



Transmission of antibiotic-resistant Enterobacteriaceae in ICUs



In an international study in 13 European intensive care units using protocolised surveillance and microbiological analysis, the transmission capacity of bacteria resistant to expanded-spectrum cephalosporins (ESCs) was 3.7 times higher for non-*Escherichia coli* Enterobacteriaceae (mainly *Klebsiella pneumoniae*) than for *E. coli*. The study findings are published in the journal *Clinical Infectious Diseases*.

The global emergence of infections caused by Enterobacteriaceae resistant to ESCs in intensive care units (ICUs) is, at least partly, driven by cross-transmission. Yet, individual transmission capacities of bacterial species have not been quantified.

Researchers conducted a post-hoc analysis of a multicentre study in 13 European ICUs that participated in the MOSAR-ICU trial. They used prospective surveillance data and a mathematical model to estimate the transmission capacity for *E. coli* and non-*E. coli* Enterobacteriaceae, all being ESC-resistant. Surveillance was based on a chromogenic selective medium for ESC-resistant Enterobacteriaceae, allowing identification of *E. coli* and of *Klebsiella*, *Enterobacter*, *Serratia*, *Citrobacter* species, grouped as non-*E. coli* Enterobacteriaceae (non-EcE).

Among 11,420 patients included in the analysis, the admission prevalence was 3.8% for non-EcE (74% being *Klebsiella pneumoniae*) and 3.3% for *E. coli*. Acquisition rates were 7.4 and 2.6 per 100 admissions at risk for non-EcE and *E. coli*, respectively. The estimated transmission capacity of non-EcE was 3.7 (95% credibility interval 1.4–11.3) times higher than of *E. coli*, yielding single admission reproduction numbers of 0.17 (95% credibility interval 0.094–0.29) for non-EcE and 0.047 (0.018–0.098) for *E. coli*.

"This was a post-hoc analysis of a large international prospective study, and, therefore, inevitably has study limitations. The surveillance method as used may have resulted in misclassification of some patients. Only the first isolate of each morphotype identified on chromogenic media was selected for species determination. Therefore, carriage with *K. pneumoniae* could have been missed in patients colonised with either *Enterobacter*, *Serratia* or *Citrobacter* species, as no further isolates were harvested and tested," the researchers note.

Furthermore, to confirm the results, the research team used the high-throughput typing method by the Raman spectroscopy for *K. pneumoniae* and *E. coli* isolates of four ICUs. The team explains: "Although validated for typing antibiotic-resistant Enterobacteriaceae, whole-genome sequencing might have provided more granularity and, thereby, more accurate estimates of transmission parameters."

As estimated single admission reproduction numbers for non-EcE and E. coli were well below the critical threshold of one (0.17 and 0.047, respectively), these data suggest that outbreaks typically remain small with current infection control policies, according to the researchers.

Source: [Clinical Infectious Diseases](#)

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