

**Title: EVALUATION OF PATHOGENIC *ESCHERICHIA COLI* IN FREE-RANGING GOLDEN-HEADED LION TAMARINS (*Leontopithecus chrysomelas*) KUHL, 1820, UNDERGOING TRANSLOCATION, BRAZIL.**

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**Abstract:**

Translocation of wild animals back to their natural habitat is an important initiative towards endangered species conservation. It requires a complete evaluation of the individuals' health status, especially regarding agents with zoonotic potential. The presence of antimicrobial resistant *Escherichia coli* with zoonotic and/or pathogenic potential may be used as an indicator of environmental contamination and/or anthropic activity. We evaluated the presence and antimicrobial resistance of pathogenic *E. coli* isolated from free-ranging Golden-headed lion tamarins – GHLT (*Leontopithecus chrysomelas*), considered an exotic and invasive species of Serra da Tiririca State Park (Niterói, RJ), while undergoing translocation to their original habitat in Southern Bahia. Rectal swabs were sampled from 330 GHLT specimens from 63 different family units. The isolated *E. coli* strains were evaluated for virulence markers of diarrheagenic strains (genes *eae*, *stx1* e *stx2*) and extraintestinal pathogenic strains (genes *sfa*, *papC*, *papEF*, *hly*, *cnf1*, *iucD*, *fyuA*, *traT*, *cvaC* e *malX*); phylogenetic groups (A, B1, D and B2); and antimicrobials resistance ( $\beta$ -lactamic, quinolone, chloramphenicol, trimethoprim/sulfamethoxazole, aminoglycosides, tetracycline). All 63 family groups were classified according to their proximity to human populations (A – high: 99 individuals; B – medium: 110 individuals; e C – low: 121 individuals). From a total of 311 isolated strains of *E. coli*, 82 were from 67 GHLT from group A (67.5%, 67/99), 115 from 95 individuals from group B (86.5%, 95/110) and 114 from 98 individuals from group C (81.0%, 98/121). A higher percentage of isolates with four or more virulence genes was found in groups A (8.5%) and B (6.0%) than in group C (2.5%), however, strains from phylogenetic groups B2 and D were higher in group C (51.5%) than groups A (44.5%) or B (30.0%). We observed an elevated percentage of strains resistant to  $\beta$ -lactamics (39.5%, 32.5%, 44.0%), followed by aminoglycosides (6.0%, 10.5%, 3.5%), tetracycline (6.0%, 9.5%, 3.5%), trimethoprim/sulfamethoxazole (6.0%, 7.0%, 1.5%), quinolone (2.5%, 1.0%, 1.0%), and chloramphenicol (2.5%, 0.0%, 0.0%), perceptual respectively, in groups A, B and C. Multi drug resistance was higher on group B (6.0%) in comparison to groups A and C (3.5%). Our results show that the microbiome of wild animals may reflect local anthropic activity and reinforce the need of health studies during wildlife reintroduction/relocation programs.

**Key words:** *Escherichia coli*, ExPEC, antimicrobial resistance, *Leontopithecus chrysomelas*, Callitrichidae

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