RESUMO SIMPLES - MICROBIOLOGIA E IMUNOLOGIA

PHENO- AND GENOTYPIC ASSESSMENT OF RESISTANCE TO COLISTIN AND B-LACTAMS IN BACTERIA ISOLATED FROM CAPYBARAS (HYDROCHOERUS HYDROCHAERIS) RESIDING ON THE SEROPÉDICA CAMPUS OF UFRRJ: IMPLICATIONS FOR ONE HEALTH

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Phenotypic and genotypic investigation of antimicrobial resistance in wildlife has become increasingly essential for understanding the dynamics of resistance gene dissemination in natural ecosystems, especially in areas with intense interface between wildlife, humans, and anthropized environments. Capybaras (Hydrochoerus hydrochaeris), due to their gregarious behavior, semi-aquatic habits and presence in urban and peri-urban areas, may serve as important

reservoirs and dispersers of multidrug-resistant (MDR) bacteria. In this context, studies involving antimicrobial susceptibility testing and molecular detection of resistance genes allow the evaluation of the potential sanitary risks posed by these animals within the One Health framework. The aim of this study was to identify bacteria resistant to critical antimicrobials, such as colistin and β-lactams, isolated from a population of capybaras residing at the Seropédica campus of UFRRJ. A total of 75 samples were collected (rectal, oral, nasal, right and left auditory canal) from 15 capybaras using sterile swabs; samples were plated on MacConkey and CLED agar, and isolates were identified using MALDI-TOF. Gram-negative bacilli (GNB) and glucose-non-fermenting GNB were subjected to phenotypic tests for β-lactam resistance, including ESBL and carbapenemase production, using the disk diffusion method with amoxicillin/clavulanic acid (30µg), aztreonam (30µg), cefotaxime (30µg), ceftazidime (30µg), cefepime (30µg) and meropenem (10µg), interpreted according to CLSI guidelines. Broth microdilution was performed to investigate resistance to colistin and meropenem, using only CLSI-defined breakpoint concentrations. DNA extraction was performed by thermal lysis, followed by PCR detection of blaTEM, blaSHV, blaCTX and mcr1-9 genes. A total of 73 Gram-negative strains were obtained, of which 66 belonged to the order Enterobacterales and 7 were non-fermenting GNB, including Pseudomonas aeruginosa, Pseudomonas stutzeri, Acinetobacter bereziniae and Stenotrophomonas maltophilia. Among Enterobacterales isolates, Escherichia coli was the most prevalent species (44% – 29/66), indicating a strong presence within the capybara microbiota, followed by 7,6% Proteus mirabilis (5/66) and Klebsiella pneumoniae (5/66). Phenotypic analysis revealed predominance of susceptibility to the β-lactams tested; however, relevant resistance profiles were detected in broth testing, such as colistin resistance in multiple E. coli isolates (31% – 9/29 – including L10, L15, L31, L32, L34, L48, L53, L79, L122), Klebsiella pneumoniae (40% – 2/5 – L36 and L97) and Enterobacter bugandensis (75% – 3/4 – L49, L50, L52). Concurrent resistance to colistin and meropenem was observed in three E. coli strains (L32, L34 and L79), a situation considered critical for public health. In total, four Proteus mirabilis strains harbored the mcr-2 gene, all isolated from rectal samples, reinforcing the role of the gastrointestinal tract as a niche for these determinants. Multiple ESBL-associated genes were also identified: 20,5% (15/73) of isolates carried blaSHV, 16,4% (12/73) carried blaCTX and 8,2% (6/73) carried blaTEM. Isolates exhibiting co-occurrence of resistance genes included P. mirabilis (L4) with blaTEM, blaCTX and mcr-2; Serratia marcescens (L11) and E. coli (L79)

with blaTEM and blaSHV; and Klebsiella aerogenes (L116) with blaSHV and blaCTX, demonstrating both phenotypic and genotypic multidrug resistance. The presence of these genes in different bacterial species and among different individuals within the same population indicates active circulation of resistance determinants among capybara microbiota. In conclusion, the studied population harbors bacteria with resistance profiles of relevance to One Health, including mcr and ESBL-encoding genes, representing potential environmental and zoonotic dissemination risks. These findings reinforce the need for continuous surveillance of wildlife as a key component in antimicrobial resistance monitoring.

Palavras-chave: wildlife; antimicrobial resistance; esbl; mcr; one health.