

Resistance to β -lactam antibiotics in *Escherichia coli*, *Klebsiella* spp. and *Enterobacter* spp. isolated from raw cow milk

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The consumption of raw milk is influenced by the concept that heating process can reduce its nutritional properties and health benefits. However, raw milk acts as an optimal growth medium for diverse microorganisms. *Escherichia coli*, *Klebsiella* spp. and *Enterobacter* spp. are widely distributed in nature and are part of the commensal microbiota of the intestinal tracts of humans and animals. Currently, *Enterobacter* species isolated from food have an importance due its association with cases of necrotizing colitis and meningitis particularly in neonates. Thereby, this study investigated the occurrence, the characterization of sensitivity profile to antimicrobials frequently used in Human and Veterinary Medicine, and the presence of resistant genes in *Escherichia coli*, *Klebsiella* spp. and *Enterobacter* spp., as well as the differentiation of *Enterobacter cloacae*, *Enterobacter aerogenes*, *Pantoea agglomerans* and *Cronobacter sakazakii*. From a total of 382 raw cow milk samples were isolated 18 *E. coli*, 63 *Klebsiella* spp. and 104 *Enterobacter* spp., of which were identified *E. cloacae* (39/104), *Pantoea agglomerans* (23/104), *Cronobacter sakazakii* (18/104) e *E. aerogenes* (9/104). The high relative frequency of resistance to β -lactam antibiotics (*E. coli* 88%, *Klebsiella* spp. 92% and *Enterobacter* spp. 85%) and the presence of positive strains to *bla*_{TEM} e *ampC* genes, respectively, *E. coli* (67%; 72%), *Klebsiella* spp. (19%; 3%) and *Enterobacter* spp. (27%; 0%) highlights the risk of infection by environmental microorganisms, resistant to antimicrobials, associated with consumption of raw cow milk. The consumers and producers should be advised about the risk of consumption of raw milk, since heat treatments do not change the nutritional properties, so that education and information are essential for provide public health.

Keywords: coliforms, antimicrobials, contamination, public health

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