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Programme

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[P292] COMPLETE SEQUENCES OF TWO *Staphylococcus aureus* PLASMIDS CARRYING GENES FOR RESISTANCE TO ANTIBIOTICS, HEAVY METALS, BIOCIDES AND/OR VIRULENCE

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Aim: To gain detailed insight into the genetic organization of two multidrug resistance plasmids, pSM31 and pSM39, from clinical *S. aureus* isolates collected in a hospital in Lisbon, Portugal, and to identify factors that may explain their selection and persistence.

Methods: Plasmid pSM31 was sequenced by Sanger sequencing using cloning and primer walking whereas pSM39 was sequenced by next generation sequencing. Sequence analysis was carried out using the BlastN and BlastP programs and the ORF Finder software from NCBI.

Results: The two plasmids fully characterized in this work were non-conjugative multiresistance plasmids. pSM31 (27,424 bp) is closely related to the family of globally dispersed plasmids from the pGSA23 group harbouring determinants for resistance to β-lactams and cadmium as well several enterotoxin genes. pSM39 (26,036 bp) is a newly described member of the pGSA11 group that carries genes conferring resistance to β-lactams, biocides, cadmium, zinc and mercury and comprises a region that may have been acquired by recombination with a *S. epidermidis* plasmid.

Conclusions: The sequence analysis of these two plasmids confirmed their involvement in antimicrobial resistance among *S. aureus* strains isolated from a clinical setting. It also provided genetic evidence for the potential risk of co-selection of antibiotic resistance genes and/or virulence genes by selective pressure of antibiotics, biocides and/or heavy metals.