

**TITLE:** OCCURRENCE AND DISTRIBUTION OF EPIDEMIOLOGICAL MARKERS AMONG *ENTEROCOCCAL* STRAINS ISOLATED FROM THE INTESTINAL MICROBIOTE OF WILD BIRDS (*ACCIPITRIFORMES*, *CATHARTIFORMES*, *FALCONIFORMES* AND *STRIGIFORMES*) IN RIO DE JANEIRO, BRAZIL

**AUTHORS:** FREITAS, A.A.R.<sup>1</sup>; FARIA, A.R.<sup>2</sup>; MERQUIOR, V.L.C.<sup>1,2</sup>; NEVES, D.M.<sup>3</sup>; PIRES, J.R.<sup>4</sup>; TEIXEIRA, L.M.<sup>1</sup>

<sup>1</sup>UFRJ - Universidade Federal do Rio de Janeiro, Av. Carlos Chagas Filho, Centro de Ciências da Saúde, Instituto de Microbiologia Paulo de Góes, Departamento de Microbiologia Médica, 21941590 - Rio de Janeiro; <sup>2</sup>UERJ - Universidade do Estado Rio de Janeiro, Faculdade de Ciências Médicas, Rio de Janeiro, RJ (Av. 28 de Setembro, 87-Fundos. 3º andar, CEP 20551-030, Rio de Janeiro - RJ, Brazil) <sup>3</sup>CETAS-RJ-Centro de Triagem de Animais Silvestres do Rio de Janeiro, BR 465, Km 3,5 Floresta Nacional Mário Xavier, Seropédica-RJ; <sup>4</sup>CRAS-UNESA – Centro de Reabilitação de Animais Silvestres da Universidade Estácio de Sá, Estrada Boca do Mato, Vargem Pequena, Rio de Janeiro, n.850, CEP: 2278332

Due to their predatory nature, birds of prey may play a role as indicators of environmental contamination, revealing the circulation of important epidemiological markers in nature. The aim of this work was to characterize enterococcal strains obtained from the feces of wild bird. Fecal samples were collected from 113 birds sent to CETAS-RJ (n=40) and CRAS-UNESA (n=73) during 2013. A total of 260 enterococcal strains were recovered from 104 (92.0%) birds and identified as *E. faecalis* 63.8%, *E. hirae* 16.2%, *E. faecium* 11.5%, *E. gallinarum* 5.4%, *E. avium* 1.5%, *E. casseliflavus* 0.8%, *E. raffinosus* 0.4% and *E. cecorum* 0.4%. Antimicrobial susceptibility was evaluated by the disk diffusion method and, in some cases, by determining the MIC. The highest percentages of nonsusceptible strains were related to enrofloxacin 75%, quinupristin/dalfopristin 70.8%, erythromycin 59.6%, rifampin 57.7%, ciprofloxacin 41.9%, norfloxacin 27.7%, nitrofurantoin 21.5% and tetracycline 21.2%, while the lowest percentages of resistance were found for streptomycin 11.9%, chloramphenicol 9.6%, levofloxacin 9.2%, penicillin 3.1%, vancomycin 2.3%, ampicillin 1.5%, gentamicin 1.5% and fosfomicin 0.8%. Multiresistance ( $\geq 3$  classes of antimicrobial) was observed among 75.8% of the strains. The following genetic markers were detected by PCR: *ant(6)-Ia*, *ant(9)-Ia* and *ant(9)-Ib* coding for high-level resistance to streptomycin; *ermA*, *ermB* and *mefA* for erythromycin; *tet(M)* and *tet(L)* to tetracycline; *aph(3')-IIIa*, *aph(2'')-Id* and *aac(6')-aph(2'')-Ia* for aminoglycoside, *vanC* for vancomycin and *vat(D)* for quinupristin/dalfopristin. The genes associated with virulence were: *efaA* 65.4%, *gelE* 63.5%, *ace* 61.5%, *eeP* 56.9%, *asa1* 53.5%, *aggA* 34.2%, *cylA* 33.5%, *esp* 11.9% and *hyl* 1.1%. Analysis of PFGE profiles after restriction with *SmaI* showed the occurrence of some predominant electrophoretic profiles among *E. faecalis* (n=106), *E. hirae* (n=27) and *E. faecium* (n=26). By MLST, eleven STs were obtained for thirteen *E. faecium* strains investigated (ST25, ST56, ST60, ST94, ST104, ST190, ST437, ST666, ST784), including two novel STs (ST1274 and ST1275). A total of 16 STs (ST4, ST47, ST81, ST82, ST116, ST123, ST192, ST287, ST300, ST314, ST330) including five new STs (ST759, ST760, ST761, ST762, ST763) were found among twenty-four *E. faecalis* strains. The results indicate that birds of prey may therefore be strategic targets in surveillance programs for the detection of these high-risk opportunistic pathogens.

**Key words:** Wild birds, *Enterococcus*, phenotypic characterization, genotypic characterization

**Development Agency:** CAPES, CNPq