

Session: P049 Living together in a world of resistance

**Category: 3b. Resistance surveillance & epidemiology: Gram-negatives**

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### **Trends in plasmids harbouring blaSHV-12 in Escherichia coli from animal and human origin**

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**Background:** *bla*<sub>SHV-12</sub> ranks amongst the most predominant resistance gene conferring extended-spectrum cephalosporin-resistant phenotype. Horizontal gene transfer via plasmids belonging to various rep/inc-types represents a key mechanism by which *bla*<sub>SHV-12</sub> disseminate among different bacterial populations. Therefore, monitoring the spread of plasmids is useful to follow the transmission of this antimicrobial resistance gene from different reservoirs. The aim of this study was to determine the plasmid rep/inc-types of a collection of *bla*<sub>SHV-12</sub> encoding Escherichia coli isolates from diverse origin.

**Material/methods:** A total of 129 non-duplicate *Escherichia coli* isolates consecutively recovered between 2009 and 2014 from humans, food-producing animals and retail meat in the Netherlands were included in the study. The isolates were recovered from MacConkey agar supplemented with 1mg/L cefotaxime during national antimicrobial resistance surveillance programmes or reference laboratory activities between 2009 and 2014. Identification of the isolates was performed using MALDI-TOF MS. The presence of acquired ESBL/AmpC genes was assessed by microarray analysis followed by PCR amplification and sequencing. Transformation experiments were performed to assess the plasmid location of the acquired ESBL/AmpC genes, while the plasmids were characterized by PCR-based replicon typing.

**Results:** Among the 129 *bla*<sub>SHV-12</sub> encoding *E. coli* recovered, 49.6% (n=64) were isolated from food-producing animals, 41.1% (n=53) from retail meat and 9.3% from humans. Plasmid-typing revealed

that *bla*<sub>SHV-12</sub> encoding plasmids belonged to nine rep/inc-types, namely IncI1 (66.7%; n=86), IncX3 (16.3%; n=21), IncX1 (4.7%; n=6), IncF (3.9%; n=5), IncB/O (3.1%; n=4), IncK (3.1%; n=4), IncN (0.8%; n=1), colE (0.8%; n=1) and multi-replicon IncF-X1 (0.8%; n=1). The predominant rep/inc-types among isolates recovered from food-producing animals and retail meat were IncI1 (64.1% and 66.0%) and incX3 (20.3% and 13.2%), while IncI1 (83.3%) among human isolates. A decrease of *bla*<sub>SHV-12</sub>-IncI1-harboring isolates was documented (100% to 90%) from 2010 to 2011, associated predominantly with a decrease among food-producing animals, and this trend continued till 2014 (55.6%). Interestingly, an increase on *bla*<sub>SHV-12</sub>-IncX3-harboring isolates was documented among food-producing animals (0% to 33.3%) between 2012 and 2013, and retail meat (0% to 25.0%) between 2011 and 2012, resulting in *bla*<sub>SHV-12</sub>-IncX3-harboring isolates being among the predominant rep/inc-types encoding *bla*<sub>SHV-12</sub> in the Netherlands from 2012 onwards.

**Conclusions:** Our data indicate that several plasmid rep/inc-types drive the epidemiology of *bla*<sub>SHV-12</sub> gene. However, the predominance of IncI1 plasmids encoding *bla*<sub>SHV-12</sub> among food-producing animals, retail meat and humans underscores the contribution of this plasmid family in the transmission of *bla*<sub>SHV-12</sub> within or between these reservoirs. Finally, the recent emergence of IncX3 plasmids encoding *bla*<sub>SHV-12</sub> implies a successful plasmid/gene combination that could facilitate the preservation and subsequent dissemination of this gene conferring extended-spectrum cephalosporin-resistant phenotype.