# SSI's overvågning af AMR i udvalgte bakterielle agens fra blodinfektioner

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# SEQ BAKTERIÆMI OVERVÅGNINGEN (RESLAB)

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- **ESBL producerende *E. coli* fra blodinfektioner (2014 -2018)**
  - 245 + 275 + 312 + 337 + ~331 = ~1500 genomer
- **ESBL producerende *K. pneumoniae* fra blodinfektioner (2018)**
  - ~70-100 genomer
- CPO fra screeninger og infektioner - inklusiv blod (2014-2018)
  - ~50 genomer fra blod (Acinetobacter, Citrobacter, Enterobacter, Escherichia, Klebsiella, Pseudomonas)
- VRE fra infektioner - inklusiv blod (2015-2018)
  - ~150 genomer fra blod

# ESBL 2014 - 2015

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- In 2014, 245 ESBL/pAmpC and carbapenemase producing *E. coli* were found
- In 2015, 280 ESBL/pAmpC and carbapenemase producing *E. coli* were found

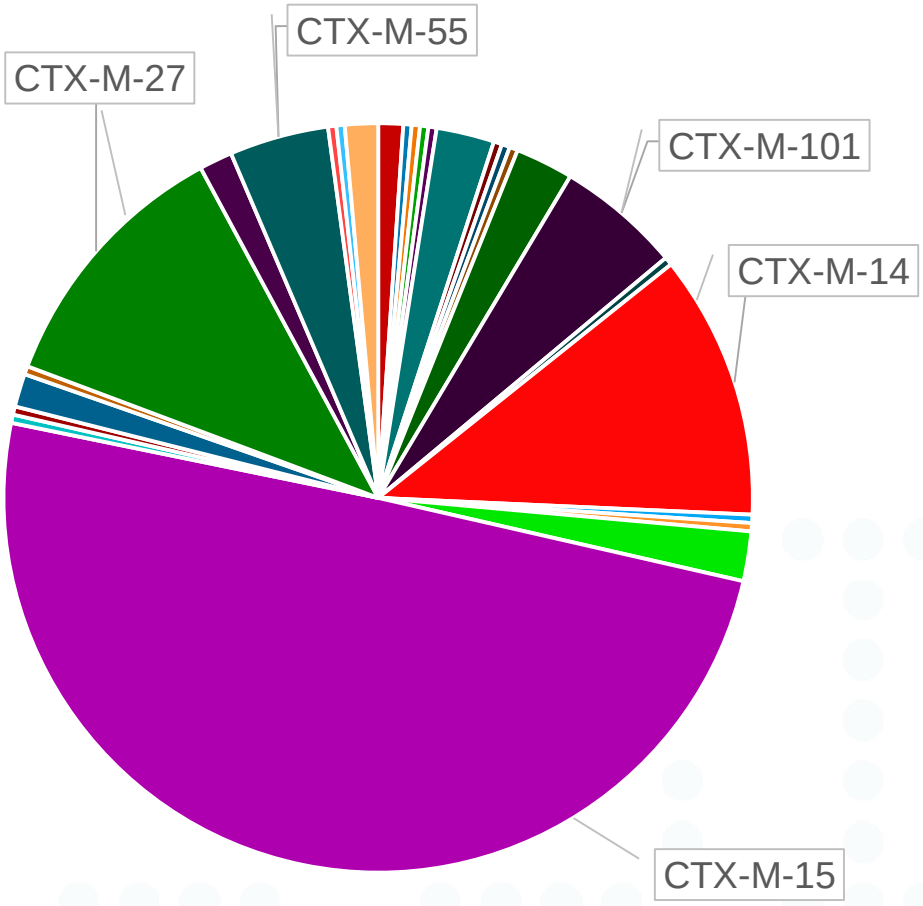
| Distribution of ESBL and Carbapenemase producing *E. coli* from bloodstream infections | | |
|---|---|---|
| | DANMAP 2014 | DANMAP 2015 |
| Region | Numbers | Numbers |
| The Capital Region of Denmark | 110 | 121 |
| The Zealand Region | 27 | 14 |
| Region of Southern Denmark | 43 | 45 |
| Central Denmark Region | 43 | 59 |
| North Denmark Region | 22 | 41 |
| Total Numbers | 245 | 280 |

# ESBL 2015 – GENE DISTRIBUTION

ESBL enzymes and Carbapenemases detected in *E. coli* from bloodstream infections

| | DANMAP 2014 | | DANMAP 2015 | |
|---|---|---|---|---|
| Enzyme | Number | % | Number | % |
| CTX-M-1 | 10 | 4% | 7 | 2% |
| CTX-M-14[1] | 38 | 15% | 34 | 12% |
| CTX-M-14b | 5 | 2% | 6 | 2% |
| CTX-M-15[1] | 121 | 48% | 141 | 49% |
| CTX-M-24[1] | 1 | 0% | 5 | 2% |
| CTX-M-27[1] | 25 | 10% | 33 | 11% |
| CTX-M-55[1] | 8 | 3% | 14 | 5% |
| CTX-M-101 | 12 | 5% | 15 | 5% |
| CMY-2[1] | 10 | 4% | 6 | 2% |
| Other CMY variants[1] | 4 | 2% | 11 | 4% |
| Other ESBL enzymes | 16 | 6% | 15 | 5% |
| OXA-48-group[1] | 3 | 1% | 3 | 1% |

[1]In some isolates more than one enzyme was detected in 2015



# ESBL 2015 – MLST DISTRIBUTION

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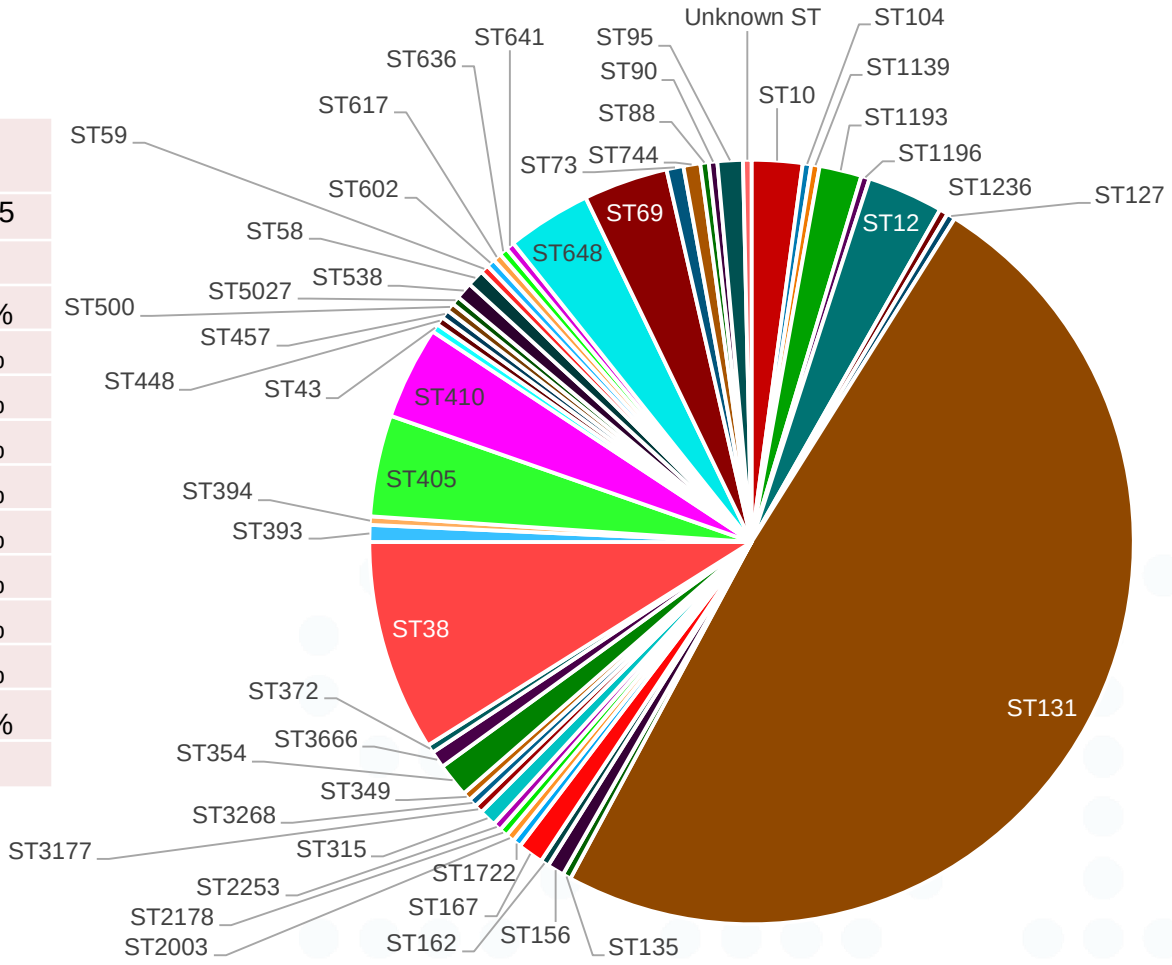
Distribution of MLSTs in *E. coli* from bloodstream infections

| | DANMAP 2014 | | DANMAP 2015 | |
|---|---|---|---|---|
| MLST | Numbers | % | Numbers | % |
| ST131 | 124 | 51% | 137 | 49% |
| ST38 | 18 | 7% | 25 | 9% |
| ST405 | 13 | 5% | 12 | 4% |
| ST410 | 4 | 2% | 11 | 4% |
| ST69 | 10 | 4% | 10 | 4% |
| ST648 | 7 | 3% | 10 | 4% |
| ST12 | 5 | 2% | 9 | 3% |
| ST10 | 0 | 0% | 6 | 2% |
| ST1193 | 2 | 1% | 5 | 2% |
| Other STs[1] | 62 | 25% | 55 | 20% |

[1] less than 5 isolates per ST in 2015



# ESBL 2015 – MLST AND GENE CORRELATION

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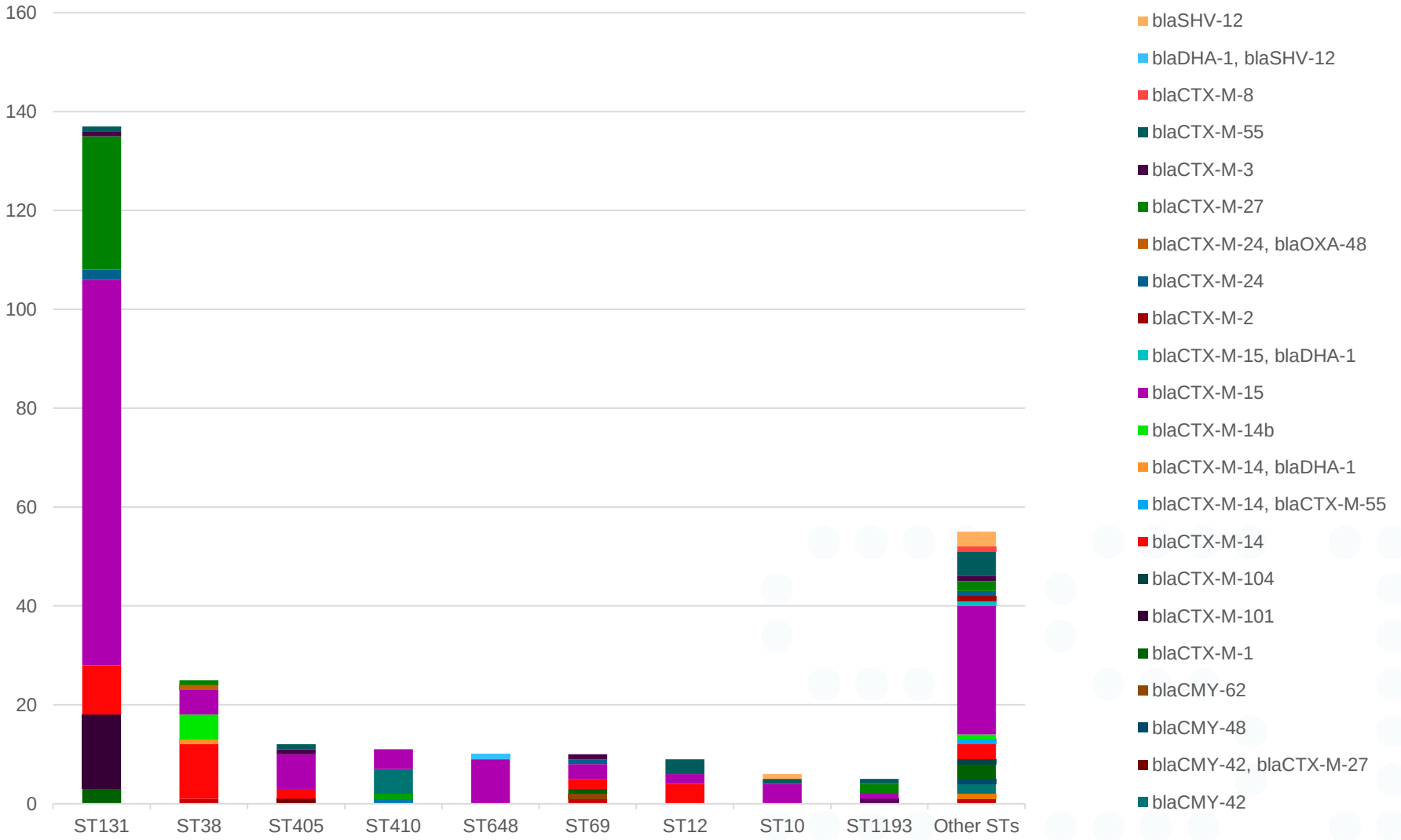

# ESBL 2014 + 2015

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Journal of Antimicrobial Chemotherapy

## WGS-based surveillance of third-generation cephalosporin-resistant *Escherichia coli* from bloodstream infections in Denmark

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# 3GC-R ENZYMES 2014-2015

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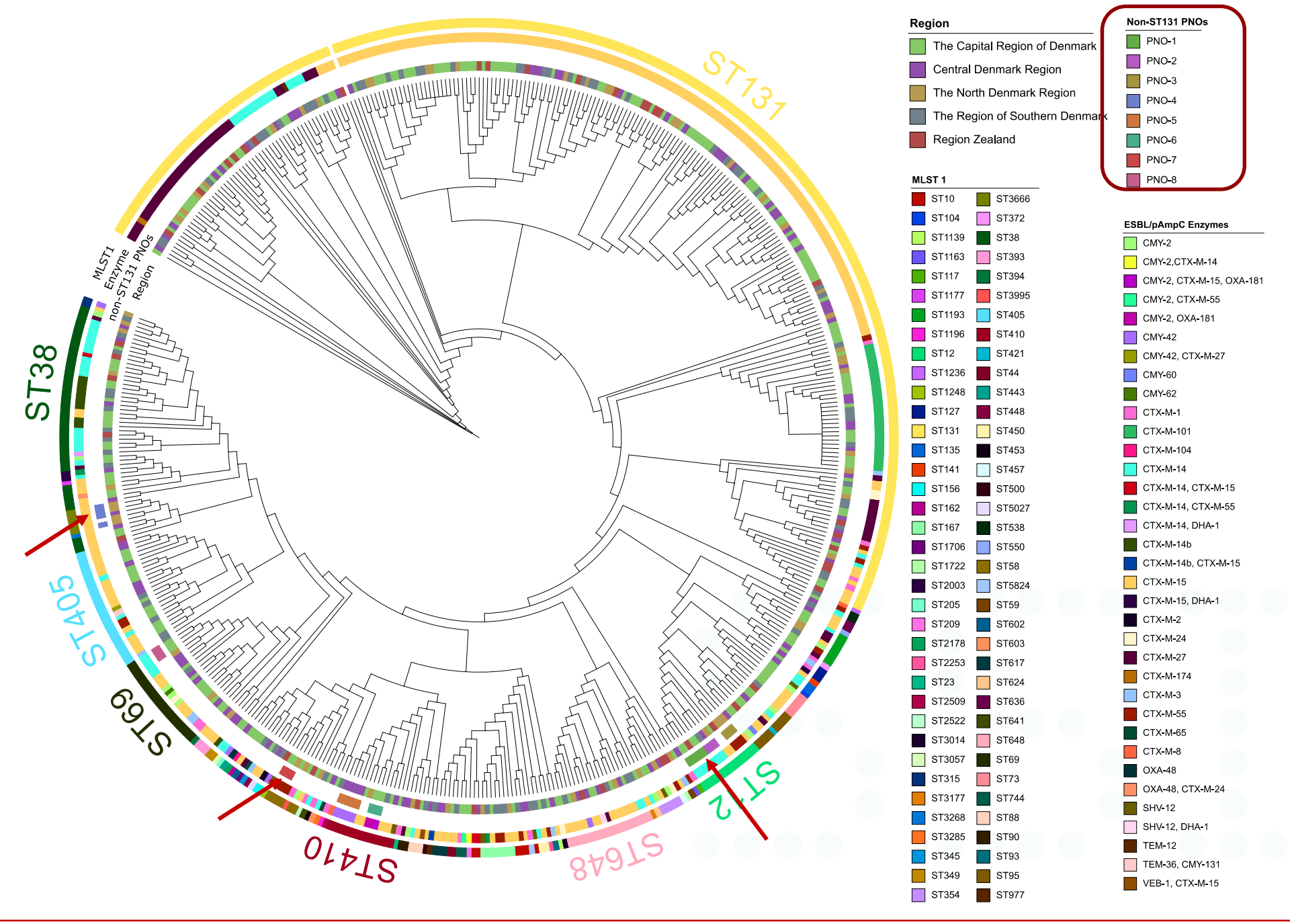
**Table 1. Distribution of Extended-Spectrum Beta-Lactamase- and AmpC Enzymes in the 552 Third-Generation Cephalosporin-Resistant *Escherichia coli* isolates**

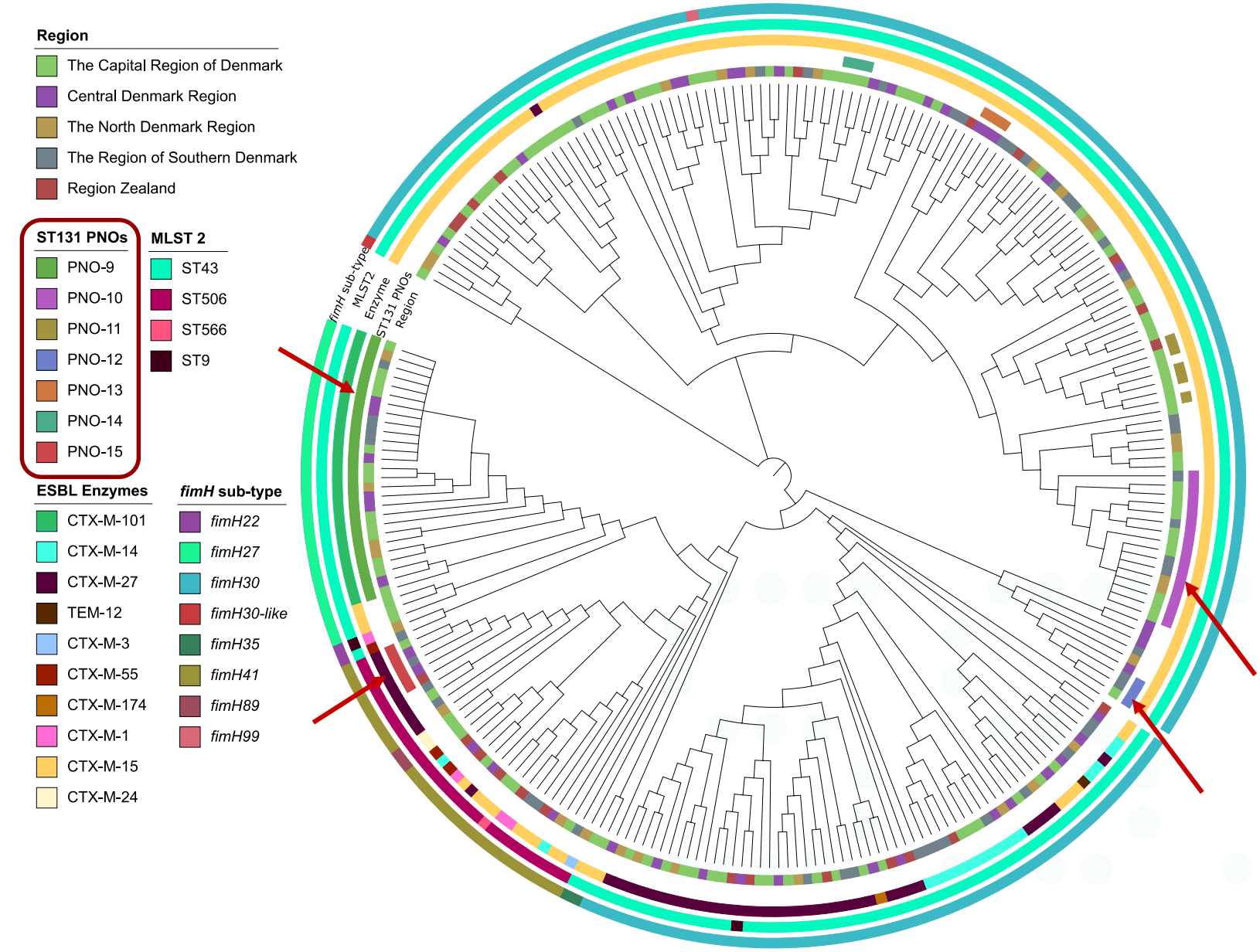
| Phenotype | Enzyme[a] | Number of Isolates | % of Isolates | Number of ST131 | % of ST131 |
|---|---|---|---|---|---|
| ESBL | | 491 | 89 % | 258 | 100% |
| | CTX-M-15 | 261 | 50 % | 155 | 60 % |
| | CTX-M-14 | 72 | 14 % | 17 | 7 % |
| | CTX-M-27 | 57 | 11 % | 47 | 18 % |
| | CTX-M-101 | 27 | 5 % | 27 | 10 % |
| | CTX-M-55 | 23 | 4 % | 3 | 1 % |
| | CTX-M-1 | 16 | 3 % | 4 | 1 % |
| | CTX-M-14b | 11 | 2 % | | |
| | CTX-M-3 | 8 | 2 % | 1 | < 1 % |
| | SHV-12 | 7 | 1 % | | |
| | CTX-M-24 | 6 | 1 % | 2 | < 1 % |
| | CTX-M-65 | 2 | < 1 % | | |
| | CTX-M-8 | 2 | < 1 % | | |
| | CTX-M-104 | 1 | < 1 % | | |
| | CTX-M-174 | 1 | < 1 % | 1 | < 1 % |
| | CTX-M-2 | 1 | < 1 % | | |
| | TEM-12 | 1 | < 1 % | 1 | < 1 % |
| | TEM-36 | 1 | < 1 % | | |
| | VEB-1 | 1 | < 1 % | | |
| pAmpC | | 34 | 6% | | |
| | CMY-2 | 18 | 4 % | | |
| | CMY-42 | 10 | 2 % | | |
| | DHA-1 | 3 | < 1 % | | |
| | CMY-131 | 1 | < 1 % | | |
| | CMY-60 | 1 | < 1 % | | |
| | CMY-62 | 1 | < 1 % | | |
| CARBA | | 5 | 1% | | |
| | OXA-181 | 3 | < 1 % | | |
| | OXA-48 | 2 | < 1 % | | |
| cAmpC | | 34 | 6 % | | |

82% i 2009
significant fald ($p$ = 0.000001)

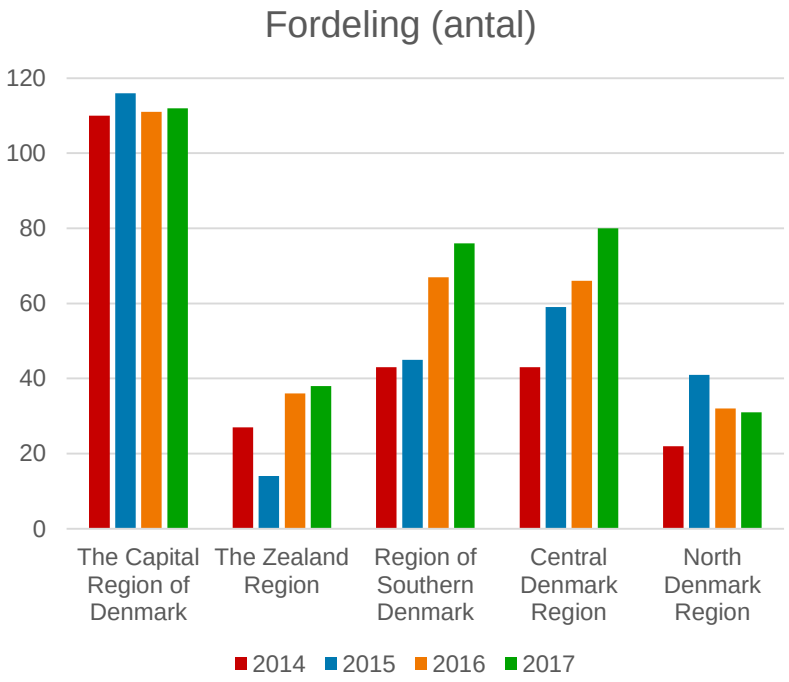
[a] In some isolates more than one enzyme was detected.

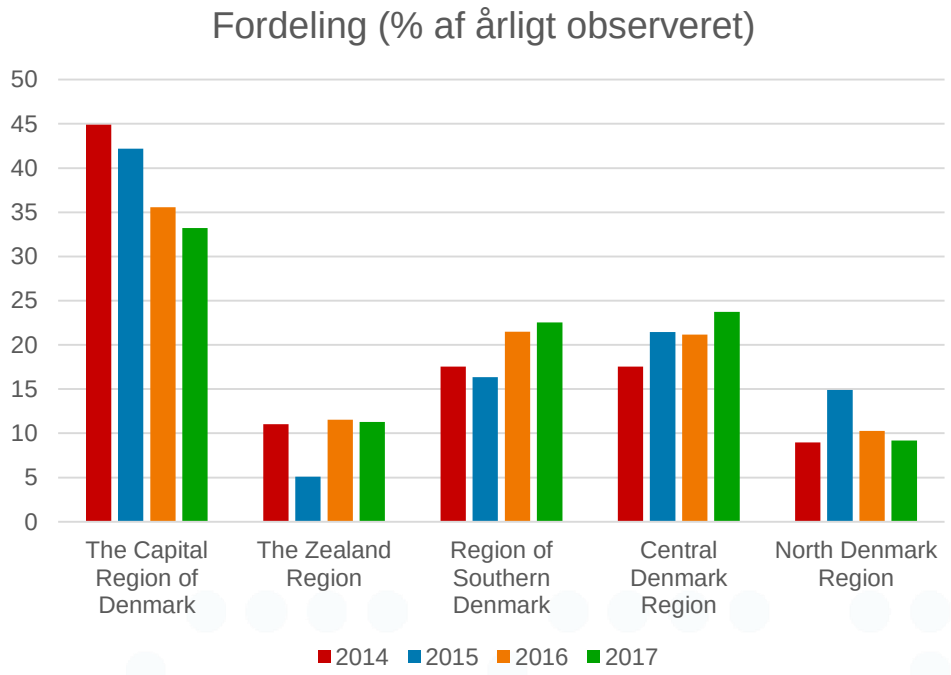

ST131
MLST1
Enzyme
non-ST131 PNOs
Region
ST38
ST405
ST69
ST410
ST2
ST648
Region
The Capital Region of Denmark
Central Denmark Region
The North Denmark Region
The Region of Southern Denmark
Region Zealand
Non-ST131 PNOs
PNO-1
PNO-2
PNO-3
PNO-4
PNO-5
PNO-6
PNO-7
PNO-8
MLST 1
ST10
ST104
ST1139
ST1163
ST117
ST1177
ST1193
ST1196
ST12
ST1236
ST1248
ST127
ST131
ST135
ST141
ST156
ST162
ST167
ST1706
ST1722
ST2003
ST205
ST209
ST2178
ST2253
ST23
ST2509
ST2522
ST3014
ST3057
ST315
ST3177
ST3268
ST3285
ST345
ST349
ST354
ST3666
ST372
ST38
ST393
ST394
ST3995
ST405
ST410
ST421
ST44
ST443
ST448
ST450
ST453
ST457
ST500
ST5027
ST538
ST550
ST58
ST5824
ST59
ST602
ST603
ST617
ST624
ST636
ST641
ST648
ST69
ST73
ST744
ST88
ST90
ST93
ST95
ST977
ESBL/pAmpC Enzymes
CMY-2
CMY-2,CTX-M-14
CMY-2, CTX-M-15, OXA-181
CMY-2, CTX-M-55
CMY-2, OXA-181
CMY-42
CMY-42, CTX-M-27
CMY-60
CMY-62
CTX-M-1
CTX-M-101
CTX-M-104
CTX-M-14
CTX-M-14, CTX-M-15
CTX-M-14, CTX-M-55
CTX-M-14, DHA-1
CTX-M-14b
CTX-M-14b, CTX-M-15
CTX-M-15
CTX-M-15, DHA-1
CTX-M-2
CTX-M-24
CTX-M-27
CTX-M-174
CTX-M-3
CTX-M-55
CTX-M-65
CTX-M-8
OXA-48
OXA-48, CTX-M-24
SHV-12
SHV-12, DHA-1
TEM-12
TEM-36, CMY-131
VEB-1, CTX-M-15

# ST131 Alene (2014 og 2015)



# ESBL FORDELT PÅ REGIONER (2014-2017)



# ESBL – LINK IMELLEM DYR OG MENNESKER?

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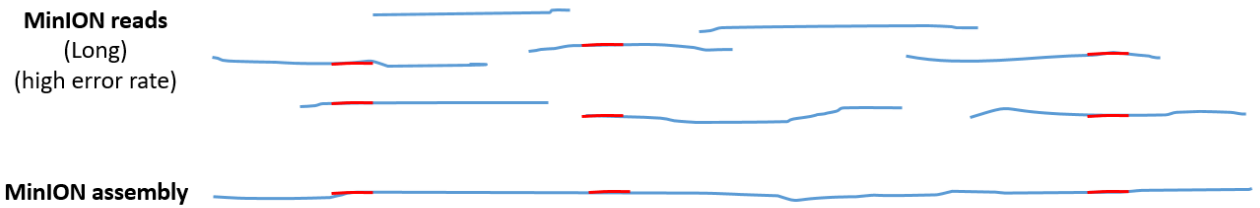
1) Samme kloner (og plasmider) i forskelige reservoirs

- ST131 med *bla*CMY-2 fra Kyllinger, kyllingekød (Europa) og blodinfektioner (DK). *JAC*

2) Samme plasmider (i forskelige kloner) i forskellige reservoirs

*bla*CTX-M-1 på IncI1 (ST3 og ST7) Kyllinger, svin, kød (WW) og blodinfektioner (DK)

# ESBL – LINK IMELLEM DYR OG MENNESKER?

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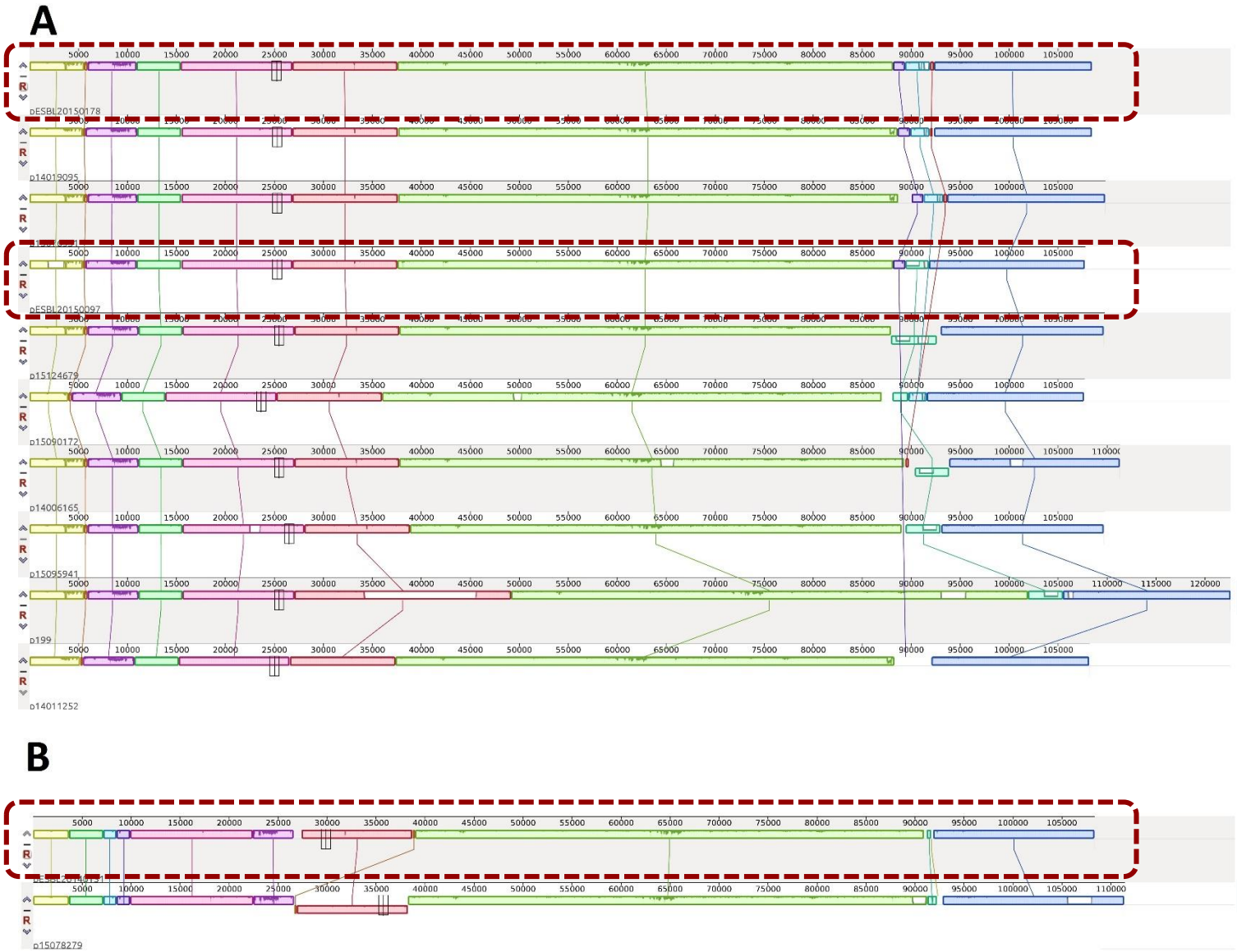
IncI1 ST3

IncI1 ST7

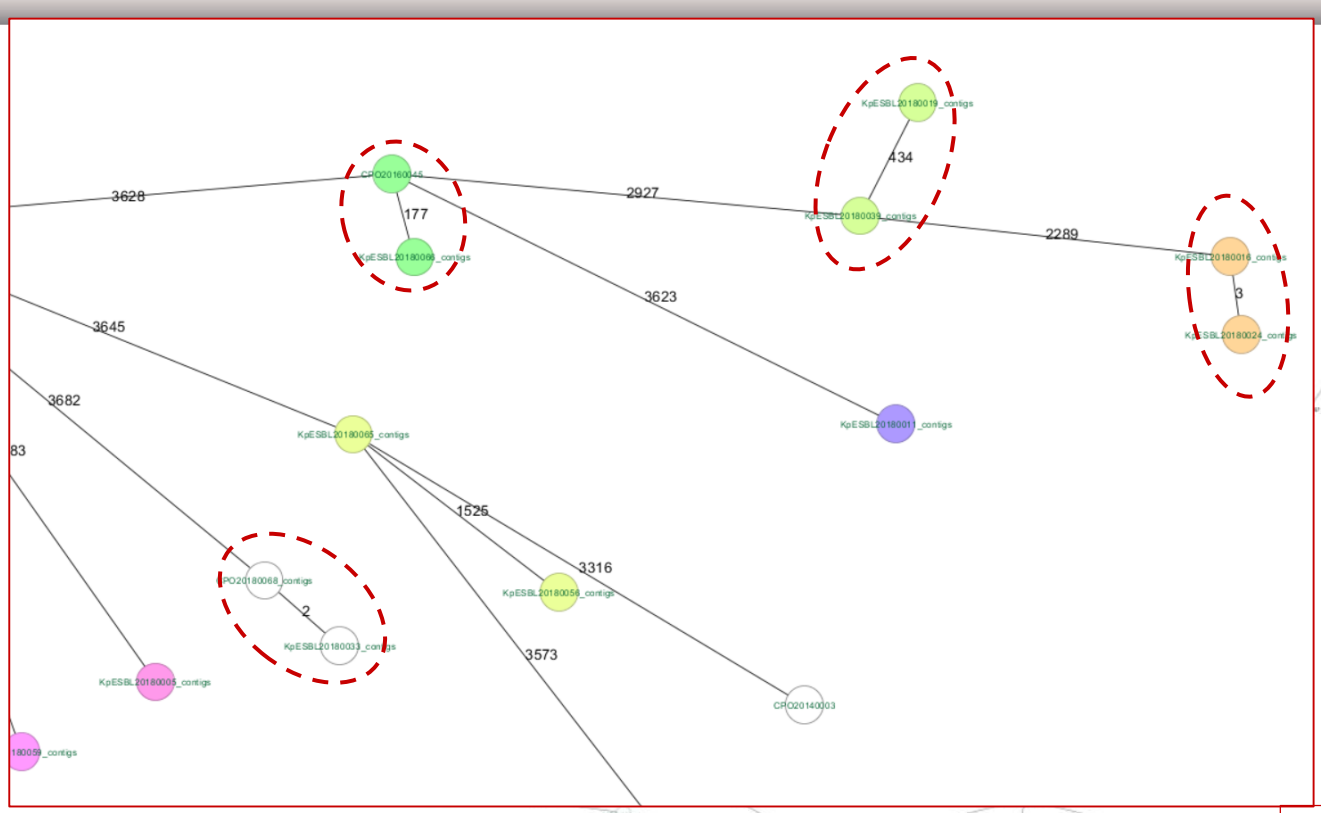


# SEQ BAKTERIÆMI OVERVÅGNINGEN (RESLAB)

STATENS SERUM INSTITUT

- **ESBL producerende *E. coli* fra blodinfektioner (2014 -2018)**
  - 245 + 275 + 312 + 337 + ~331 = ~1500 genomer
- **ESBL producerende *K. pneumoniae* fra blodinfektioner (2018)**
  - **~100 genomer**
- CPO fra screeninger og infektioner - inklusiv blod (2014-2018)
  - ~50 genomer fra blod (Acinetobacter, Citrobacter, Enterobacter, Escherichia, Klebsiella, Pseudomonas)
- VRE fra infektioner - inklusiv blod (2015-2018)
  - ~150 genomer fra blod

# ESBL *KLEBSIELLA PNEUMONIAE* - cgMLST




Fortsættelse følger i 2019….
…fra Sanne Grønvall Kjær Hansen (OUH)

# ESBL bacteriæmi humant - konklusion

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- Mange forskellige enzymer (dog primært CTX-M-15)
- Mange Sekvens typer (men ST131 i 50% af tilfældene)
- Også små udbrud i flere tilfælde


- Samme type ESBL-producerende *E. coli* kan findes hos patienterne efter mere end 12 måneder
- I enkelte tilfælde ses link i imellem dyr/fødevarer og humane blodinfektioner. Disse kan både være klon- og plasmid-relaterede.
- Massere af spændende data…hvis nogen har lyst til at grave videre i dem..