

Antimicrobial resistance profiles of *Escherichia coli* and prevalence of extended-spectrum beta-lactamase-producing *Enterobacteriaceae* in calves from organic and conventional dairy farms in Switzerland

Magdalena Nüesch-Inderbinnen¹, Claudia Hänni¹, Sonja Hartnack¹, Katrin Zurfluh¹, and Roger Stephan¹

¹University of Zurich

February 10, 2022

Abstract

This study compared the antimicrobial resistance (AMR) among commensal *Escherichia coli* in the fecal microbiota of young calves raised on organic and on conventional dairy farms in Switzerland. Further, fecal carriage of extended-spectrum beta-lactamase (ESBL) producing *Enterobacteriaceae* was assessed for calves from both farming systems. Where possible, data on antimicrobial usage (AMU) were obtained. Antimicrobial susceptibility testing was performed on a total of 71 isolates using the disk diffusion method. ESBL producers were characterized by PCR-based multilocus sequence typing and sequencing of the *bla*ESBL genes. Organically raised calves were significantly more likely to harbor *E. coli* that showed antimicrobial resistance to ampicillin (OR 2.78, 95%CI 1.02–7.61, $p=0.046$), streptomycin (OR 3.22, 95%CI 1.17–8.92, $p=0.046$), kanamycin (OR 11.3, 95%CI 2.94–43.50, $p<0.001$), and tetracycline (OR 3.25, 95%, 95%CI 1.13–9.31, $p=0.028$). Calves with reported AMU were significantly more likely to harbor *E. coli* with resistance to ampicillin (OR 3.91, 95%CI 1.03–14.85, $p=0.045$), streptomycin (OR 4.35, 95%CI 1.13–16.7, $p=0.045$), and kanamycin (OR 8.69 95%CI 2.01–37.7, $p=0.004$). ESBL-producing *Enterobacteriaceae* (18 *E. coli* and 3 *Citrobacter braakii*) were detected exclusively among samples from conventionally farmed calves (OR infinity ([?]), 95%CI 2.3–[?], $p<0.0013$). The observations from this study suggest that AMR is highly prevalent among commensal *E. coli* in young dairy calves, irrespective of the farm management system, with proportions of certain resistance phenotypes higher among organic calves. By contrast, the occurrence of ESBL producers among young dairy calves may be linked to factors associated with conventional farming.

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