β-lactamase-encoding gene identification by microarrays in phenotypically resistant *Escherichia coli* from young calves in Wallonia, Belgium.

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Since 2016, a decrease of β-lactam resistance of *Escherichia* (*E.*) *coli* from calves is observed at ARSIA, maybe as a consequence of the regulation of the use of human critical antibiotics in livestock, like 3rd/4thG cephalosporins. The most frequent β-lactam resistance mechanism is the production of β-lactamase enzymes (BLA). Their classification is highly complex, but 4 groups can be proposed: classical BLA (BLA_C), cephalosporinases (AmpC), extended spectrum BLA (ESBL) and carbapenemases (CPE). The aim of this study was to identify the BLA-encoding genes present in *E. coli* from calves with a β-lactam resistance phenotype at the disk diffusion assay (DDA). For 4 months, *E. coli* with β-lactam resistance profiles were collected at ARSIA from calves with enteritis or septicaemia. After initial growth on Gassner agar plates, 3 colonies from faeces or intestinal contents were tested to identify their virulotype and one positive isolate per calf was tested by DDA. When pure culture was obtained from organs one isolate was also tested by DDA. Of the collected isolates, 94 with different resistance profiles were chosen to be tested with the Check-MDR CT103XL® microarray. A concordance of 72% between the detected genes and the phenotypes was observed. In isolates with ESBL resistance profiles, only $bla_{CTX\text{-}M}$ genes were detected. In isolates with AmpC resistance profiles $bla_{CMY\ II}$ and bla_{DHA} genes were identified. The $bla_{TEM\text{-}WT}$ genes were detected in isolates with BLA_C resistance profiles and also in isolates harbouring ESBL/AmpC-encoding genes. In the future, PCR will be performed on the whole collection to identify the genes present and to follow their incidence for 3 years.