

**TITLE:** GENOTYPING OF *Klebsiella pneumoniae* ISOLATES FROM ANIMALS AND HUMANS IN CUIABÁ, MATO GROSSO.

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**ABSTRACT:**

*Klebsiella pneumoniae* (*K. pneumoniae*), is a bacterium known as multidrug-resistant (MDR) due to the development of enzymatic mechanisms, being considered responsible for many infectious diseases. The severity of the infection is often associated with the multiresistance capability of the isolate due to the exacerbated use of antimicrobials. The Multilocus sequence typing (MLST) technique is being used to detect the degree of similarity between the isolates originat from different lesion sites in domestic animal, wild animals and humans with the aim of tracing the degree of similarity between the isolates of *K. pneumoniae*. For this study, we used 47 isolates from different clinical samples from the Laboratory of Microbiology, previously biochemically characterized and by sequencing the 16S rRNA gene. For the isolates of animals, the antimicrobial susceptibility test was done bythe disc diffusion technique using 11 classes of antimicrobials with 20 antibiotics, whereas for the human isolates it was based on the Minimum Inhibitory Concentration (MIC) performed in Bact / Alert 3D systems and Vitek2, and 7 classes of antimicrobials with 17 antibiotics have been tested. The extracted isolates were submitted to MLST technique as described by the Pasteur Institute. In the isolates, high resistance rates to ampicillin (94%) and low resistance to amikacin (13%) were observed, and 85% (40/47) of the isolates were multiresistant (MDR). The analyses generated a total of 47 Sequence Typing (ST) formed and of these, 20 were considered new STs, since new alleles were detected. The most common STs were ST 70 (6% 03/47), ST 534 (6% 03/47), ST 1089 (4% 02/47) and ST12 (4% 02/47). In this study, a high resistance rate to beta-lactams and a low aminoglycoside resistance rate was detected, with a high prevalence of multiresistance of the isolates, agreeing with several studies. In domestic animals the ST 15 is widely disseminated, but it was not observed in our study. In human isolates, the ST 11 and the ST 437 have been identified as having global epidemiological importance because they are associated with nosocomial infections and the dissemination of carbapanemases. The knowledge of the population structure of *K. pneumoniae* is necessary to determine the relationship between MDR organisms as well as the source of infection during outbreaks providing data for greater control in public health.

**Keywords:** MDR, MLST, molecular diagnosis, nosocomial infection

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