

DISTRIBUTION OF SPECIES, ANTIMICROBIAL RESISTANCE AND VIRULENCE DETERMINANTS AMONG *ENTEROCOCCUS* ISOLATED FROM THE INTESTINAL MICROBIOTA OF *RUPORNIS MAGNIROSTRIS* IN RIO DE JANEIRO, BRAZIL

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Due to their predatory nature, raptor birds like *Rupornis magnirostris* may serve as indicators of environmental contamination. As members of *R. magnirostris* feed on small rodents and birds that easily circulate in different habitats, their intestinal microbiota can reflect that of the animals on which they feed. Consequently, they may play a role in the spread of microorganisms that may represent a threat to human health, such as the multidrug-resistant enterococci. The purpose of this study was to characterize *Enterococcus* isolates obtained from the intestinal microbiota of *R. magnirostris*, by using phenotypic and genotypic methods. Cloacal swabs were collected from 38 birds sent to the CETAS-RJ and CRAS-UNESA, during 2013. Enterococci were recovered from cloacal samples of all the birds evaluated, and 80 isolates were selected based on colony morphology. The isolates were identified, by using conventional phenotypic and PCR-based tests, as: *E. faecalis* 78.75 %, *E. hirae* 8.75%, *E. faecium* 5%, *E. gallinarum* 5%, *E. casseliflavus* 1.25% and *E. raffinosus* 1.25%. They were submitted to antimicrobial susceptibility tests, by using disk-difusion and demonstrated full resistance to ciprofloxacin 5%, chloramphenicol 10%, enrofloxacin 6.25%, erythromycin 10%, levofloxacin 1.25, linezolid 1.25%, nitrofurantoin 5%, norfloxacin 1.25%, penicillin 2.5%, quinupristin/dalfopristina 1.25% (non-*E. faecalis*), rifampin 31.25%, streptomycin 7.5% and tetracycline 7.5%. A higher number of isolates demonstrated intermediate level susceptibility to ciprofloxacin 38.75%, enrofloxacin 55%, erythromycin 60%, norfloxacin 21.25%, and rifampin 25%. Multidrug resistance (resistance to ≥ 3 classes of antimicrobials) was found in 10% of the isolates. Resistance was related to the presence of the following genes: *ant(6)-Ia*, *ermB*, *mefA*, *tet(M)*, *tet(L)* and *vanC*. Virulence-associated genes were detected as follows: *efaA* 81.25%, *ace* and *gelE* 78.75%, *asa1* 71.25%, *eeP* 68.75%, *cylA* 57.5%, *aggA* 47.5%, *esp* 17.5% and *hyl* 3.75%. Chromosomal DNA fragmentation profiles after restriction with *Sma*I (n=37) demonstrated high genetic diversity among the *E. faecalis* isolates, with a tendency of unique electrophoretic profiles among isolates from each individual bird. The results indicate that *R. magnirostris* circulating in Rio de Janeiro may represent a reservoir of potentially health-threatening microorganisms warranting the need for additional monitoring.

Key words: Roadside hawk, *Enterococcus*, antimicrobial resistance, genotypic characterization

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