P1645
Poster Session VI
MDR Enterobacteriaceae from animal sources

ANTIMICROBIAL RESISTANCE AND REP-PCR GENOMIC FINGERPRINTING OF PSEUDOMONAS SP. ISOLATED FROM WILD FREE-LIVING SEA TURTLES IN THE GULF OF GUINEA

D. De Vos[1], J. Santos[2], F. Bilocq[1], P. Soentjens[3], S. Jennes[4], W. Heuninckx[5], A. Leitao[6], R. Seixas[2], M. Oliveira[2], J. Pirnay[1]

[1]Laboratory for Molecular and Cellular Technology, Queen Astrid Military Hospital, Brussels, Belgium ; [2]Laboratório de Bacteriologia da Faculdade de MedicinaVeterinária de Lisboa, Universidade de Lisboa, Lisboa, Portugal ; [3]Queen Astrid Military Hospital Department of Infectiology and Travel Clinic, Queen Astrid Military Hospital, Brussels, Belgium ; [4]Burn Wound Centre, Queen Astrid Military Hospital, Brussels, Belgium ; [5]Clinical microbiology, Queen Astrid Military Hospital, Brussels, Belgium ; [6]Institutode InvestigaçãoCientífica Tropical CVZ Faculdade de MedicinaVeterinária, Universidade de Lisboa, Lisboa, Portugal

Objectives:
Data on the incidence, prevalence and spread of antimicrobial resistance (ABR) among wild animals, worldwide, but specifically from remote tropical areas are still very scarce and inconsistent. The genus Pseudomonas is emerging as a group of increasingly reported opportunistic organisms in human as well as veterinary medicine with high resistance levels. Seen there ubiquity, they could be used as a tool for ABR-surveillance in the environment. Therefore we characterized a batch of pseudomonads isolated from wild, apparently healthy, wild sea tutles on the presence of ABR.
Methods:
Our batch included all gram-negative, oxidase positive bacilli isolated from oral and cloacal swabs of free-living turtles (Eretmochymys imbricata and Cheloniamydas) in Principe isalnd in the gulf of Guinea. The isolates where screened by multiplex-PCR for oprI/oprL pseudomonad specific lipoproteins.The oprI-positives (12) were considered as pseudomonads. One isolte was oprI/oprL positive meaning P. aeruginosa. The isolates were subsequently identified biochemically at species level (Vitek-2, BioMérieux) while ABR profiling was done using the Vitek-2 AST-N237 card (BioMérieux). Antibiotics tested were temocillin (TEM), ticarcillin (TIC), ticarcillin+calvulanic acid (TCC), piperacillin+tazobactam (TZP), ceftazidime (CAZ), cefepime (FEP), aztreonam (ATM), imipenem (IPM), meropenem (MEM), amikacin (AN), gentamycin (GM), tobramycin (TM), ciprofloxacin ((CIP), tigecyclin (TGC), fosfomycin (FOS), colistin (CS), and trimethoprim+sulfamethoxazole (SXT). All Pseudomonas strains were genotyped by Rep-PCR (Diversilab, BioMérieux). Additionally the P. aeruginosa was serotyped in order to compare the strain with isolates from our world population structure collection (Pirnay et al. PlosOne 2009).
Results:
the 13 isolates positive for the presence of oprI were identified as Pseudomonas aeruginosa (N=1, was also oprL+), Pseudomonas mendocina (N=1), Pseudomonas stutzeri (N=6) and Alcaligenes faecalis (N=5). The latter were however not yet further investigated. Concerning ABR-profiles, P. aeruginosa was only resistant to TEM, TGC and SXT, considered natural resistances for this psecies. P. mendocina was resistant to TEM, TIC, ATM, TGC and FOS. P. stutzeri profiles were TEM/FOS (N=3), TEM/TGC/FOS (N=1), TEM/TIC/ATM/FOS (N=1) and TEM/TIC/TCC/ATM/FOS (N=1),. This last was considered as multidrug resistant (MDR). The only P.aeruginosa was serotyped as 6. Genomic fingerprinting did not show any specific clonal-cluster.The P. aeruginosa isolate showed high similarity (≥95%) with other animal as well as human clinical isolates with also similar ABR profile and serotype.
Conclusions:
Monitoring ABR in free-living wild animals should be considered as surveillance tool to help us better describe and understand ABR spread and incidence which will result in better strategies to deal with this worldwide problem. Even in remote locations MDR-bacteria can be found which may represent a risk for human populations in those areas, considering limited health assistance and therapeutic

options. It clearly shows also the worldwide spread of ABR and our deep links with the global environment.