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Poster Session VI
Zoonotic antimicrobial resistance

PLASMID DIVERSITY AMONG ENTEROCOCCUS FAECALIS OF DIFFERENT ORIGINS INCLUDING MIGRATORY BIRDS, FARM ANIMALS AND HUMANS

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Introduction: Strains from birds and insects have a number of physiological differences with those of humans, but might serve as vehicles of antibiotic resistance among different hosts. This work highlight the diversity of mobile genetic elements associated with AbR in *Efs* from different origins.

Methods: *Efs* isolates from wild birds (n=100) attended at two Spanish Veterinarian Centers of Wild Nature Conservation, patients (n=69, 37 blood, 29 feces, 3 other), and other (n=210) were analyzed (2001-2010). Clonal relationship (PFGE/ MLST), and antibiotic susceptibility (CLSI) was established. Plasmid analysis included identification of replication initiation proteins (Rep); relaxases (Rel); and toxin-antitoxin systems (TA). Conjugative transposons (CTns) were identified based on integrases and excisionases.

Results: *Efs* clonal diversity was analyzed in wild birds (8 major PFGE clusters, 75% similarity, diverse STs, mostly singletons) and hospitalized patients (47 PFGE-types, 38 STs of 19 CCs, 9 singletons). Wild birds and humans have differences in tetracycline susceptibility (67% *vs* 58%), chloramphenicol (42% *vs* 17%) erythromycin (28% *vs* 71%), streptomycin (26% *vs* 46%; high-level breakpoint), and gentamicin (5% *vs* 36%). All isolates contain plasmids (1-3 plasmids per cell; 3-155kb). RepA_N pheromone plasmids were identified at similar rates among all isolates (rep9, 70%), which correspond to subgroups rep9A$_{pAD1}$, rep9B$_{pTEF2}$, and rep9C$_{pCF10}$. The rep8$_{pAM373}$ was absent among bird but common among human isolates (23%). Differences in the carriage of Inc18 plasmids (rep1$_{pIP501,}$ 12% vs 17%; and rep2$_{pVEF1/pRE25}$,5% *vs* 20%), and Rep_trans-RCR (rep7$_{pS194\text{-}like,}$ 44% *vs* 0%, rep17$_{pRUM}$, 16% *vs* 0%, rep14/orf1$_{pEFNP1}$; 5% *vs* 0%) were found between birds and humans respectively. While Rep3_small_theta plasmids were identified at similar rates (rep18$_{pEF418}$, 5%; rep18c$_{pCIZ2}$, 2%; rep6$_{pAMα1/pS86}$, 30%). MOB$_C$ (Orf57$_{pAD1}$), MOB$_P$ (*pcfG*$_{pCF10}$/$_{pBEE99,}$ orf5$_{pCIZ2}$, orf29$_{EF62pC}$); and MOB$_V$ (*mobE*$_{pAMα1}$) were found among birds and humans (44%/56%/0%/0%/2% *vs* 65%/36%/4%/3%/20%) respectively. MOB$_Q$ (Orf1$_{pIP501}$, 19%) was only found in hospital. Differences in TA systems, *fst*$_{pAD1}$ (23% vs 78%), ε-ζ$_{Inc18}$ (7% *vs* 0%), were found among birds and humans. All but pheromone-related plasmid sequences were highly homologous (≥99%). CTn*916*-like (Tn*916*, Tn*5801*, Tn*5397*, Tn*6000)* and Tn*3*-Erm^R (Tn*917*, Tn*5398*) elements were detected, the rate of isolates carrying ≥2 CTn being higher in birds than humans (24% *vs* 10%). Virulence genes were found in higher proportions, *gel* (100% vs 84%)*, asa* (84% vs 52%), *esp* (61% vs 55%)*,* and *cyl* (35% vs 20%) in birds than in humans.

Conclusions: Clonal diversity among *Efs* from different origins confirms high levels of recombination and adaptation, probably determining its broad host-range. While ubiquitous presence of pheromone plasmids suggest co-evolution of such elements with the bacterial host, differences in the rate of other plasmid families and AbR genes indicates an intrincate network of both barriers and effective transfer events among *Firmicutes* of animals and humans. The high frequency of putative virulence genes among wild birds is remarkable.