

Triplex PCR to detect CTX-M-1, CTX-M-2 and CTX-M-9 extended-spectrum- β -lactamase-encoding genes in bovine *Escherichia coli* isolates

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Extended-spectrum-BLA (ESBL) confer a resistance to some antibiotics classified as critical in human medicine, like 3rd/4th generation cephalosporins. Though the use of critical antibiotics in livestock is regulated since 2016, it remains important to follow the evolution of ESBL resistance, especially in enterobacteria. The aim of the study was therefore to identify the ESBL-encoding genes in *Escherichia (E.) coli* from young calves in Wallonia with an ESBL phenotype at the disk diffusion assay. During 2 calving seasons (A: 2017-2018 and B: 2018-2019), 152 (A) and 161 (B) *E. coli* with ESBL resistance profiles were collected at ARSIA from calves with enteritis or septicemia. Of them, 50 were tested with microarrays and only *bla*_{CTX-M} genes, coding for cefotaximases, were detected. Based on these results, all 313 *E. coli* of the collection were tested with PCR for the different genes coding for the CTX-M-1, CTX-M-2 and CTX-M-9 ESBL groups: 103 (A) and 84 (B) were positive for the CTX-M-1 group; 26 (A) and 24 (B) isolates, for the CTX-M-2 group; 25 (A) and 37 (B) isolates, for the CTX-M-9 group; and 4 (A) and 5 (B) isolates were negative. In 4 (A) and 1 (B) isolates, genes coding for CTX-M-1 and CTX-M-2 groups were simultaneously detected. In conclusion, the *bla*_{CTX-M} genes are the most prevalent ESBL-encoding genes in our collection and of them, the genes coding for the CTX-M-1 group are the most prevalent, as described in the literature. The PCR-negative *E. coli* will be further tested with PCR for the other *bla*_{CTX-M} genes, if any. Moreover, a third collect of isolates is already planned during the next calving season to follow the prevalence of ESBL *E. coli*.