

GNSOP Referred Isolates

Current state of play:

E. coli, *Klebsiella* spp., *Proteus* spp. and *Salmonella* spp. with ceftazidime or ceftriaxone MIC

>1 mg/L, or ceftiofloxacin MIC >8 mg/L

any other Enterobacteriaceae with cefepime MIC >1 mg/L [ESBL, pAmpC]

all isolates with ciprofloxacin MIC >0.25 mg/L [PMQR]

all isolates with meropenem MIC >0.25 mg/L [Carbs]

all isolates with amikacin MIC >32 mg/L [RMT]

all isolates with colistin > 2 mg/L [MCR]

plus any isolate where no AST results were available

All referred isolates screened for the presence of the *bla*TEM and *bla*SHV genes using a real-time polymerase chain reaction (PCR) platform (LC-480)

A multiplex real-time TaqMan PCR used to detect CTX-M-type genes. Isolates probed for plasmid-borne AmpC enzymes and subjected to molecular tests for MBL (*bla*VIM, *bla*IMP, and *bla*NDM), *bla*KPC and *bla*OXA-48-like genes using real-time PCR.

Known plasmid-mediated quinolone resistance mechanisms (*qnr*, efflux [*qepA*, *oqxAB*] and *aac* (6')-*Ib-cr*) examined by PCR on all referred isolates with ciprofloxacin MIC >0.25 mg/L.

All referred *E. coli* are examined for membership of the O25b-ST131 clone.

All isolates with carbapenemase activity subjected to whole genome sequencing using the Illumina MiSeq platform. Data analysed using the Nullarbor bioinformatic pipeline. The pipeline was used to identify the multi-locus sequence type and the resistome.