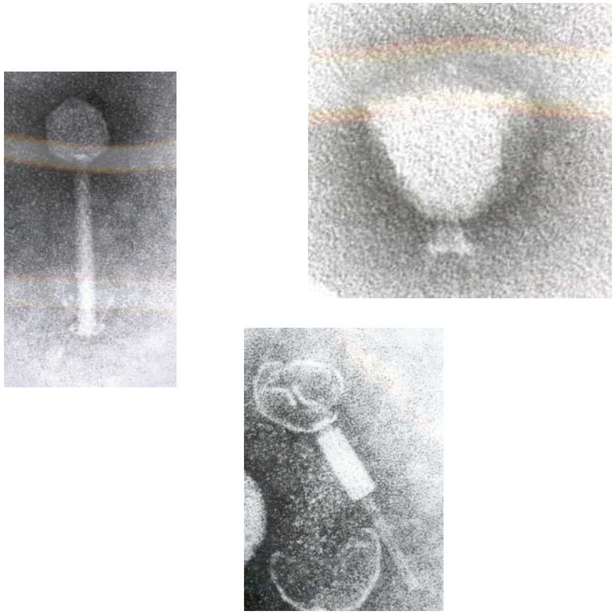
Many TEM enzymes vary by just one SNP

There exists large discrepancies in the functional subclass assignment (e.g. narrow-spectrum, ESBL etc.) of beta-lactamases across the various AMR databases.

Functional class assignment for the SHV beta-lactamases is particularly complicated because some intrinsic SHV alleles seem to have been mis-identified as causal variants of extended-spectrum or inhibitor resistances, due to the difficulties in distinguishing chromosomal and mobile variants.

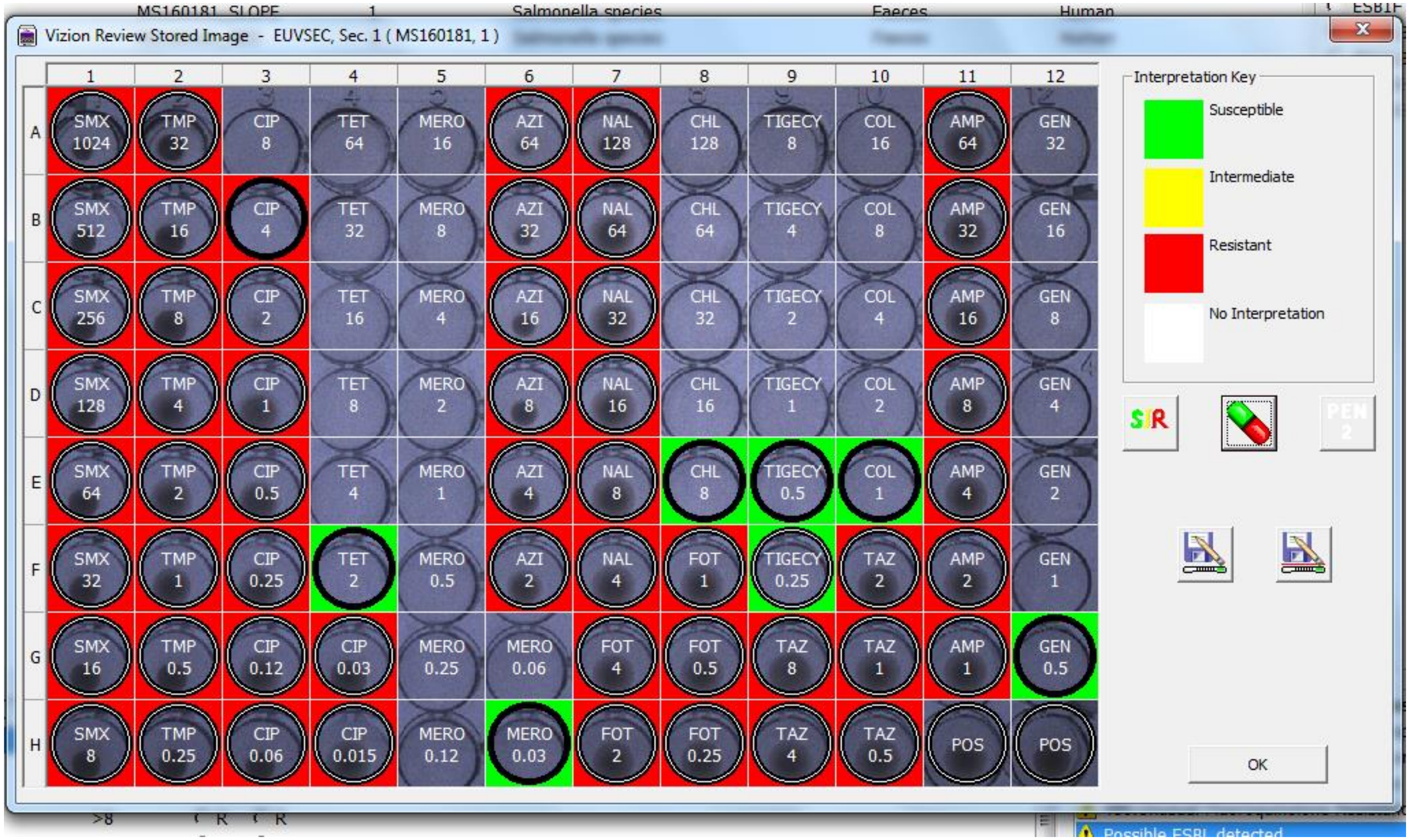
Mobile Genetic Elements

- Plasmids
- Phages
- Transposons
- Integrons
- Insertion sequences



MDR ST13 *S*.Agona

ASuTmNaCpCazCtxAzt



Vizion Review Stored Image - EUVSEC, Sec. 1 (MS160181, 1)

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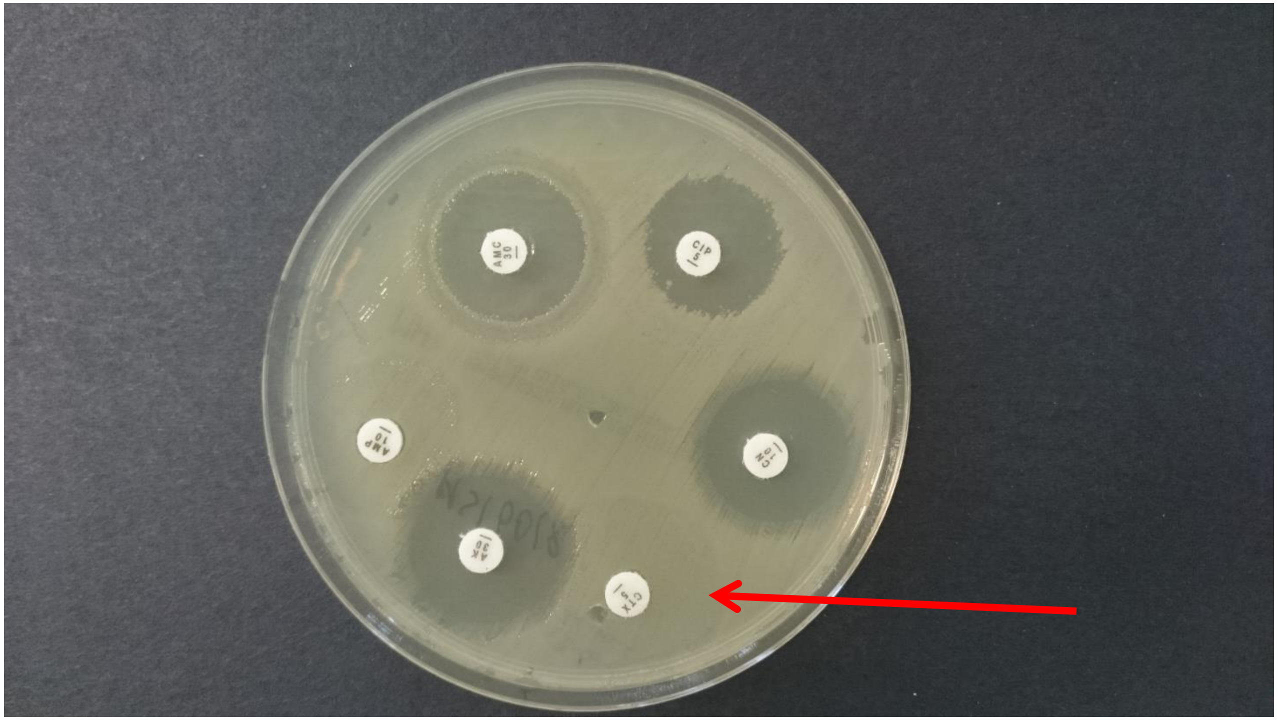
B	SMX 512	TMP 16	CIP 4	TET 32	MERO 8	AZI 32	NAL 64	CHL 64	TIGECY 4	COL 8	AMP 32	GEN 16
C	SMX 256	TMP 8	CIP 2	TET 16	MERO 4	AZI 16	NAL 32	CHL 32	TIGECY 2	COL 4	AMP 16	GEN 8
D	SMX 128	TMP 4	CIP 1	TET 8	MERO 2	AZI 8	NAL 16	CHL 16	TIGECY 1	COL 2	AMP 8	GEN 4
E	SMX 64	TMP 2	CIP 0.5	TET 4	MERO 1	AZI 4	NAL 8	CHL 8	TIGECY 0.5	COL 1	AMP 4	GEN 2
F	SMX 32	TMP 1	CIP 0.25	TET 2	MERO 0.5	AZI 2	NAL 4	FOT 1	TIGECY 0.25	TAZ 2	AMP 2	GEN 1
G	SMX 16	TMP 0.5	CIP 0.12	CIP 0.03	MERO 0.25	MERO 0.06	FOT 4	FOT 0.5	TAZ 8	TAZ 1	AMP 1	GEN 0.5
H	SMX 8	TMP 0.25	CIP 0.06	CIP 0.015	MERO 0.12	MERO 0.03	FOT 2	FOT 0.25	TAZ 4	TAZ 0.5	POS	POS

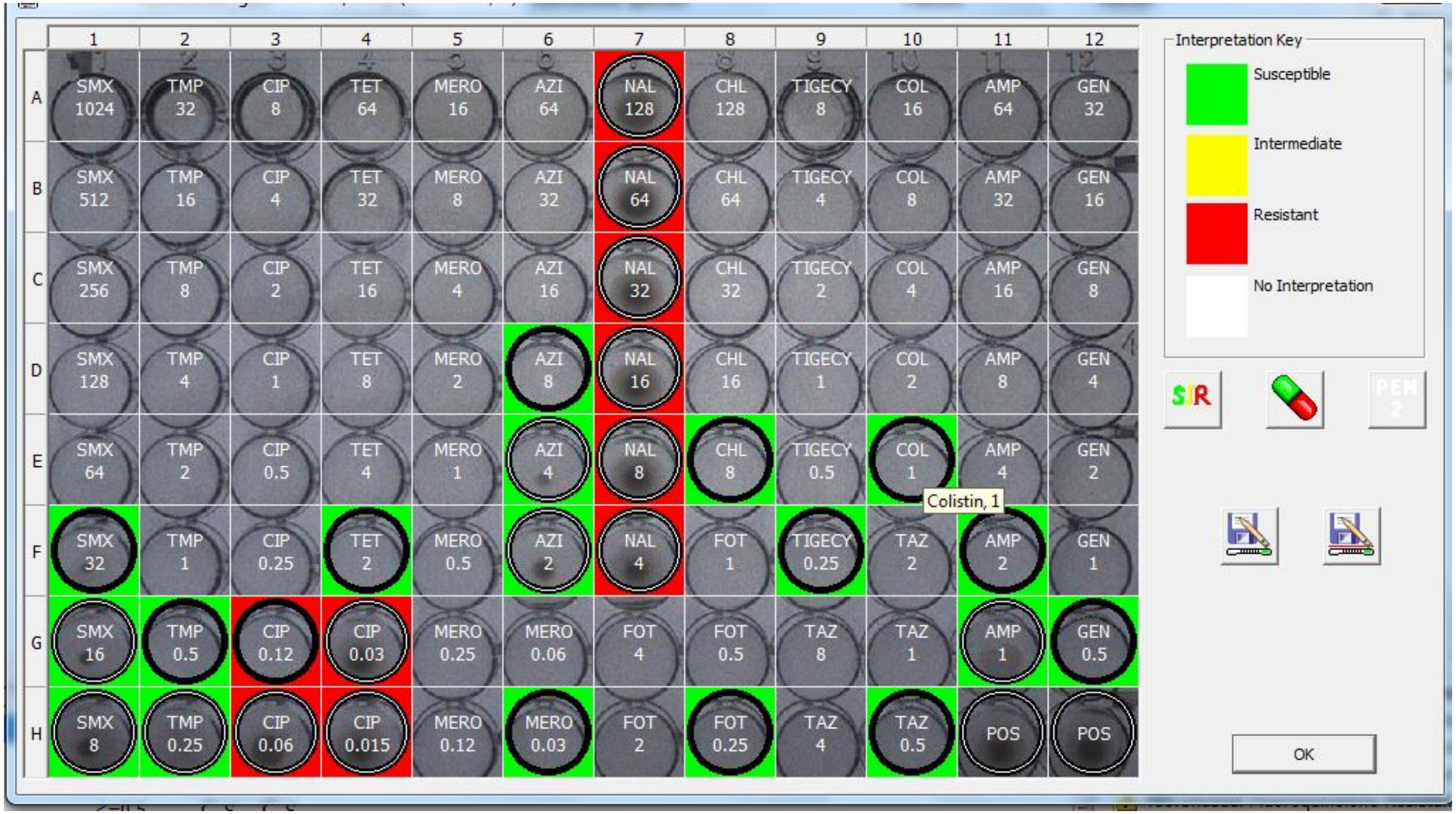
Interpretation Key

- 🟩 Susceptible
- 🟨 Intermediate
- 🟥 Resistant
- ⬜ No Interpretation

Disk Diffusion



NaCp



	1	2	3	4	5	6	7	8	9	10	11	12
A	SMX 1024	TMP 32	CIP 8	TET 64	MERO 16	AZI 64	🟥 NAL 128	CHL 128	TIGECY 8	COL 16	AMP 64	GEN 32
B	SMX 512	TMP 16	CIP 4	TET 32	MERO 8	AZI 32	🟥 NAL 64	CHL 64	TIGECY 4	COL 8	AMP 32	GEN 16
C	SMX 256	TMP 8	CIP 2	TET 16	MERO 4	AZI 16	🟥 NAL 32	CHL 32	TIGECY 2	COL 4	AMP 16	GEN 8
D	SMX 128	TMP 4	CIP 1	TET 8	MERO 2	🟩 AZI 8	🟥 NAL 16	CHL 16	TIGECY 1	COL 2	AMP 8	GEN 4
E	SMX 64	TMP 2	CIP 0.5	TET 4	MERO 1	🟩 AZI 4	🟥 NAL 8	🟩 CHL 8	TIGECY 0.5	🟩 COL 1	AMP 4	GEN 2
F	🟩 SMX 32	TMP 1	CIP 0.25	🟩 TET 2	MERO 0.5	🟩 AZI 2	🟥 NAL 4	FOT 1	🟩 TIGECY 0.25	TAZ 2	🟩 AMP 2	GEN 1
G	🟩 SMX 16	🟩 TMP 0.5	🟥 CIP 0.12	🟥 CIP 0.03	MERO 0.25	MERO 0.06	FOT 4	FOT 0.5	TAZ 8	TAZ 1	🟩 AMP 1	🟩 GEN 0.5
H	🟩 SMX 8	🟩 TMP 0.25	🟥 CIP 0.06	🟥 CIP 0.015	MERO 0.12	🟩 MERO 0.03	FOT 2	🟩 FOT 0.25	TAZ 4	🟩 TAZ 0.5	POS	POS

Colistin, 1

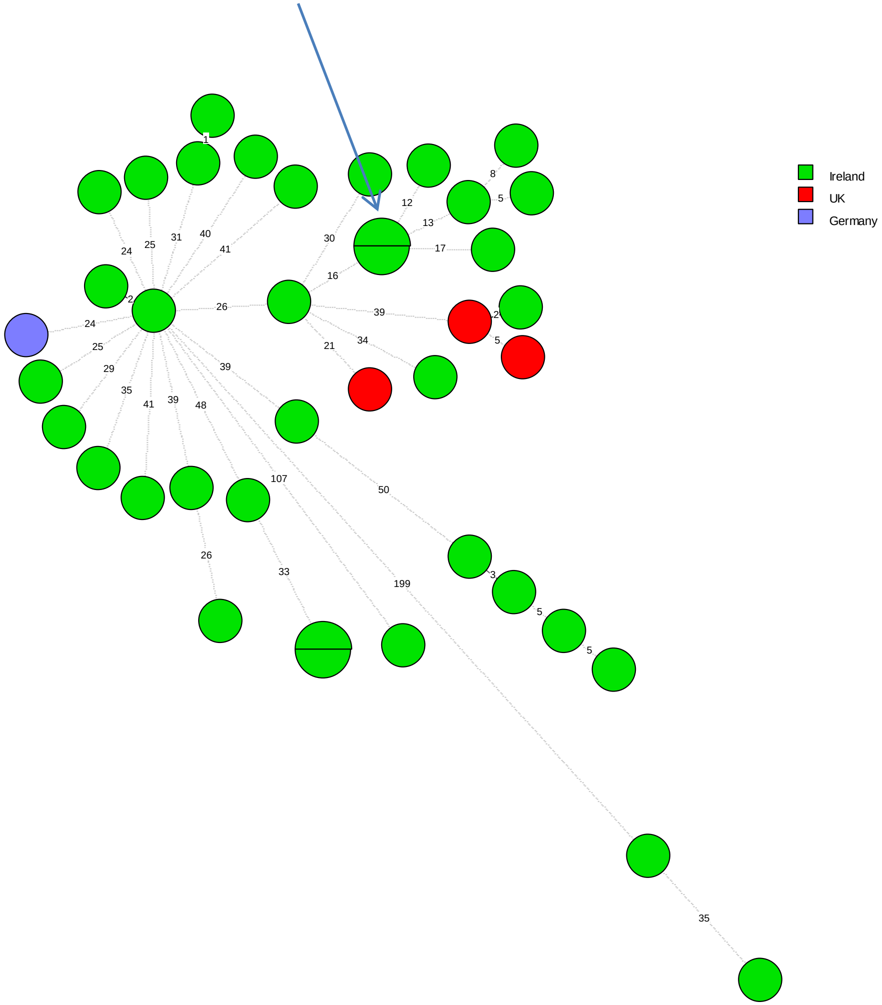
Interpretation Key

- 🟩 Susceptible
- 🟨 Intermediate
- 🟥 Resistant
- ⬜ No Interpretation

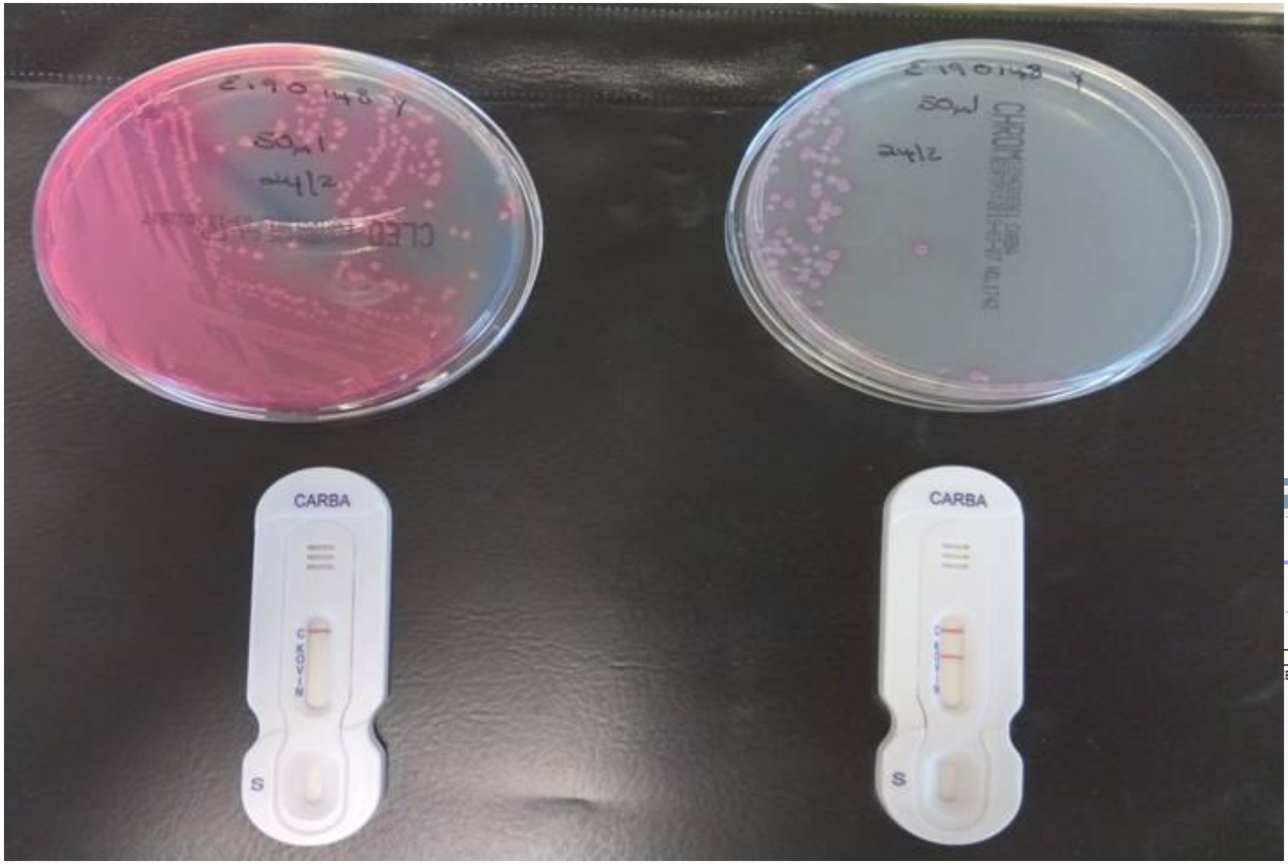
- Agona
  - ASuTmNaCpCazCtxAzt
  - *bla*CTX-M-15, *sul*1, *dfrA*12, *mph*(A), gyrA:p.D87Y,
  - Plasmid IncL/M (96.69%), IncR (100%)

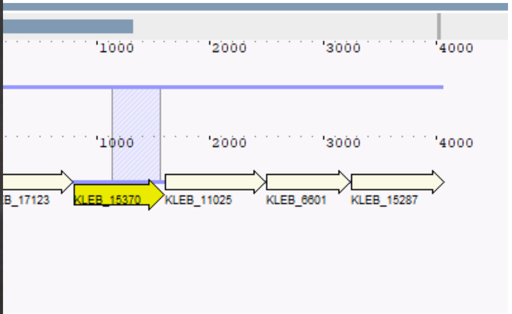
- Agona without Plasmid
  - NaCp
  - *gyr*A:p.D87Y

cgMLST of ST13 *S.*Agona



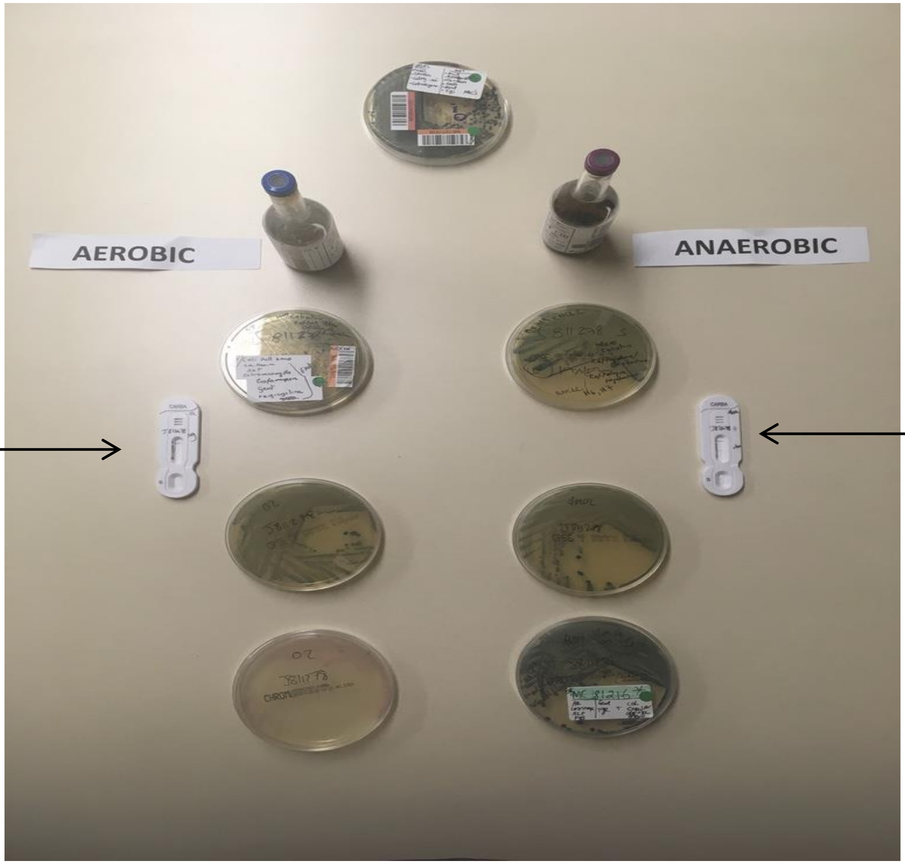
*bla*OXA-48 PCR pos ,WGS Neg





- *bla*OXA48 only present in <1% of cells

Now You See it, Now You Don’t



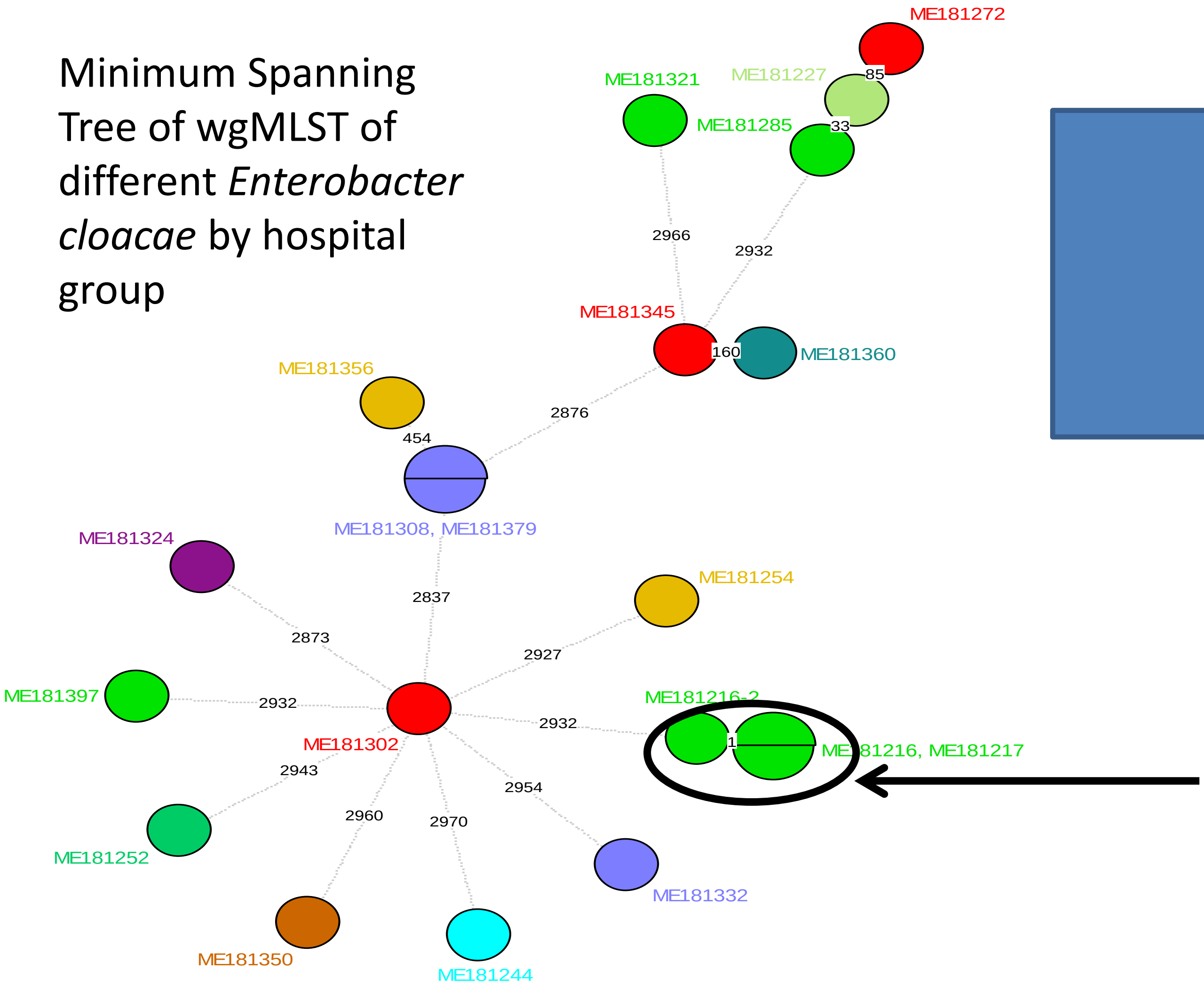
Meropenem
MIC=0.25 mg/L

Meropenem
MIC=8mg/L

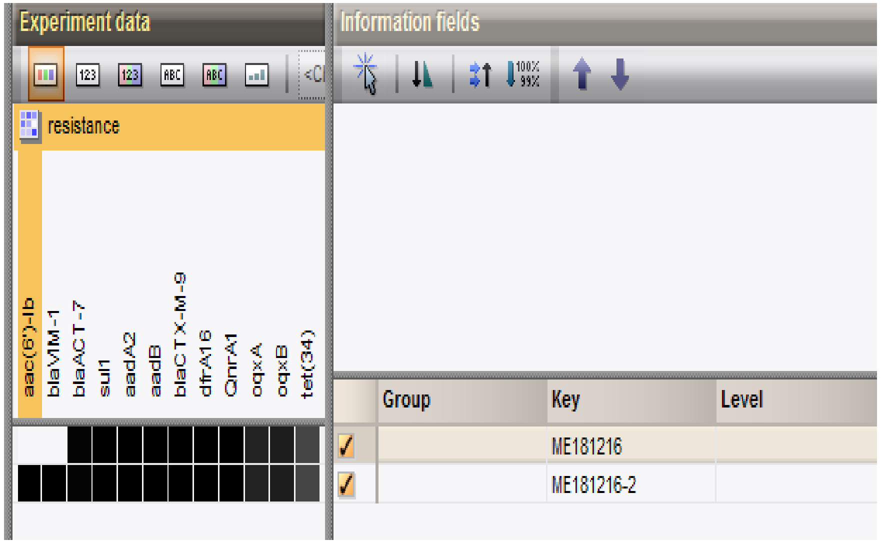
Negative →

← Positive
VIM

Minimum Spanning Tree of wgMLST of different *Enterobacter cloacae* by hospital group



[redacted]

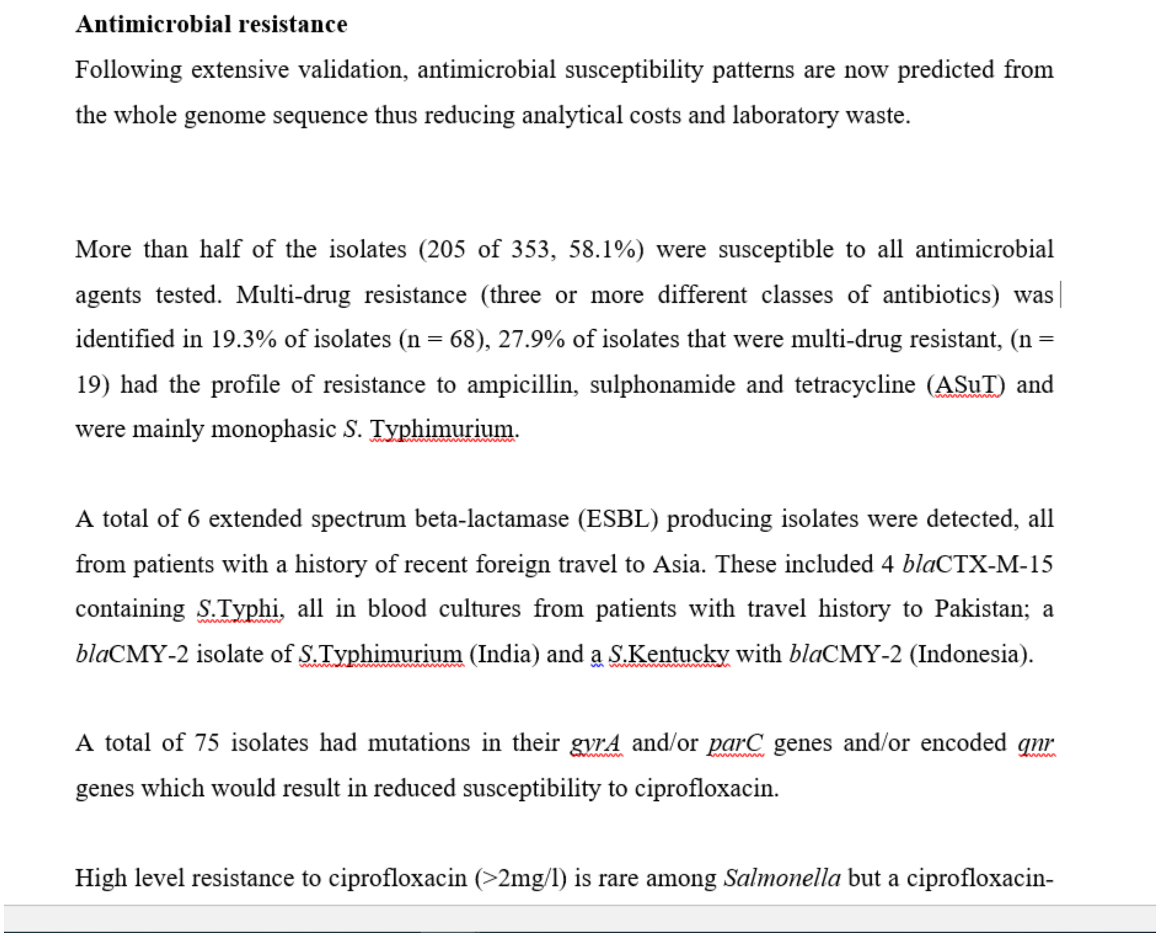


aac(6')-Ib	blaVIM-1	blaACT-7	sul1	aadA2	aadB	blaCTX-M-9	dfrA16	QnrA1	oqxA	oqxB	tet(34)
□	□	■	■	■	■	■	■	■	■	■	■
■	■	■	■	■	■	■	■	■	■	■	■

	Group	Key	Level
☑		ME181216	
☑		ME181216-2	

- Two resistance genes missing from isolate from aerobic bottle
  - blaVIM-1
  - aac(6')1b

Annual Report



Antimicrobial resistance

Following extensive validation, antimicrobial susceptibility patterns are now predicted from the whole genome sequence thus reducing analytical costs and laboratory waste.

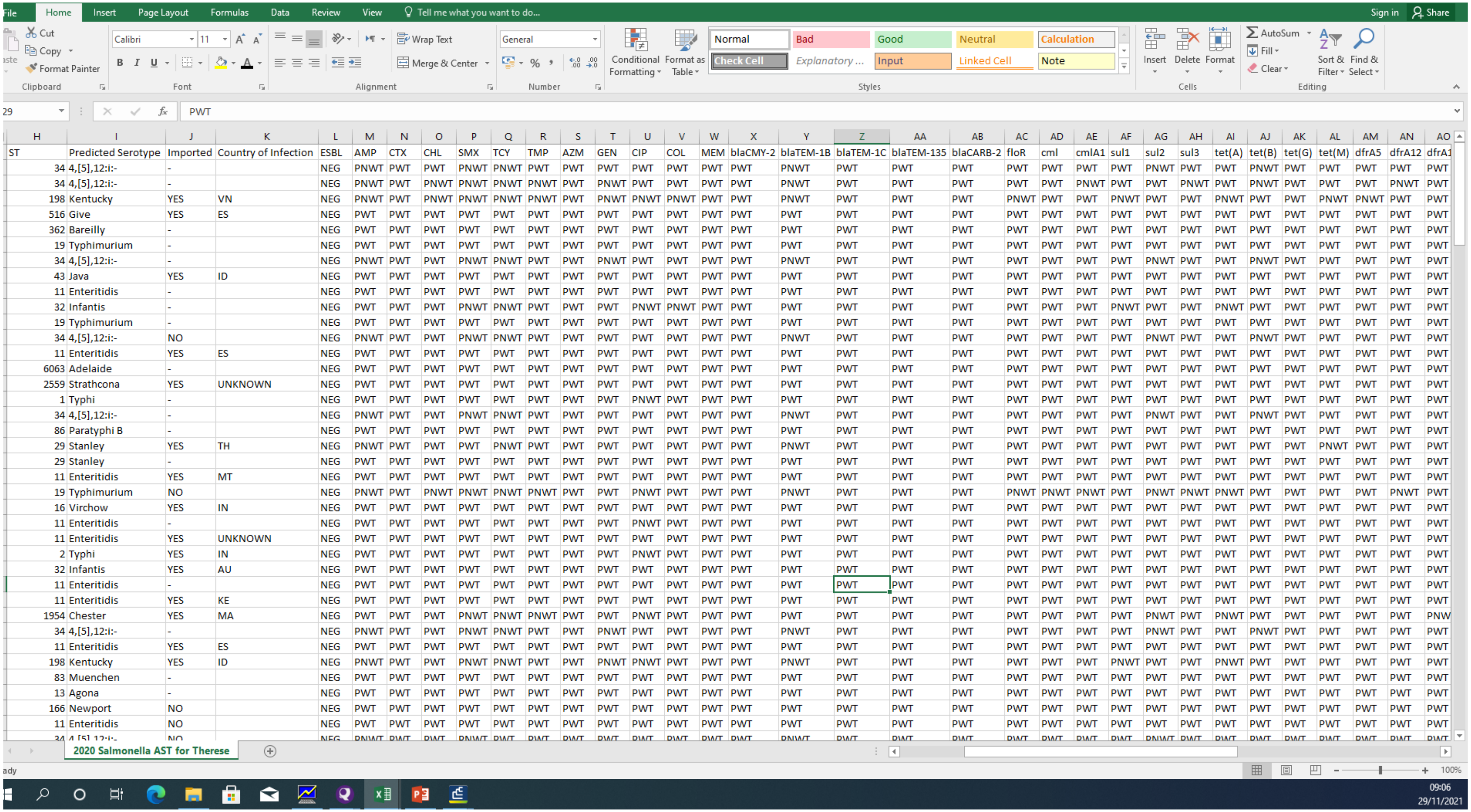
More than half of the isolates (205 of 353, 58.1%) were susceptible to all antimicrobial agents tested. Multi-drug resistance (three or more different classes of antibiotics) was identified in 19.3% of isolates (n = 68), 27.9% of isolates that were multi-drug resistant, (n = 19) had the profile of resistance to ampicillin, sulphonamide and tetracycline (ASuT) and were mainly monophasic *S*. Typhimurium.

A total of 6 extended spectrum beta-lactamase (ESBL) producing isolates were detected, all from patients with a history of recent foreign travel to Asia. These included 4 *bla*CTX-M-15 containing *S*.Typhi, all in blood cultures from patients with travel history to Pakistan; a *bla*CMY-2 isolate of S.Typhimurium (India) and a S.Kentucky with *bla*CMY-2 (Indonesia).

A total of 75 isolates had mutations in their *gyrA* and/or *parC* genes and/or encoded *qnr* genes which would result in reduced susceptibility to ciprofloxacin.

High level resistance to ciprofloxacin (>2mg/l) is rare among *Salmonella* but a ciprofloxacin-

Files for ECDC



ST	Predicted Serotype	Imported	Country of Infection	ESBL	AMP	CTX	CHL	SMX	TCY	TMP	AZM	GEN	CIP	COL	MEM	blaCMY-2	blaTEM-1B	blaTEM-1C	blaTEM-135	blaCARB-2	floR	cml	cmlA1	sul1	sul2	sul3	tet(A)	tet(B)	tet(G)	tet(M)	dfrA5	dfrA12	dfrA1
34	4,[5],12:i:-	-		NEG	PNWT	PWT	PWT	PNWT	PNWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PNWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PNWT	PWT	PWT	PNWT	PWT	PWT	PWT	PWT	PWT
34	4,[5],12:i:-	-		NEG	PNWT	PWT	PNWT	PNWT	PNWT	PNWT	PWT	PNWT	PWT	PWT	PWT	PWT	PNWT	PWT	PWT	PWT	PWT	PWT	PNWT	PWT	PWT	PNWT	PWT	PNWT	PWT	PWT	PWT	PNWT	PWT
198	Kentucky	YES	VN	NEG	PNWT	PWT	PNWT	PNWT	PNWT	PNWT	PWT	PNWT	PNWT	PNWT	PWT	PWT	PNWT	PWT	PWT	PWT	PNWT	PWT	PWT	PNWT	PWT	PWT	PNWT	PWT	PWT	PNWT	PNWT	PWT	PWT
516	Give	YES	ES	NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
362	Bareilly	-		NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
19	Typhimurium	-		NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
34	4,[5],12:i:-	-		NEG	PNWT	PWT	PWT	PNWT	PNWT	PWT	PWT	PNWT	PWT	PWT	PWT	PWT	PNWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PNWT	PWT	PWT	PNWT	PWT	PWT	PWT	PWT	PWT
43	Java	YES	ID	NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
11	Enteritidis	-		NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
32	Infantis	-		NEG	PWT	PWT	PWT	PNWT	PNWT	PWT	PWT	PWT	PNWT	PNWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PNWT	PWT	PWT	PNWT	PWT	PWT	PWT	PWT	PWT	PWT
19	Typhimurium	-		NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
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11	Enteritidis	YES	ES	NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
6063	Adelaide	-		NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
2559	Strathcona	YES	UNKNOWN	NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
1	Typhi	-		NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PNWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
34	4,[5],12:i:-	-		NEG	PNWT	PWT	PWT	PNWT	PNWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PNWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PNWT	PWT	PWT	PNWT	PWT	PWT	PWT	PWT	PWT
86	Paratyphi B	-		NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
29	Stanley	YES	TH	NEG	PNWT	PWT	PWT	PWT	PNWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PNWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PNWT	PWT	PWT	PWT
29	Stanley	-		NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
11	Enteritidis	YES	MT	NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
19	Typhimurium	NO		NEG	PNWT	PWT	PNWT	PNWT	PNWT	PNWT	PWT	PWT	PNWT	PWT	PWT	PWT	PNWT	PWT	PWT	PWT	PNWT	PNWT	PNWT	PWT	PNWT	PNWT	PNWT	PWT	PWT	PWT	PWT	PNWT	PWT
16	Virchow	YES	IN	NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
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11	Enteritidis	YES	UNKNOWN	NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
2	Typhi	YES	IN	NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PNWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
32	Infantis	YES	AU	NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
11	Enteritidis	-		NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
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1954	Chester	YES	MA	NEG	PWT	PWT	PWT	PNWT	PNWT	PNWT	PWT	PWT	PNWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PNWT	PWT	PNWT	PWT	PWT	PWT	PWT	PWT	PNW
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11	Enteritidis	YES	ES	NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
198	Kentucky	YES	ID	NEG	PNWT	PWT	PWT	PNWT	PNWT	PWT	PWT	PNWT	PNWT	PWT	PWT	PWT	PNWT	PWT	PWT	PWT	PWT	PWT	PWT	PNWT	PWT	PWT	PNWT	PWT	PWT	PWT	PWT	PWT	PWT
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166	Newport	NO		NEG	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT	PWT
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GISAID for FWD Pathogens?

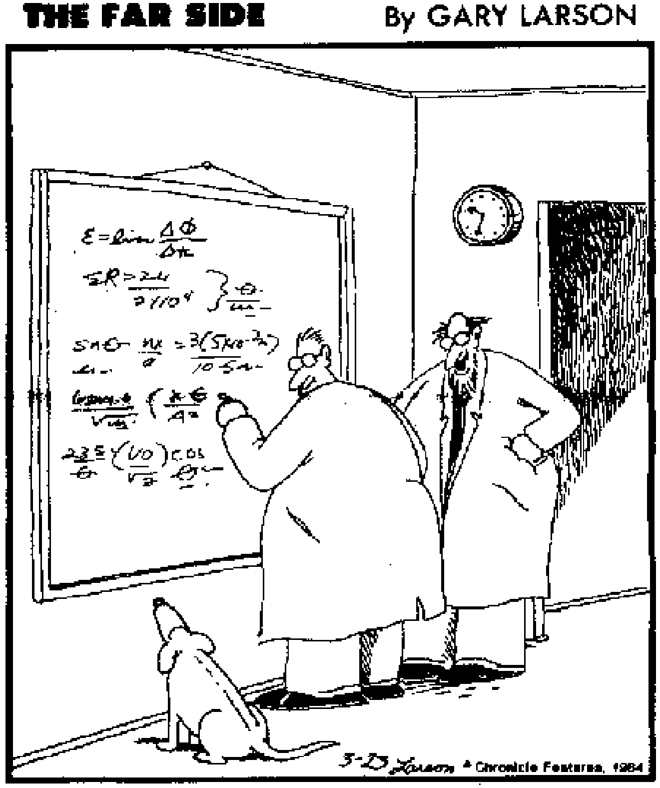
VOC Omicron GR/484A (B.1.1.529) first detected in Botswana/Hong Kong/South Africa

Map of tracked variant occurrence

Circle size proportional to number of variant genomes, zoom into region for more detail. Color by recency with red being most recent.

Acknowledgements

- Genevieve, Alma, Ger, Stuart, Martin



"Ohhhhhhh . . . Look at that, Schuster . . . Dogs are so cute when they try to comprehend quantum mechanics."