

# PREVALENCE OF MACROLIDE RESISTANCE GENES IN *Staphylococcus aureus* (SAU) CLINICAL ISOLATES FROM ARGENTINA



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## BACKGROUND

The most frequent macrolide-resistant phenotypes are MLS<sub>S</sub> (methylase) constitutive (c) and inducible (i) mediated by *erm* genes, and MS<sub>S</sub> (efflux) by *msrA*. Recently emerged in SAU from our country the L phenotype (mediated by lincosamide nucleotidyltransferases) encoded by *InuA* gene, erythromycin and lincomycin

## OBJECTIVE

TO DETERMINE THE NATIONAL PREVALENCE OF MACROLIDE RESISTANCE GENES AND CLONALITY IN SAU ISOLATES.

## RESULTS

1. RELATION BETWEEN PHENOTYPE AND GENOTYPE 60 hospitals from 23 provinces and Buenos Aires city.

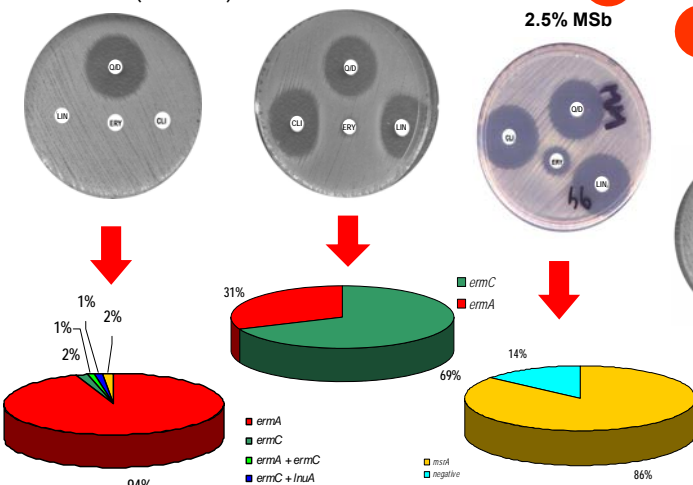
By triple-disc diffusion assay (CLI, ERY, LIN) 242 (38%) isolates were macrolide-resistant.

## MATERIALS AND METHODS

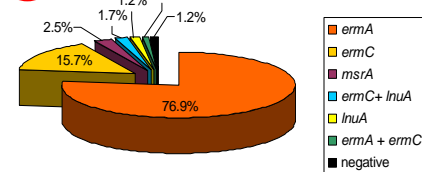
242 isolates were further studied by PCR for *ermA*, *ermC*, *msrA* and *InuA* genes. 200/242 were methicillin resistant (MRSA).

MICs were performed by agar dilution (CLSI). Molecular typing by *Sma*I PFGE, was performed to 107 representative of all genotypes (76 *ermA*, 17 *ermA* + *ermC*, 6 *msrA*, 3 *InuA*, + *InuA*).

PVL determined by PCR, SCCmec type by multiplex PCR and MLST was performed to one isolate of the

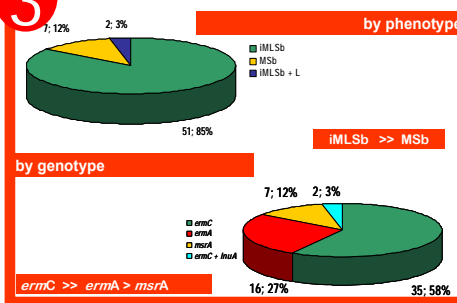


## 2 GENOTYPES OF MACROLIDES RESISTANCE

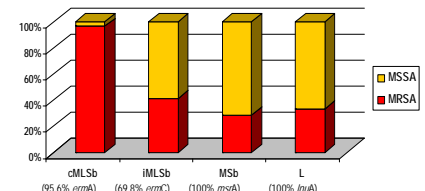


*ermA* 76.9% (n: 186), *ermC* 15.7% (n: 38), *msrA* 2.5% (n: 6), *ermC* + *InuA* 1.7% (n: 4), *InuA* 1.2% (n: 3), *ermA* + *ermC* 0.8% (n: 2) and negative 1.2% (n:3)

## 3 ERY R and CLI S PHENOTYPE

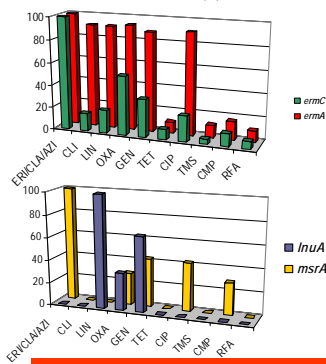


## 4 METHICILLIN RESISTANCE BY PHENOTYPE / GENOTYPE

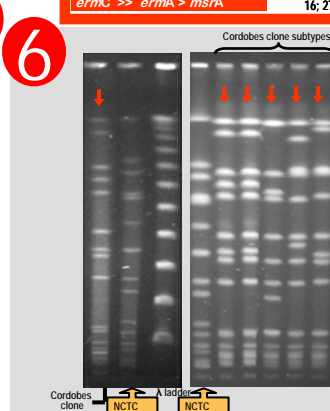


cMLSb >>> % MRSA iMLSb >>> % MSSA  
Methicillin resistance was more frequent in *ermA* isolates (93%) than in other genotypes.

## 5 ANTIMICROBIAL RESISTANCE (R) BY GENOTYPE



R OXA, GEN and CIP >> *ermA* isolates



## 6 CLONAL DIVERSITY BY GENOTYPE

**ermA**  
**Sma**I PFGE  
• PFGE was performed to 76/186 *ermA* isolates and 16 clonal types were identified.  
• 76.5% of them belonged to the dominant Cordobes clone (red arrows), R to OXA (100%), GEN (93%) and CIP (98%) and susceptible to SXT and RFA.  
• This clone was confirmed as: ST5-SCCmecI and PVL(-)

## 7 ermC, msrA, InuA

Among the 31 isolates with *ermC*, *msrA* and *InuA* or combination of these, 13 different clonal types were detected.

Genotype	Nro. total	Nro. isolates PFGE	Nro. of clonal types
<i>ermC</i>	38	17	10
<i>msrA</i>	6	6	3
<i>InuA</i>	3	3	2
<i>ermC</i> + <i>InuA</i>	4	3	2
<i>ermA</i> + <i>ermC</i>	2	2	1

## CONCLUDING REMARKS

- In Argentina macrolide resistance in SAU is 38%. There were association between phenotypes and genotypes: cMLS<sub>S</sub>/*ermA*, iMLS<sub>S</sub>/*ermC*, MS<sub>S</sub>/*msrA*, L/*InuA* and iMLS<sub>S</sub>+L/*ermC*+*InuA*.
- The most prevalent genes were *erm*: *ermA* 76.5% and *ermC* 15.6%.
- ERY R and CLI S phenotype was mainly associated with iMLS<sub>S</sub> and *ermC* genes.
- cMLS<sub>S</sub> phenotype was associated principally with MRSA and iMLS<sub>S</sub> with MSSA.
- Strains carrying *ermA* gene were more resistant to OXA, GEN
- According to *Sma*I PFGE restriction pattern and antibiotic resistance profile, most (76.5%) of the isolates carrying *ermA* gene belong to Cordobes clone.
- In contrast, strains carrying *ermC*, *msrA* and *InuA* genes were less prevalent and highly diverse.
- This is the first study to address the prevalence of macrolide resistance in SAU from Argentina. It showed that macrolide resistance was principally associated with the epidemic hospital acquired MRSA Cordobes clone: *ermA* - ST5 - SCCmecI - PVL(-), resistant to GEN and CIP, and susceptible to SXT and RFA.