

## **Prevalence of Macrolide Resistance Genes in Staphylococcus aureus (SAU) Clinical Isolates from Argentina**

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**Background and aims:** The most frequent macrolide-resistant phenotypes are MLS<sub>B</sub>(methylase) constitutive(c) and inducible(i) mediated by erm genes, and MS<sub>B</sub> (efflux) by msrA. Recently emerged in our country the L phenotype mediated by lnuA gene in SAU (erythromycin(ERY)/clindamycin(CLI) susceptible and lincomycin(LIN) resistant). The aim was to determine the national prevalence of macrolide resistance genes and clonality in SAU isolates.

**Methods:** 631 SAU were collected in 60 hosp from 23 provinces in April 2006. By triple-disc diffusion assay (ERY,CLI,LIN) 242(38%) resulted macrolide-resistant and were further studied by PCR for ermA, ermC, msrA and lnuA genes. MICs were performed by agar dilution (CLSI). SCCmec type was determined by multiplex PCR, and molecular typing by SmaI PFGE and MLST.

**Results:** The genes detected were (%): ermA(76.9), ermC(15.6), ermA+ermC(0.8), msrA(2.5), lnuA(1.3), ermC+lnuA(1.6). Three strains were negative for the 4 genes. Five phenotypes were observed: 74.4% cMLS<sub>B</sub> (170 ermA, 3 ermC, 2 ermC+lnuA, 2 ermA+ermC, and 3 were negative); 21.1% iMLS<sub>B</sub> (35 ermC, 16 ermA); 2.5% MS<sub>B</sub> phenotype (6 msrA), 1.2% L (3 lnuA) and 0.8% iMLS<sub>B</sub>+L (2 ermC + lnuA). Methicillin resistance was more frequent in ermA (93%) than in other genotypes. PFGE was performed to 107 isolates which represent all genotypes (76 ermA, 17 ermC, 2 ermA+ermC, 6 msrA, 3 lnuA, 3 ermC+lnuA). 76.5% of the strains with ermA belonged to the dominant Cordobes/Chilean clone ST5-SCCmecI, resistant to oxacillin(100%), gentamicin(93%) and ciprofloxacin(98%) and susceptible to thrimethoprim/sulfamethoxazole and rifampicin. Among the 31 isolates with ermC, msrA and lnuA or combination of these, 24 clonal types were detected.

**Conclusion:** 1) ermA was the prevalent genotype and it was related with the hospital associated Cordobes/Chilean dominant clone: ST5-SCCmecI 2) ermC, msrA and lnuA genes were less prevalent and showed genetic diversity