GENOMIC CHARACTERIZATION OF MULTIDRUG-RESISTANT STAPHYLOCOCCUS EPIDERMIDIS IN A WILD RUFOUS-BELLIED THRUSH

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Introduction: *Staphylococcus epidermidis* is an opportunistic bacteria greatly associated with healthcare associated infections and has increasing relevance in One Health when associated with methicillin resistance profile. **Objectives:** To make the genomic categorization of a multi-drug resistant *S. epidermidis* strain isolated from a fatal skin lesion found on a wild rufous-bellied thrush.**Materials and Methods:** In 2025, a swab sample was collected from a skin lesion found in a rufous-bellied thrush at a wild animal rehabilitation center. The swab was streaked on Blood Agar (5% v/v) and incubated at 37°C overnight. White circular colonies were identified as *Staphylococcus epidermidis* by MALDI-TOF. The MIC was determined for the following antimicrobials: amikacin (AMK), cefoxitin (CFO) , chloramphenicol (CHL), ciprofloxacin (CIP), clindamycin (CLI), gentamicin (GEN), oxacillin (OXA), penicillin (PEN), rifampicin (RIF), sulfamethoxazole-trimethoprim (SXT), tetracycline (TET) and vancomycin (VAN). Whole genomic sequencing was performed using the MiSeq platform, the quality of the reads was assessed by FastQC, and trimming was made using Trimmomatic. Unicycler was used to assemble the draft genome, while annotation was performed later using Prokka. The antimicrobial resistance genes were screened by ABRicate v1.0.1 platform, and bacterial typing tools were used to identify Multi-Locus Sequence Typing. For phylogenomic analysis, a phylogenetic tree was constructed using IQ-TREE to compare the isolate with the 50 closest genomes from the NCBI database. **Results:** The isolate, designated as SL01, was identified as *Staphylococcus epidermidis* belonging to Sequence Type 208 (ST208). The MIC test found that the strain had elevated resistance to beta-lactams, specifically to CFO (MIC = 16 µg/mL), PEN (MIC = 0.5 µg/mL) and OXA (MIC = 1 µg/mL), as well as to aminoglycosides, including AMK and GEN (both MIC = 32 µg/mL). Besides, resistance was observed for CIP (MIC = 8 µg/mL), CHL (MIC = 64 µg/mL), RIF (MIC = 8 µg/mL), and SXT (MIC = 4 µg/mL). The isolate carried genes that conferred resistance to β-lactams (*mecA*; *blaZ*), aminoglycosides (*aadD*; *aac(6´)-aph(2´´)*), fosfomycin (*fosB*), and macrolides (*erm(C)*). Phylogenomic and epidemiological analysis found that the closest genomic resemblance belonged in samples acquired from humans in the United States in 2014, followed by isolates from bovine origin, also from the United States. Most of *S. epidermidis* strains (90,1%; 46/51) were reported in humans, and presented antimicrobial resistance encoding genes for aminoglycosides (70,5%; 36/51), beta-lactams (94,1%; 48/51) and phosphomycin (100%). All studied samples carried the fosfomycin resistance gene

fosA, 46 samples (90,1%; 46/51) were positive for *mecA* and 26 (50,9%;26/51) were positive for *blaZ*. **Discussion:** The fatality of the skin lesion in the wild bird is linked closely to the extensive multi-drug resistant profile of the SL01 isolate. The genomic cluster formed with human and bovine strains from the United States highlights the intercontinental dissemination and ecological plasticity of the ST208 clone. The infection of this bird demonstrates its role as an epidemiological sentinel, serving as an indicator of antimicrobial pollution in urban environments. **Conclusion:** The intercontinental and interspecies dissemination of this lineage underscores the urgent need to incorporate wildlife monitoring into One Health surveillance models.

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