ANTIMICROBIAL RESISTANCE AND GENETIC DETERMINANTS IN ENTEROBACTERALES ISOLATED FROM ILLEGALLY TRADED REPTILES

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Introduction: Illegal wildlife trade is a major threat to biodiversity. In addition to causing ecological imbalance, illegally traded wild animals may carry and disseminate pathogens of public health concern, including antimicrobial-resistant bacteria, and may also develop infections caused by these agents. **Objectives:** To characterize the phenotypic and genotypic antimicrobial resistance profiles of Enterobacterales isolated from reptile species originating from wildlife trafficking. **Materials and Methods:** Cloacal and oral samples were collected from 34 illegally traded reptiles (16 *Crocodilurus amazonicus*, 6 *Dracaena guianensis*, 5 *Pelodiscus sinensis*, 2 *Iguana iguana*, 2 *Boa constrictor*, 1 *Siphlophis cervinus*, 1 *Platemys platycephala*, and 1 *Podocnemis expansa*) rescued by environmental authorities.. Samples were streaked on MacConkey agar supplemented with ceftriaxone (4.0 µg/mL) and incubated at 36 °C overnight. Lactose-fermenting colonies were identified by MALDI-TOF and stored in 10% glycerol at −20 °C. Antimicrobial susceptibility was evaluated using the broth microdilution method with a panel of 15 antibiotics: β-lactams [amoxicillin/clavulanic acid (2:1), aztreonam, cefoxitin, cefepime, cefotaxime, ceftazidime, meropenem, imipenem, and ertapenem], aminoglycosides (amikacin and gentamicin), quinolones (ciprofloxacin and nalidixic acid), sulfamethoxazole/trimethoprim (19:1), and tetracycline. Resistance genes to β-lactams (bla_{TEM}, bla_{SHV}, bla_{CMY}, bla_{CTX-M} groups 1, 2, 8, and 9), quinolones (*qnrA, qnrB, qnrS, oqxA, oqxB, and qepA*), and aminoglycosides (*aadA, aac(6′)-Ib, aac(3′)-IIa, ant(2″)-Ia*, and *aph(3′)-VI*) were screened by PCR. **Results:** A total of 33 isolates were obtained, including *Enterobacter cloacae* (N=12), *Enterobacter asburiae* (N=9), *Klebsiella pneumoniae* (N=7), *Enterobacter bugandensis* (N=2), *Citrobacter freundii* (N=2), and *Enterobacter kobei* (N=1). High resistance rates were observed for cefotaxime, tetracycline, gentamicin, amoxicillin/clavulanate, ciprofloxacin, trimethoprim-sulfamethoxazole, aztreonam, and ceftazidime (100%, 33/33). Cefepime (96.9%, 32/33) and cefoxitin (93.9%, 31/33) also showed high resistance rates. Chloramphenicol (75.8%, 25/33), amikacin (57.6%, 19/33), and nalidixic acid (48.5%, 16/33) showed moderate resistance. In contrast, meropenem remained highly effective, with 97.0% susceptibility (32/33). All isolates (100%, 33/33) carried *aac(6′)-Ib, aadA,* and *qnrB genes*. A high frequency was also observed for bla_{CTX-M} group 1 (90.9%, 30/33) and *aac(3′)-IIa* (93.9%,

31/33). The *bla*$_{SHV}$ gene was detected in 78.8% (26/33) of isolates, while *qnrS* was present in 48.5% (16/33). The *ant(2″)-Ia* gene was identified in 36.4% (12/33), and *oqxB* in 15.2% (5/33). In contrast, *bla*$_{CMY}$ and *bla*$_{CTX-M}$ group 2 were detected at low frequencies (6.1%, 2/33 each), and *bla*$_{TEM}$ was found in only one isolate (3.0%, 1/33). No isolates carried *bla*$_{CTX-M}$ groups 8 or 9, *qnrA, oqxA*, *qepA,* or *aph(3′)-VI.* **Discussion:** The high frequency of antimicrobial resistance genes in Enterobacterales from illegally traded reptiles likely reflects pressures from poor hygiene, stress, and overcrowding. These conditions may promote multidrug-resistant bacteria and their spread across the human–animal–environment interface. **Conclusion:** Wildlife trafficking represents a significant pathway for the emergence and spread of multidrug-resistant Enterobacterales, reinforcing its relevance as a critical One Health concern.

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