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

Catherine Ludden*[1], Dearbhaile Morris[2], Derek J. Pickard[3], Tim Downing[4], Alasdair P. Macgowan[5], Nicholas Brown[6], Julian Parkhill[7], Sharon Peacock[1], Gordon Dougan[3], Martin Cormican[8]

[1]*London School of Hygiene & Tropical Medicine*

[2]*National University of Ireland; Antimicrobial Resistance and Microbial Ecology Group*

[3]*Wellcome Trust Sanger Institute*

[4]*Dublin City University; School of Biotechnology*

[5]*North Bristol NHS Trust; Southmead Hospital ; Department of Medical Microbiology*

[6]*Cambridge University Hospitals NHS Foundation Trust*

[7]*Wellcome Trust Sanger Institute, Hinxton*

[8]*National University of Ireland Galway; School of Medicine*

**Background:** *Escherichia coli* sequence type (ST) 131 is globally disseminated and associated with antimicrobial resistance and with urinary tract and blood stream infections. ST131 has been linked to colonisation and infection in vulnerable nursing home residents. The movement of patients between nursing homes and hospitals is a means for patients within both healthcare facilities to interact. We collected *E. coli* isolates from routine clinical samples from one nursing home (NH) over 7 years and compared them to a large global population of *E. coli* ST131 using genome sequencing to define the success of a nursing home specific clone.

**Material/methods:** From 2005 and 2011, we collected 69 ESBL *E. coli* ST131 isolates from 63 residents of a NH in Ireland. All isolates were sequenced using the Illumina Hiseq platform and compared to *E. coli* ST131 submitted to the referral hospital in 2010, from 8 hospitalised patients, 11 from other NHs and 2 from general practitioners. These genomes were also compared to *E. coli* ST131 from patients with bacteraemia at 4 geographically unrelated Irish hospitals (n=20; 2006-2011), 11 major UK tertiary hospitals (n=221; 2003-2013) and also to previously characterised global genomes (n=184, 1967-2011). Phylogenetic and other bioinformatics analyses were performed using a suite of open-access software.

**Results:** Genome-based comparison of 69 *E. coli* ST131 isolates from the individual nursing home with the 446 *E. coli* ST131 isolates from Ireland (n=41) and worldwide (n=405) demonstrated three distinct NH lineages (Clade A=11/69, Clade B=5/69, Clade C=47/69) and 6 outliers. However, Clade C was strongly associated with the NH clustering. Only 3 of the 446 non-NH isolates clustered with these. The 3 isolates were associated with the referral hospital (n=2) and 1 from a nearby NH. A time signature was observed for the 2 largest lineages, with the earlier NH isolates predominately belonging to Clade A and the later isolates mainly forming the displacement clade, Clade C. Comparative genomic analysis identified phage and plasmid elements to be highly associated with Clade C ($P < 0.01$). In addition, multidrug resistance and virulence genes were more commonly associated with Clade C isolates ($P<0.01$). Absence of gene flow between the subtypes and distinct differences between lineages, eliminates the possibility of evolution of Clade C from Clade A/B within the NH or from the other global collections analysed

**Conclusions:** A resident ST131 strain (Clade A/Clade B) in a NH was substantially displaced by a newly introduced ST131 variant (Clade C) with more mobile elements, which appear to be contributing to the differences in virulence and resistance genes. PacBio sequencing is underway to compare the mobile elements that differ between NH lineages to determine the success of the NH displacement clone which outcompeted the pandemic clones disseminating worldwide.