

# Escherichia coli from bloodstream infections in a tertiary referral hospital belong to a wide variety of MLST and show no sign of hospital outbreaks

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### BACKGROUND AND AIM

*Escherichia coli* is the most common cause of bloodstream infections (BSI) with a mortality of up to 15%. We investigated all *E. coli* isolates that were isolated from blood cultures of patients admitted to the University Hospital of Copenhagen - Rigshospitalet within a sampling period of 18 months

The purpose was to study

- (1) whether increasingly observed BSIs can be assigned to specific clones
- (2) whether resistance genes are more common in blood isolates compared to isolates from other infections
- (3) whether BSI isolates are disseminated in the hospital.

### METHODS

- *E. coli* from all clinical samples at Rigshospital, Copenhagen, Denmark for a period of 18 months (Dec 2019 - June 2021).
- Whole-genome sequencing (Illumina): ST types (tseemann/mlst) and prevalence of resistance genes (Abricate, Resfinder).
- SNP distances were calculated with Parsnp/1.5.0, raxml/8.2.11, harvesttools/1.3 and snpdist/0.7.0.

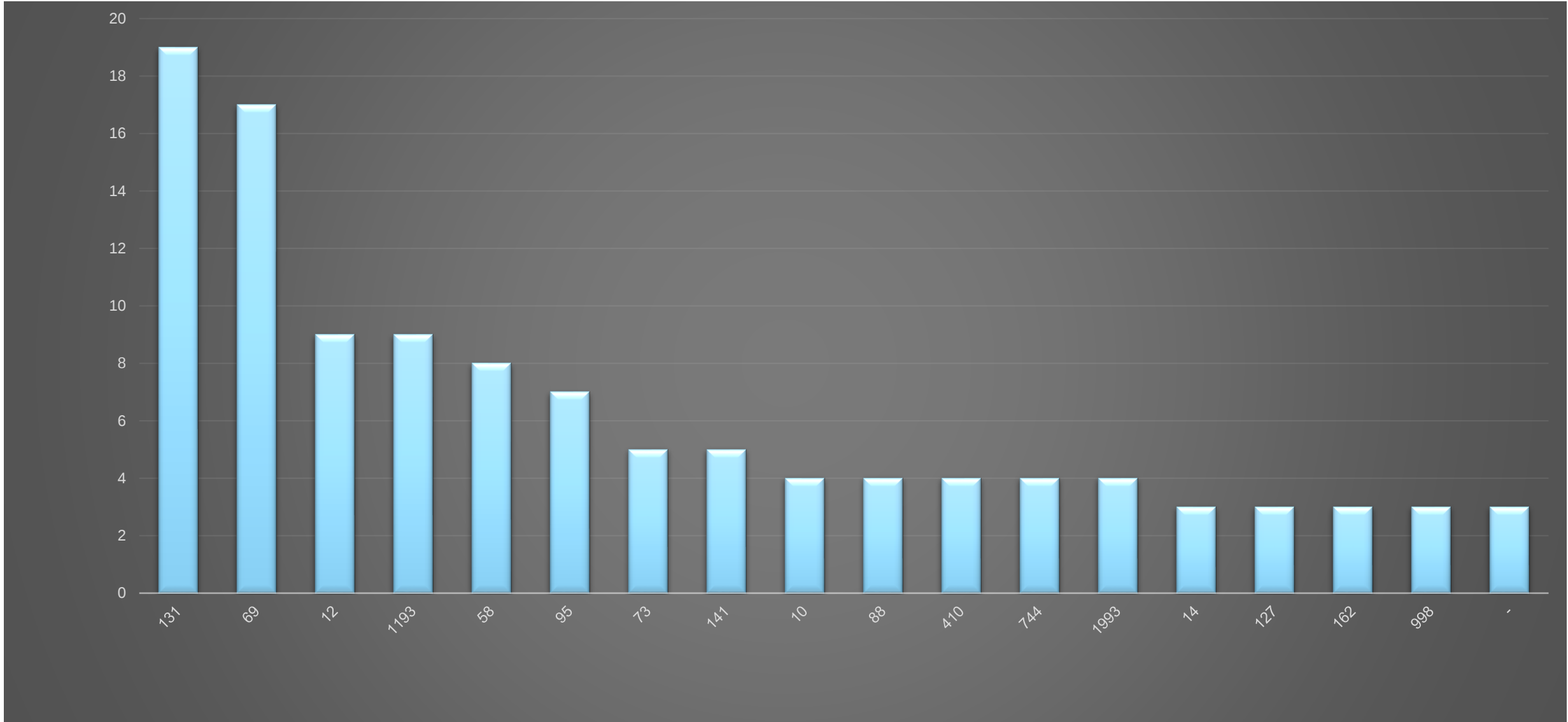
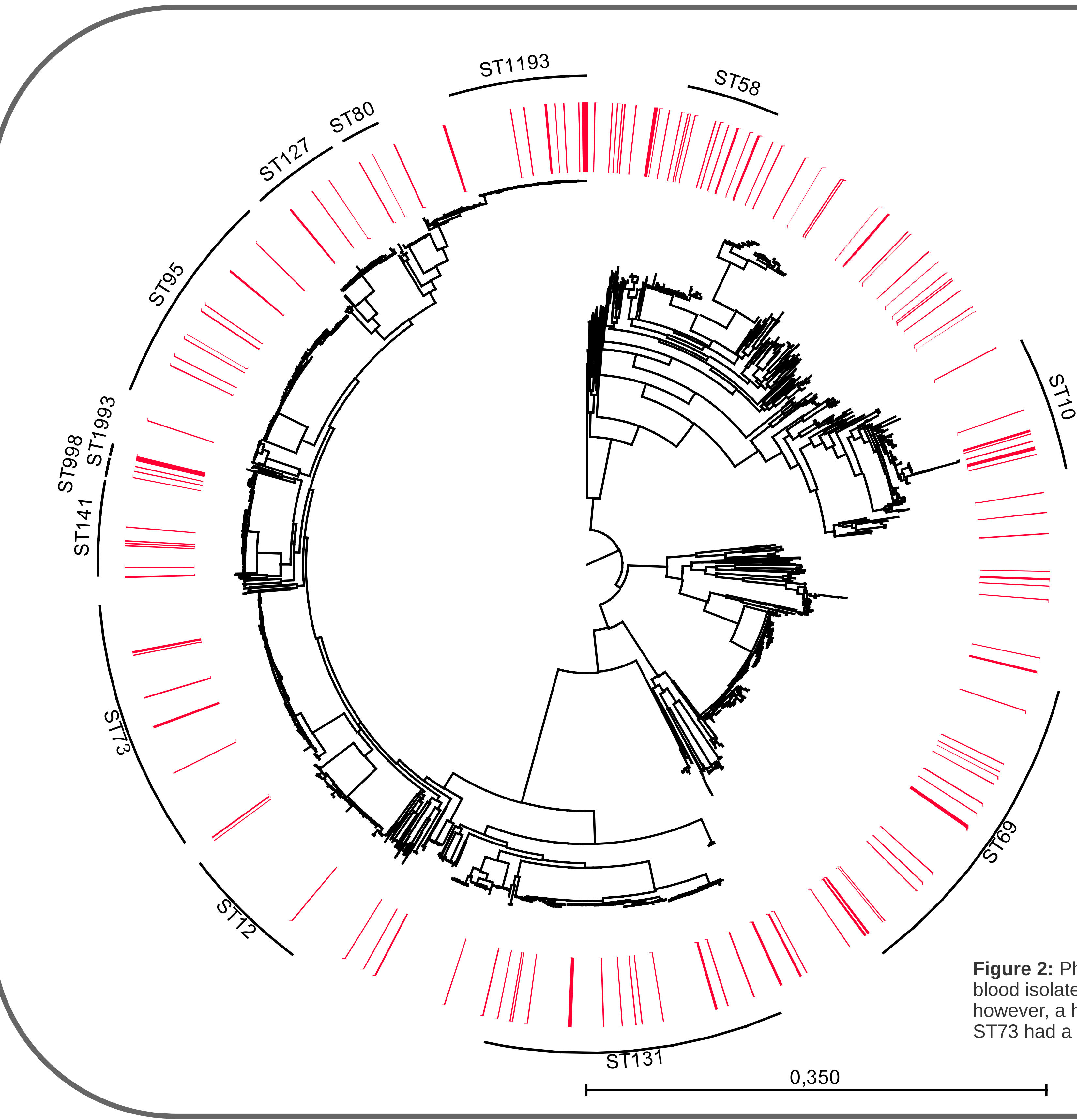


Figure 1: MLST types of blood isolates ≥3.



### RESULTS

- 190 *E. coli* blood isolates in a collection of 2857 *E. coli* isolates (6.7%) were analyzed
- The BSI isolates belong to 78 different MLSTs; three isolates were non-typeable by MLST. 45 were singletons.
- ST131, ST1193, ST73 and ST69 were the most prevalent MLSTs in all sources.
- The relative fraction of ST1193 was higher in BSI isolates, while we found a higher proportion of ST73 in the non-blood culture isolates.
- ST131, ST73 and ST1193 carried resistance genes in 32/33 BSI isolates. The blood isolates of the four major MLSTs combined carried resistance genes significantly more often compared to non-blood isolates.
- No indications of transmission of BSI isolates between patients based on epidemiological data or SNPs.

Figure 2: Phylogenetic tree of all 2926 *E. coli* isolates collected and highlighted with red are blood isolates. The phylogeny illustrates no specific clustering of BSI isolates in the tree, however, a higher fraction of ST1193 in blood compared to non-blood isolates. Oppositely, ST73 had a lower proportion in blood compared to non-BSI isolates.

Table 1: MLST types of blood isolates and resistance genes

|                                | ST69 n(%) | ST73 n(%) | ST131 n(%) | ST1193 n(%) |
|--------------------------------|-----------|-----------|------------|-------------|
| <i>E. coli</i> all sources     | 264 (9.2) | 246 (8.6) | 260 (9.1)  | 126 (4.4)   |
| <i>E. coli</i> blood (% of ST) | 17 (6.4)  | 5 (2.0)   | 19 (7.3)   | 9 (7.1)     |
| All sources                    |           |           |            |             |
| + resistance genes             | 201 (76)  | 132 (54)  | 216 (83)   | 112 (88)    |
| + resistance genes             | 63 (24)   | 114 (46)  | 44 (17)    | 14 (12)     |
| BSI                            |           |           |            |             |
| + resistance genes             | 12 (71)   | 5 (100)   | 18 (95)    | 9 (100)     |
| + resistance genes             | 5 (29)    | 0 (0)     | 1 (5)      | 0 (0)       |

### CONCLUSION

- The *E. coli* from BSI belong to a wide range of MLST types and resistance types.
- The blood isolates of the four major MLSTs more often carried resistance genes compared to non-blood isolates.
- BSI isolates showed no signs of transmission between the patients

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