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Paper Poster Session
The MDR enterococcus

Prevalence of extended spectrum beta-lactamase-producing Enterobacteriaceae and vancomycin-resistant enterococci in hospitals and the community in the Northern Netherlands

Silvia García-Cobos*[1], Xuewei Zhou[1], Gijs J.H.M. Ruijs[2], Greetje Kampinga[1], Jan Arends[1], Dirk M. Borst[1], Lieke V. Möller[3], Nicole D. Holman[4], Theo A. Schuurs[5], Lesla E. Bruijnesteijn van Coppenraet[2], Jan F. Weel[6], Jan H. van Zeijl[6], John W.A. Rossen[1], Alexander W. Friedrich[1]

[1]*Department of Medical Microbiology, University of Groningen, University Medical Center Groningen, Groningen, Netherlands*

[2]*Laboratory for Medical Microbiology and Infectious Diseases, Isala, Zwolle, Netherlands*

[3]*Department of Microbiology, Certe, Groningen, Netherlands*

[4]*Department of Intensive Care Medicine, Martini Hospital, Groningen, Netherlands*

[5]*Izore, Centre for Infectious Diseases, Friesland, Leeuwarden, Netherlands*

[6]*Centre for Infectious Diseases Friesland, Izore, Leeuwarden, Netherlands*

Background: Extended spectrum β-lactamase (ESBL)-producing *Enterobacteriaceae* are increasingly reported in hospitals and in faecal samples collected from people in the community. In addition, vancomycin resistant enterococci (VRE) have emerged as an important nosocomial pathogen worldwide. However, its prevalence remains low within the community. We investigated the prevalence of both pathogens in hospitalized patients and its faecal carriage in healthy people in the Northern Netherlands.

Material/methods: In total 445 rectal swabs were collected from patients in 4 hospitals between 2012-2013 and additionally 400 stool samples were collected from healthy people in the community between 2010-2012. Detection of ESBL/plasmid AmpC (pAmpC)-*Enterobacteriaceae* and VRE was done on selective medium after pre-enrichment. Species determination was done by MaldiTof-MS and susceptibility testing by the VITEK®2 system according to EUCAST breakpoints. DNA array assays were used to determine ESBL genes. Typing of ESBL/pAmpC positive *E. coli* was performed using multiple locus sequence typing (MLST) (Wirth *et al*.). *E. coli* phylogenetic groups were determined by a multiplex PCR assay as described by Clermont *et al*. Enterococci intermediate or resistant to amoxicillin and/or resistant to vancomycin were screened by PCR for the presence of *IS16*, *vanA* and *vanB* genes.

Results: A total of 34 hospital isolates from 27 patients (6.1%) were confirmed to be ESBL and/or pAmpC positive. Thirty-two isolates were *E. coli,* of which 29 were ESBL positive (CTX-M-1-like (n=17), CTX-M-9 group (n=9), TEM_{ESBL} (n=2), SHV_{ESBL} (n=1)) and 3 were pAmpC producers (CMY-II (n=2) and DHA (n=1)). ST131-phylogroup B2 was the most prevalent among *E. coli* isolates (15.6%). The other two positive isolates were an *E. cloacae* (containing a CTX-M-1-like gene) and a pAmpC CMY-II producing *P. mirabilis*. In the community samples, 10 *E. coli* (2.5%) were confirmed to be

ESBL positive (CTX-M-1 like (n=5), CTX-M-15-like (n=3), CTX-M-9 group (n=1) and SHV_{ESBL} (n=1)), and 1 (0.3%) was pAmpC CMY-II positive. Among the 11 *E. coli* community isolates ST10-Cplx was the most prevalent (27.3%) whereas only one isolate belonged to ST131 (phylogroup F). A total of 105 hospitalized patients (23.6%) were colonized with ampicillin resistant *E. faecium* (AREfm), six (1.3%) of them were also colonized with vancomycin resistant *E. faecium* (VREfm). All AREfm were positive for the IS16. All VREfm had the *vanB* gene. Six AREfm (1.5%) were found in the community samples, three (0.75%) of them were confirmed *IS16* positive and one was a *vanA*-VREfm (0.25%).

Conclusions: A higher prevalence of ESBL/pAmpC-*Enterobacteriaceae* was observed in hospitals compared to the community in the Northern Netherlands. The most prevalent ESBL gene appeared to be CTX-M-1-like in both settings. The results suggest ESBL/pAmpC-*E.coli* circulate in the hospital and the community. AREfm is a more prevalent nosocomial pathogen whereas VREfm prevalence was low both in the hospital environment and the community.