Clonal displacement of one *E. coli* ST131 variant by a distinct variant in a nursing home

Catherine Ludden
London School of Hygiene and Tropical Medicine
Background

- The rise in multi-drug resistant *E. coli* is a global concern
  - ST131
- Nursing homes (NHs) represent potential reservoirs of ST131 causing several outbreaks
- In 2006 multiple individuals in a NH in Ireland presented with urinary tract infection caused by ESBL *E. coli*.
  - High levels of asymptomatic carriage in residents
- Study aims:
  - Collect all ESBL-*E. coli* submitted from the NH to the Microbiology Laboratory at Galway University Hospital (GUH) from 2005-2011
  - Examine ESBL type
  - Use whole genome sequencing to investigate strain differences over time, in the context of a large global population of *E. coli* ST131
Study Design: Global contextual database

<table>
<thead>
<tr>
<th>Collection</th>
<th>Number of samples (n=812)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nursing home (2005-2011)</td>
<td>69</td>
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<tr>
<td>GUH (2010)</td>
<td>21</td>
</tr>
<tr>
<td>BSAC MDR - Ireland (2001-2012)</td>
<td>20</td>
</tr>
<tr>
<td>BSAC – UK and Ireland (2001 -2012)</td>
<td>146</td>
</tr>
<tr>
<td>UK teaching hospital</td>
<td>75</td>
</tr>
<tr>
<td>UK nursing home</td>
<td>297</td>
</tr>
<tr>
<td>Global studies (Petty et al., 2014, Price et al., 2013)</td>
<td>184</td>
</tr>
</tbody>
</table>
Methods

• For the 90 ST131 nursing home and associated clinical strains, Pulsed field gel electrophoresis (PFGE) using XbaI was performed in accordance with the Pulse-Net protocol.
  • Clusters were identified based on a similarity $\geq 85\%$ were identified
• MLST confirmed based on Achtman scheme.
• Ribosomal Multilocus Sequence Typing (rST) inferred using The Bacterial Isolate Genome Sequence Database (BIGSdb).
  • 53 genes encoding the bacterial ribosome protein subunits
• Identified antimicrobial resistance genes using Short Read Sequence Typing for Bacterial Pathogens (SRST2).
• Phylogenetic analysis of the core genome.
• Pan-genome analysis
rST Prevalence

- rST1850 was widely present in the nursing home study (n=44/90)
- 16 rST1850 from UK (n=12), Canada (n=3) and Galway-BSAC (n=1)
- 51 rSTs in total collection, with rST1503 predominant (648/812; 80%)
SNP-based phylogenetic tree of 90 Galway ST131 isolates

- Core genome phylogeny
- 2 distinct ST131 lineages identified
- 1 resident changed lineages
Phylogeny of Global ST131

- Global spread of rST1503 (red)
- rST1850 forms a distinct lineage (purple)
  - Ireland
  - UK
  - Canada
- Nursing home clade is specific to Galway, Ireland
- Global clade suggests possible emergence of new strain
5 NH strains for PacBio (marked in red)

- Different clades
  - 3 rST1850
  - 2 rST1503
- Same Resident
PacBio Analysis

5 NH strains for PacBio (marked in red)
- Different clades
  - 3 rST1850
  - 2 rST1503
- Same Resident

- Plasmid CTX-M-15
  - Inc FII and FIA

- Plasmid CTX-M-14
  - Inc FII

- Chromosomal CTX-M-15

Source
- Outbreak Nursing home
- Other Nursing homes
- Clinical
- Community

rST
- 1503
- 1505
- 1507
- 1548
- 1849
- 1850
- 1851
- 1858

NCTC13441
Antimicrobial resistance and virulence gene summary

ESBL gene summary

• Only CTX-M-15 found in rST1850
  • CTX-M-15 is chromosomally encoded in the 3 PacBio samples

• CTX-M-15 predominates in other rST1503 on a plasmid
  • Highly similar to pEK499 (<99% identity)

• CTX-M-14 found in one rST1503 clade on a plasmid
  • Highly similar to CTX-M-14 plasmids disseminated in Asia

Pan-genome comparisons of rST1850 Vs other rSTs

• Chromosome: Phage encoding 7 PapK proteins (C, D, E, F, G, H, J, K), PagN (Adhesin/invasin), PrsF (fimbrial protein)

• Plasmid encoding catA1 and tetB resistance genes
Conclusion

- A resident global ST131 strain (rST1503) in a NH was substantially displaced by a newly introduced ST131 variant (rST1850)

- rST1850 found also in the UK, Canada and the receiving hospital
  - Associated with Pap virulence genes, plasmid encoding tetB and cat A1 and CTX-M-15 being chromosomally encoded

- Rep typing would have proved misleading for the CTX-M-15

- H30R and H30Rx typing could not differentiate the clades

- rST may be used as a surveillance tool to detect new clones

- Further surveillance of rST1850 is required.
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