TITLE: VIRULENCE, ANTIMICROBIALS RESISTANCE OF *Klebsiella* spp. AND GENOMIC CHARACTERIZATION OF *Klebsiella pneumoniae* EXTENDED SPECTRUM β-LACTAMASES PRODUCERS ISOLATED FROM PSITACINNE BIRDS WITH RESPIRATORY DISEASE

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ABSTRACT

Psittacine birds are among the most seized bird species in São Paulo, commonly kept as pet. The maintenance of these birds in captivity may represent a zoonotic risk and contribute to the propagation of multiresistant and beta-lactamase extended-spectrum (ESBLs) enterobacteria, such as *Klebsiella* spp. The aim of this study was to identify and characterize strains of *Klebsiella* spp. isolated from respiratory secretions of 46 diseased psittacines, determining virulence and resistance profile to 15 antimicrobials. Isolation was performed on MacConkey agar with incubation at 37ºC for 24 h. The colonies were identified by MALDI-TOF MS. The antibiotic susceptibility was determined by the agar diffusion method. Amplified spectrum beta-lactamase detection was performed by double-disc synergism test. The virulence genes profile performed was *iro*N, *iuc*D, *irp*-2, *rmp*A, *mag*A, K2, *kfu*, *uge*, K1, *kpn*, *mrk*D, *fim*H, cc258, and *all*S. ESBL-producing *K. pneumoniae* strains were subjected to whole genome sequencing on Illumina NextSeq platform using paired-end library. MLST, resistance genes, plasmids, pMLST were determined using online tools of Center for Genomic Epidemiology. Among the 19 strains of *Klebsiella* spp., 16 (16/19) were identified as *K. pneumoniae*, and three (3/19) as *K. oxytoca*. The antimicrobial susceptibility profile demonstrated high resistance to ampicillin (89.5%), multiple resistance (at three or more antimicrobial categories) was detected in 31.6% (6/19) of the strains, and the standard of resistance to ampicillin, sulfonamide, and gentamicin was the most prevalent (50%, 3/6). The virulence profile demonstrated a high prevalence of *fim*H (94.7%), *kpn* (89.4%), *uge* (84.2% %) and *irp*-2 (78.9%). Three strains of *K. pneumoniae* were positive for extended-spectrum beta-lactamase production. These strains were classified in sequence types (STs) ST15, ST147 and ST307. These three clonal groups represent the main responders for outbreaks of *K. pneumoniae* nosocomial infections worldwide. However, this is the first account of these clones as causing disease in birds. These data indicate the occurrence of *K. pneumoniae* producing CTX-M-15 and CTX-M-8 in captive parrots and confirm the zoonotic and anthropozoonotic potential of the agent, highlighting the clinical relevance for humans and animals.

Keywords: Psittacines. *Klebsiella* spp. Microbiology. Bacterial resistance. ESBL.