

Phenotypic and Genotypic Characterization of *Klebsiella* spp. Isolated from the Nasal Cavity of Healthy Swine

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Klebsiella spp. are ubiquitous in nature and, in mammals, they are commensal bacteria found in mucosal microbiota. However, they can also act as opportunistic pathogens, causing a wide range of infections that are challenging to treat due to their significant antibiotic resistance (AR) profile. Information on *Klebsiella* spp. in clinically healthy swine is scarce in the literature. Therefore, the objective of this study was to characterize *Klebsiella* spp. isolates from the nasal cavity of healthy swine raised under antimicrobial-free diets and without antibiotic administration throughout all growth phases. Samples were obtained from the nares of 15 animals using the swab technique and streaked onto Simmons citrate with 1% inositol agar and McConkey agar. The isolates obtained through culture-dependent methods were confirmed as *Klebsiella* using the Modified Rugai medium followed by 16S rDNA sequencing. Genetic polymorphism of the isolates was investigated using rep-PCR (ERIC PCR). Antimicrobial susceptibility was evaluated using the disk diffusion test and CLSI-Vet breakpoints. The presence of resistance genes, including *bla*CTX-M, *bla*OXA, *bla*SHV, *bla*TEM, *mcr*-1, *qnr*S, *str*A, *sul*2, and *tet*A, was assessed through conventional PCR. Results revealed 24 *Klebsiella* isolates that were confirmed both biochemically and molecularly. The species were identified as *Klebsiella aerogenes* (n=3), *Klebsiella africana* (n=3), *Klebsiella grimontii* (n=2), *Klebsiella pneumoniae* (n=5), *Klebsiella quasivariicola* (n=5), *Klebsiella variicola* (n=4) and *Klebsiella* spp. (n=2). Genetic polymorphism analysis showed that 11 isolates from different animals exhibited identical genetic profiles (similarity > 90%). Regarding the antimicrobial susceptibility profile, 100% of the isolates were resistant to macrolide; 91.6% to beta-lactam; 66.6% to cephalosporin; 16.6% to tetracycline; 12.5% to sulfonamide; 8.3% to aminoglycoside; 8.3% to phenicol, and 4.16% to polymyxins. PCR analysis identified the *bla*OXA gene in 41.6% of the isolates, *sul*2 in 41.6%, *tet*A in 41.6%, *str*A in 37.5%, *qnr*S in 29.16%, *bla*CTX-M in 25%, *bla*SHV in 58.3%, and *bla*TEM in 12.5%. Phenotypic and molecular analyses were conclusive in revealing a profile of antimicrobial-resistant isolates, even under growth conditions without selection pressure. This study reveals that healthy swine without antimicrobial use naturally harbor nasal cavity microbiota composed of *Klebsiella* spp. resistant to antimicrobials commonly employed in the field for infection treatment.

Key-Word: *Klebsiella*, resistance, nasal cavity, health swine

Caracterização Fenotípica e Genotípica de *Klebsiella* spp. Isolada da Cavidade Nasal de Suínos Saudáveis

Klebsiella spp. são comensais da mucosa de mamíferos, mas podem ser patógenos oportunistas. Até o momento, nenhum estudo caracterizou isolados da cavidade nasal de suínos. Portanto, este trabalho caracterizou o genótipo e fenótipo de resistência de isolados da cavidade nasal de suínos saudáveis. Como resultado, identificamos 6 espécies de *Klebsiella*, das quais, os testes de susceptibilidade a antimicrobianos revelaram alta resistência a macrolídeos, beta-lactâmicos e cefalosporinas. Análises de PCR detectaram genes de resistência, incluindo *bla*OXA, *sul*2 e *tet*A. Concluímos que, esses suínos abrigavam *Klebsiella* resistentes a antimicrobianos mesmo sem exposição prévia a antibióticos, sugerindo um reservatório natural de resistência.

Palavras-chave: *Klebsiella*, resistência, cavidade nasal, suínos saudáveis
