

O248

1-hour Oral Session

Escherichia coli ST131: successful and intriguing

Multidrug-resistant extra-intestinal pathogenic *Escherichia coli* sequence type 131 subclones H30-R and H30-Rx in retail chicken meat, Italy

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Background: Extraintestinal pathogenic *Escherichia coli* ST131 (ExPEC ST131) belongs to the virulent phylogenetic group B2 and has been reported to cause a wide range of extraintestinal infections. Recent molecular epidemiologic and whole-genome phylogenetic studies have elucidated the clonal structure of ST131, which comprises multiple ST131 subclones with distinctive resistance profiles, including the (nested) H30, H30-R, and H30-Rx subclones.

Material/methods: A collection of 237 fluoroquinolone resistant and ESBL/AmpC producing *E. coli* isolates, which had been isolated from processed retail chicken meat in the period May 2013-April 2015, was analyzed. Established polymerase chain reaction methods were used to define ExPEC ST131 and its H30 subclones, ESBL, AmpC, and plasmid-mediated quinolone resistance (PMQR) determinants.

Results: Out of 237 *E. coli* isolates, 12 isolates (5.1%) belonged to the phylogenetic group B2. Based on the molecular definition of ExPEC, all isolates were attributed with the status of ExPEC. SNP-PCR results confirmed that nine out of 12 (75%) B2 isolates were ST131. SNP-PCR for H30-R and H30-Rx subclones showed that six and three ExPEC ST-131 were positive for H30-R and H30-Rx, respectively.

Conclusions: Among clinical isolates, ST131, primarily its H30-R and H30-Rx subclones, accounts for most antimicrobial-resistant *E. coli* and is the dominant *E. coli* strain worldwide. To the best of our knowledge, this is the first report of these subclones in animal food samples. Our finding can strengthen the hypothesis of an animal food source for their acquisition by humans.