

Molecular Characterization and Antibiotic Resistance Profiling of *Campylobacter* Species Isolated from Chicken in Gauteng Abattoirs

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Abstract

Food-producing animals such as chickens are the primary hosts of several zoonotic foodborne pathogens, including *Campylobacter* species. Foodborne pathogens pose a serious risk to the public's health and have significant socioeconomic repercussions. Poultry meat is a major source of foodborne pathogens that can cause disease and/or death in humans. This study is aimed to determine the molecular epidemiology of antibiotic-resistant *Campylobacter* spp., isolated from chicken carcasses in Gauteng abattoirs. A total of 404 samples were examined for the presence of *Campylobacter* spp., which were putatively detected using selective media and confirmed as such by PCR for specific genes. *Campylobacter* species were found ($P < 0.05$) in 68.8% (287/404) samples. *Campylobacter* had the majority of positive samples from Emfuleni (92.5%), West Rand (76.2%), Ekurhuleni (68.8%), City of JHB (60.0%), and, City, of Tshwane (46.3%) and the differences were statistically significant ($P = 0.004$). The positive isolates were characterized by, antibiotic resistance, and more than 96% of the *Campylobacter* spp. isolates were resistant to quinolones and tetracyclines. Positive isolates will also be characterized given speciation and virulence genes using PCR. Clonal relatedness will be determined using Enterobacterial Repetitive Intergenic Consensus (ERIC)-PCR fingerprinting and Multilocus Sequence Types. Data generated from the study will indicate the extent of meat contamination by *Campylobacter* spp., in Gauteng abattoirs and, more importantly, a potential risk to human health.