Clonal profile of *Klebsiella pneumoniae* isolated in a Veterinary Teaching Hospital in Botucatu, Sao Paulo State, Brazil

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In a public health perspective there is potential for spread of pathogenic bacteria and commensal resistant to antimicrobials, from animals to humans, via direct contact or food chain. Bacteria from the genera Klebsiella are opportunistic pathogens isolated from various diseases in humans and animals. Antimicrobial resistance has become a serious problem in this genus. The need to investigate the relationship among bacterial groups made that the traditional methods were replaced to molecular methods. Six Klebsiella pneumoniae, resistant to at least six classes of antimicrobial, isolated from diseased animals, five dogs and one horse, were characterized by Xbal-macrorestriction analysis (PFGE) in order to establish genetic relationships among them. An 80% coefficient of similarity was chosen for the cluster definition. More than eight chromosomal DNA fragments were generated for each isolate. Among the six K. pneumoniae, one cluster with three isolates (two isolates from dogs with gastroenteritis or sepsis, and one equine with orchitis) was identified. The comparison between strains, relating them phylogenetically, is due the fact that those epidemiologically related come from the spread of a single ancestor, being considered clones. PFGE is one of the most techniques used, with a high discriminatory power, and have been considered as the gold standard in molecular epidemiology. The presence of genetically related strains, isolated from different species of domestic animals unrelated, suggests the spread of a K. pneumoniae clone at the Veterinary Teaching Hospital. The knowledge of the bacteria involved in infectious disease outbreaks is essential to complete epidemiological studies, especially focused on prevention and no dissemination of these microorganisms in animal populations, and consequently in human populations.

Keywords: Enterobacteriaceae; pulsotype; hospital infection; pets.