

P1833 Characterization of *ermB*-positive staphylococci isolated in Greece from samples of animal origin

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Background: Macrolides and lincosamides are extensively used in human and veterinary medicine for the treatment of staphylococcal infections. Resistance to these antibiotics is mainly associated with the adenine-N6-methyltransferase-encoding genes, *ermA*, *ermB* and *ermC*. In Greece, however, *ermB*-positive staphylococci are very rare. Here, we describe the characterization of *ermB*-positive staphylococci, isolated from samples of animal origin.

Materials/methods: Macrolides- and lincosamides-resistant staphylococci were recovered from milk samples from ewes, with clinical mastitis, from farms located throughout Greece. Identification to species level and susceptibility testing against various antimicrobial agents was performed by the automated system Vitek 2 (BioMerieux, France). Genes encoding for resistance to macrolides and lincosamides were detected by PCR. All *ermB*-positive isolates were typed by multilocus sequence typing analysis (MLST). Plasmid analysis comprised transfer of the *ermB* to *Escherichia coli* by transformation. Chromosomes and plasmids were sequenced using the Illumina MiSeq platform. Annotation and comparative analysis were performed using software available on the Internet.

Results: One *Staphylococcus aureus* belonged to ST133 (Sau-392Lar,) and one *Staphylococcus lentus* (Sle-091Lar), being positive for *ermB* gene, were identified. Both isolates exhibited resistance to erythromycin (MIC: 256 mg/L) and lincomycin (MIC: 64 mg/L), but were susceptible to the remaining antibiotics. Plasmid analysis and de novo assembly indicated that, in Sau-392Lar, *ermB* was carried by a 7770-bp plasmid (pSau-392Lar), which was highly similar (94% coverage, 98% identity) to the *ermB*-positive plasmid pAFS11 from ST398 *S. aureus* isolates (GenBank accession no. FN806789). Additionally, in Sle-091lar, *ermB* was part of the transposon Tn917, which was originally described from *Streptococcus faecalis* DS16 (GenBank accession no. M11180), integrated into the *S. lentus* chromosome.

Conclusions: This study reported the presence of *ermB*, associated with different mobile elements, in *S. aureus* and *S. lentus* isolates, emphasizing the diversity of mobile elements that can be implicated in the dissemination of resistance determinants in staphylococci.