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Poster Session VI

Zoonotic antimicrobial resistance

TEMPORAL AND SPATIAL DISSEMINATION OF TWO MAIN GENOTYPES OF STREPTOCOCCUS DYSGALACTIAE SUBSP. EQUISIMILIS ISOLATES IN BRAZIL AND EVIDENCE FOR ZONOTIC TRANSMISSION

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Group C streptococci (GCS) include different species usually penicillin-susceptible found in both human and animals, as part of their microbiota and as etiological agents of several infections. Besides the already reported tetracycline resistance, many authors have described increased prevalence in antimicrobial resistance to other antimicrobial agents clinically employed, such as clindamycin and erythromycin. The most frequently GCS species isolated from humans is *S. dysgalactiae* subspecies *equisimilis* (SDSE). An increased prevalence of invasive infections caused by microorganisms of this subspecies has been observed in the last years. Thus, it is important to trace the occurrence and spread of possible well-adapted SDSE clones, in order to better understand the epidemiology of these infections. **Objectives.** In this work we have analyzed the antimicrobial profiles and clonal characteristics of 115 SDSE isolates, obtained from human and equines, carries and infections, and different clinical sites. **Methods.** These isolates were collected from different Brazilian cities located in the southeast region. Biochemical tests were used to confirm the species and subspecies. Antimicrobial susceptibility testing was carried out using the disk-diffusion method (to determine resistance rates for clindamycin, erythromycin and tetracycline, and macrolide-lincosamide resistance phenotypes) and the agar-dilution method (to determine minimum inhibitory concentration – MIC – for penicillin and for erythromycin-resistant isolates). In addition, polymerase chain reaction (PCR) was used to detect antimicrobial resistance encoding genes. The genetic diversity of the isolates was analyzed by pulsed-field gel electrophoresis (PFGE). Additionally, multilocus sequence typing (MLST) was performed for the isolates obtained from distinct hosts that displayed the same genotype defined by PFGE. **Results.** All isolates displayed penicillin MIC ranging from 0.0075 mg/L to 0.06 mg/L, confirming that all isolates were penicillin susceptible. As expected, these isolates displayed high tetracycline resistance (66.7%), and this resistance was mainly encoded by the *tetM* gene. PFGE revealed a temporal and spatial dissemination of two main genotypes, A (52.0% of the isolates) and B (23.6%). Two isolates from genotype B₂, each obtained from different hosts (human and equine), were submitted to MLST analyses, and both were allocated in the ST 129. **Conclusions.** These data raise the hypothesis of zoonotic transmission of SDSE isolates between humans and equines, similarly to what occurs for *Streptococcus equi* subspecies *zooepidemicus*. In addition, these results demonstrate the occurrence of clonal expansion among isolates of *S. dysgalactiae* subspecies *equisimilis*.