**O379**
**2-hour Oral Session**
**New insights in the control of multi-resistant Gram-negatives**

## The prevention paradox of extended-spectrum beta-lactamase-producing Enterobacteriaceae (ESBL-E): species-specific risk and burden of transmission

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**Background:** The ESCMID guideline on 'infection control measures to reduce transmission of multidrug resistant Gram-negatives' recommends applying contact precautions for all patients colonised with ESBL-E, with the exception of *Escherichia coli*. The aim of this study was to quantify the species-specific risk and burden of ESBL-E transmission in Dutch hospitals.

**Material/methods:** The SoM study is a multi-centre cluster-randomised study comparing contact isolation strategies for known ESBL-E carriers, and was performed between 2011 and 2014 in 14 Dutch hospitals. All consecutive adult patients that were identified with ESBL-E were placed on contact precautions and enrolled in the study (index patient). Ward-based ESBL-E prevalence surveys, using perianal swabs, were performed 5-9 days after enrolment of the index patient. The swabs were selectively pre-enriched and cultured on a selective ESBL screening agar plate (EbSA, AlphaOmega). Phenotypic ESBL confirmation was performed using the combination disk diffusion method (Neo-Sensitabs, Rosco). Whole genome sequencing was performed for all phenotypic confirmed ESBL-E isolates, on either a MiSeq or a HiSeq 2500 sequencer (Illumina). *De novo* assembly was performed using CLC genomics Workbench 7.0.4 (Qiagen). Assembled genomes were uploaded to the ResFinder web-service of the Center for Genomic Epidemiology (version 2.1), to identify the presence of ESBL genes. Genetic relatedness between the index isolate and wardmate isolates was assessed by whole genome multilocus sequence typing (wgMLST) (SeqSphere, Ridom), using a 2% cut-off value for genetic distance to define transmission.

**Results:** A total number of 662 index patients and 11,677 wardmates were enrolled. ESBL-E was cultured in 1,076 (9.2%) wardmates. Transmission of ESBL-E to wardmates was detected for 36 (5.4%) index patients. The risk of transmission was 4.4% (22/501) for *E. coli*, 11.0% (10/91) for *Klebsiella pneumoniae*, 10.0% (4/40) for *Enterobacter cloacae*, and 0% (0/30) for other

Enterobacteriaceae. Although the risk of transmission was higher for *K. pneumonia* (RR 2.59; 95% CI 1.31-5.32) and *E. cloacae*, 10.0% (RR 2.28; 95% CI 0.68-6.43) compared to *E. coli,* 61.1% [44.8%-75.3%] of all ESBL-E transmissions were attributable to *E. coli*, whereas only 27.8% [95% CI 15.7%-44.1%] and 11.1% [3.8%-25.9%] were attributable to *K. pneumoniae* and *E. cloacae*, respectively.

**Conclusions:** In a low-endemic setting, where contact precautions were applied for all ESBL-E carriers, transmission of ESBL-E was observed for 5% of known ESBL-E carriers. The risk of transmission was higher for *K. pneumoniae* and *E. cloacae*, compared to *E. coli*, but due to the higher prevalence of ESBL producing *E. coli,* 61% of all transmissions were attributable to *E. coli*. These findings illustrate that both the prevalence and the intrinsic transmission capacity of pathogens must be considered when designing infection control strategies for ESBL-E.