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**Poster Session VI**
**MDR Enterobacteriaceae from animal sources**

# DRUG SENSITIVITY PROFILES AND GENOMIC REP-PCR FINGERPRINTS OF PSEUDOMONAS AERUGINOSA STRAINS FROM ANIMALS ON THE BACKGROUND OF P. AERUGINOSA'S GLOBAL POPULATION STRUCTURE.

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**Objectives:**
Antimicrobial resistance (ABR) is an established worldwide problem. It typically emerges as a phenomenon of highly complex and self-organizing system evolving at the edge of chaos. over-consumption and often inapropriate use of antibiotics play certainly a causative role, but fundamental issues are still not well understood, like ABs role(s) in natural settings. Data of the incidence and prevalence of ABR among animals, domesticated and wild, are also only fragmentary available and not integratively interpreted.
The here reported data could contribute to a better understanding of the antibiotic crisis situation.
**Methods:**
Our batch (N=74) included P. aeruginosa isolates from 50 pets (dog, cat, turtle, parrot), 15 farm animals (cow, sheep, horse, pig, goat), 7 zoo animals (seal, dolphin, kangaroo, tamarind) and 1 free-living sea turtle. The strains were biochemically (Vitek-2, BioMérieux) and genomically identified (PCR for pseudomonad oprI/L lipoproteins) before ABR profiling and serotyping was done. Antibiotics tested were temocillin (TEM), ticarcillin (TIC), ticarcillin+clavulanic acid (TCC), piperacillin+tazobactam (TZP), ceftazidime (CAZ), cefepime (FEP), aztreonam (ATM), imipenem (IPM), meropenem (MEM), amikacin (AN), gentamycin (GM), tobramycin (TM), ciprofloxacin (CIP), tigecycline (TGC), fosfomycin (FOS), colistin (CS) and trimethoprim+sulfamethoxazole (SXT). All strains were genotyped by Rep-PCR (Diversilab, BioMérieux) and compared wih our global P.aeruginosa population structure database (Pirnay et al,PlosOne 2009).All isolates originated from Portugal except the turtle isolate who was sampled in Principe island in the gulf of Guinea.
**Results:**
Seroptypes 1,3,4,6,9,10,11,12,15 were detected while 6 (21%) and 1 (17%) were the most common. Multidrug-resistant P. aeruginosa were isoleted among pets (20%) and farm animals (13%) while none was found among wild animals (zoo and free living).The MDR profiles were TCC/ATM/FOS (7/12), TCC/ATM/CIP/FOS (4/12) and GN/TM/CIP/FOS (1/12). One extensively drug-rresistant (XDR) bacterium, only susceptible to aminoglycosides and colistin and intermediate for cephalosporins was isolated from a dog with infected sugical wound. it was serotyped as 12, a serotype associated with human XDR clonal cluster. resistance levels ranged from ≥95% (temocillin, tygecycline, trimethoprim+sulfamethoxazole) to ≤5% (piperacillin+tazobactam, ceftazidime, cefepime, imipenem, meropenem, amikacin, gentamycin, tobramycin, colistin). Genotyping did not show any animal specific cluster. Isolates were homogeniously scattered in the global P. aeruginosa population structure.
**Conclusions:**
These data show the overall presence of MDR among P. aeruginosa isolates sampled from different, domesticated or not, animals. The genotypic Rep-PCR analysis showed that no specific animal cluster exists and showed a rather homogeniously scattered distribution of these strains among a worldwide collection of P. aeruginosa. Pets showed most MDR and even XDR. We confirmed that most MDRs belonged to the prevalent serotypes previously observed. The limited therapeutic options in human and veterinary medicine to face MDR P. aeruginosa is a major concern.