Uropathogenic *Escherichia coli* population structure & antimicrobial susceptibility in Norfolk, UK

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Genomic surveillance is underutilised for urinary tract infections (UTIs) which are a global health concern for their widespread occurrence and high frequency of antibiotic prescription.

We conducted a preliminary genomic surveillance study on the main etiological agent for UTIs, Uropathogenic *E. coli* (UPEC), in Norfolk – the first study of its kind in this region.

The objective was to identify clonal groups and antimicrobial resistance determinants disseminating in the community and hospitals in Norfolk.

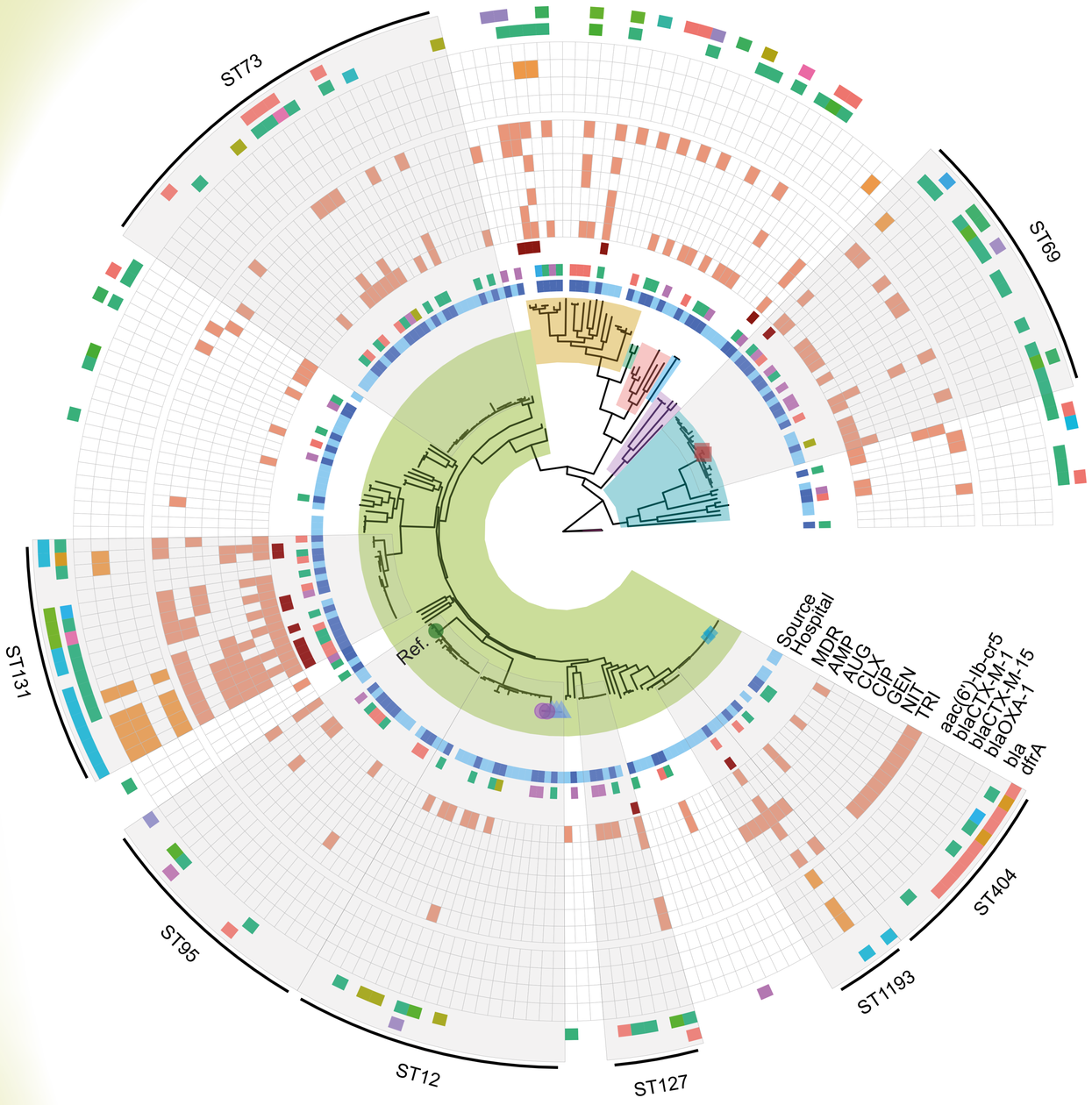

FIGURE Nº 1

Phylogenomic tree of 217 *E. coli* isolates from UTI cases in Norfolk.

Branch backgrounds are coloured by phylogroup. Reference genome, *E. coli* UTI89, is indicated by a dark green filled circle at the tip of the branch and labelled "Ref." Four rUTI cases are numbered and colour/shape coded at the branch tips.

Abbreviations

Hospital of origin

JPUH	James Paget University Hospital
NCH	Norwich Community Hospital
NNUH	Norfolk & Norwich University Hospital
NSFT	Norfolk & Suffolk Foundation Trust
QEH	Queen Elizabeth Hospital King's Lynn

Phenotypic resistance

AMP	Ampicillin
AUG	Co-amoxiclav
CLX	Cefalexin
CIP	Ciprofloxacin
GEN	Gentamicin
NIT	Nitrofurantoin
TRI	Trimethoprim

About Norfolk

Rural county in East Anglia, England

Population: 916,200

In 2021, 88,459 antibiotic prescriptions for uncomplicated UTIs under NHS Norfolk and Waveny costed £860,161

Methods

217 *E. coli* isolates and metadata from UTI patients were collected from from the Clinical Microbiology laboratory at Norfolk and Norwich University Hospital irrespective of personal characteristics. Patients could provide more than one sample for the study for the inclusion of recurrent (r)UTIs.

Isolates were whole genome sequenced using the Illumina platform for in silico multi-locus sequence typing and antibiotic resistance determinant detection (AMRFinderPlus).

Core genome alignment was made using Snippy for input into RAxML for the maximum likelihood phylogenomic tree. Visualisation was performed using ggtree in R.

FIGURE Nº 2

Source attribution

Non-exhaustive list of sources where the predominant clonal groups (see Figure 1) have been reported in the literature.

Results

57% of isolates represented by 8 global lineages.
Suggests Norfolk is no exception to the global movement of pathogens

92% of isolates were broadly susceptible.
Suggests *E. coli* causing UTIs in Norfolk are largely treatable with first-line drugs like nitrofurantoin. However, cost effective options like trimethoprim and ciprofloxacin were limited for many cases (25.1% and 9.0% resistant, respectively).

Future consideration

Problem: 8 of 11 nitrofurantoin resistant isolates did not harbour a known nitrofurantoin resistance determinant.

Significance: Nitrofurantoin is the current empirical treatment for UTIs.

Unmet need: Effective means of monitoring resistance mechanisms for nitrofurantoin are still needed.

Want to know more?

Scan QR code to read the pre-print.

Carter *et al.*, (2023) Uropathogenic *Escherichia coli* population structure and antimicrobial susceptibility in Norfolk, UK.

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