

TITLE: GENETIC PROXIMITY AND ALTERATION OF ANTIMICROBIAL RESISTANCE PROFILE IN SESSILE AND PLANKTONIC *Campylobacter jejuni*

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ABSTRACT:

Campylobacter is one of the main etiological agents of gastroenteritis of food origin in the world, with *C. jejuni* being the species more involved in the human campylobacteriosis when compared to the other species. Consumption of contaminated animal products is the main source of human infection, with chicken meat being the most prominent. The aim of this study was to evaluate the susceptibility to antimicrobials in planktonic and sessile forms by traditional methodology with chicken juice (CJ) supplementation and to determine the genetic similarity of 30 strains of *C. jejuni* isolated from chickens carcasses produced by an exporting company in the state of Minas Gerais in the years of 2015 and 2016. The diffusion disc technique was used to determine the antibiotic resistance to amoxicillin / clavulanic acid, azithromycin, erythromycin, ciprofloxacin and tetracycline. The genetic similarity between the strains was determined using the RAPD-PCR technique. The sessile form presented a higher percentage of resistance to all antimicrobials tested, with difference being significant for amoxicillin / clavulanic acid and tetracycline. The highest percentages of resistance were observed for tetracycline (73.3% and 93.3%), amoxicillin / clavulanic acid (33.3% and 60.0%) and ciprofloxacin (60.0% and 63.3%), for the planktonic and sessile forms, respectively. The high resistance to tetracycline and amoxicillin / clavulanic acid can be explained due to the fact that these drugs are of therapeutic use in veterinary medicine, exerting selective pressure on the microorganism, as well as ciprofloxacin and enrofloxacin. Resistance to fluoroquinolone is a cause for concern as this drug is used to treat serious human infections. Multiresistance was identified in 40% (12/30) of *C. jejuni* sessile and in 23.3% (7/30) of strains in planktonic form. The phylogenetic evaluation showed the presence of seven clusters with similarity superior to 80%, being two considered clones, with 100% of homology. In general, the phylogenetic analysis indicated a possible occurrence of cross contamination and of persistent genotypes in the slaughter environment. The higher resistance found in the sessile form addresses the need for more rigorous methodologies in the hygiene processes, besides the risk associated with the dissemination of this profile among the strains.

Keywords: Antibiotics, Campylobacteriosis, Chicken juice, multiresistance, RAPD-PCR

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