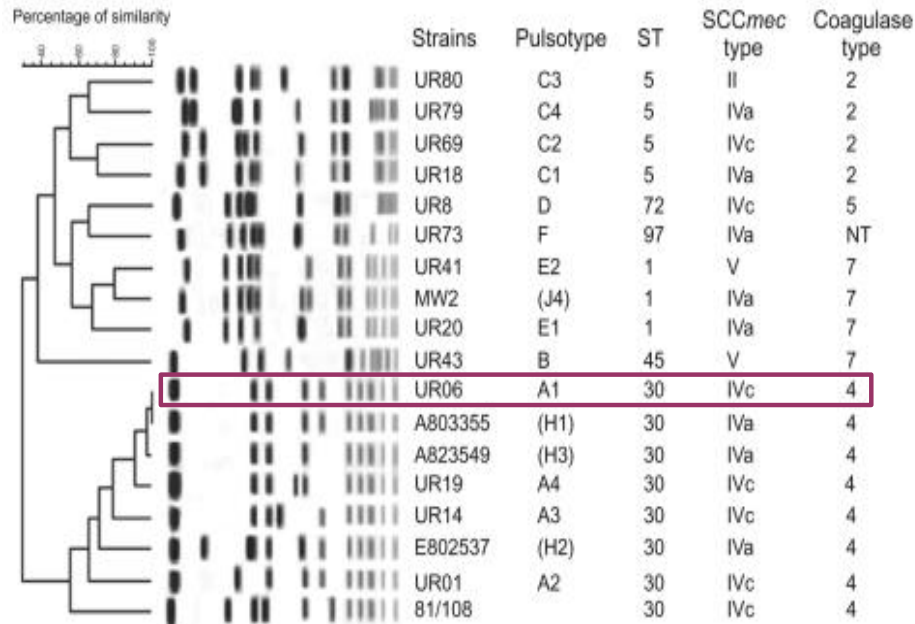


# StaphNET South America: Establishing a network for genomic surveillance of *Staphylococcus aureus* in South America. Buenos Aires, 2018.



The outbreak of CA-MRSA that occurred in Uruguay between 2002 and 2003 involved >1,000 patients

Boils and abscesses were the most prevalent infections (85%), followed by hidradenitis and cellulitis.

Clone represented by UR 06 (Uruguay clones) was considered to have been the cause of this outbreak.

# StaphNET South America: Establishing a network for genomic surveillance of *Staphylococcus aureus* in South America. Buenos Aires, 2018.

Between 2004-2005 we studied 90 MRSA isolates recovered from adults from different areas of the country.

On each isolate we study:

Alpha-hemolysin

$\beta$ -hemolysin

CP typing

The presence of *cna*, *mecA* and *lukS-lukF* genes was determined by PCR

SCC*mec* typing was done on only 23 isolates

*Sma*I-PFGE

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TABLE 1: Phenotypic and genotypic characteristics of CA-MRSA isolates recovered in Uruguay between 2004-2005. CP, capsular polysaccharide; iMLS<sub>B</sub>, inducible macrolide-lincosamide-streptogramin B resistance; PVL, Panton-Valentine leukocidin.

Group	PFGE type	CP	iMLS <sub>B</sub> Phenotype	PVL	Number of strains
1	A	8	–	+	62 <sup>(a),(b)</sup>
2	A, A1, A2	8	+	+	19
3	A3	8	–	–	1
4	B	8	+	+	4 <sup>(c)</sup>
5	C	8	–	+	1
6	D	8	–	+	1
7	E	NT	+	–	1 <sup>(d)</sup>
8	F	5	–	–	1
Total					90

<sup>(a)</sup>Fifty-nine isolates showed positive result by colony immunoblot method with CP8 antibody and 3 strains showed positive result by PCR for the *cp8* gene.

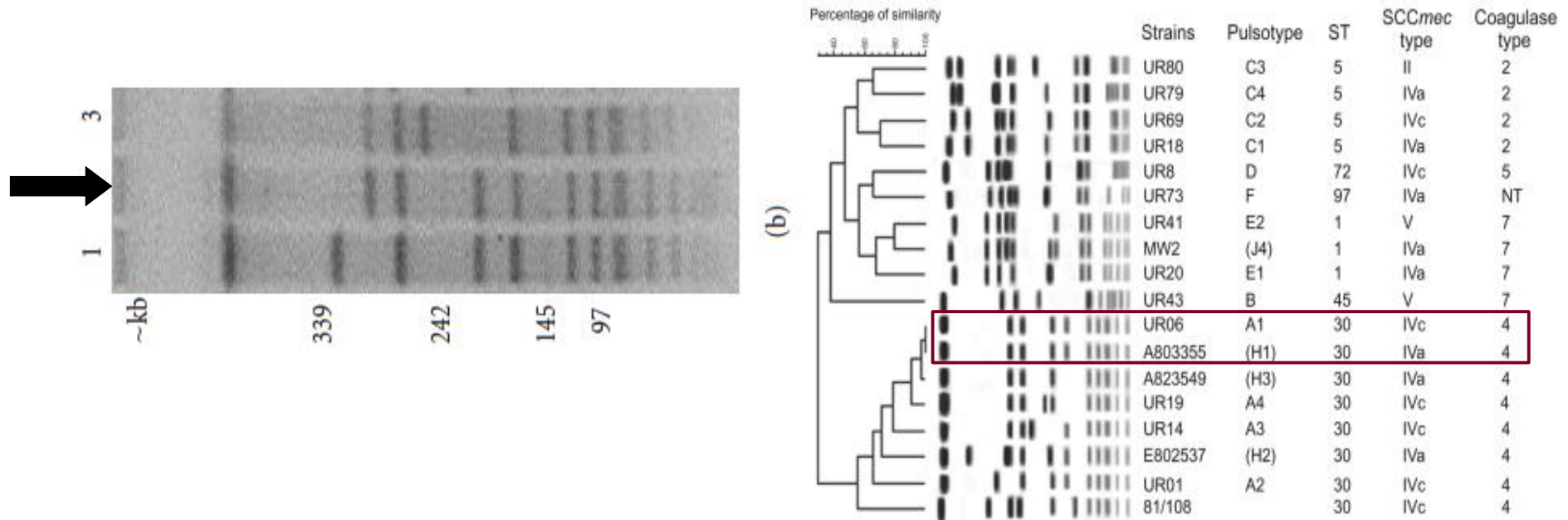
<sup>(b)</sup>Twenty-three strains showed SCC*mec* type-IV. <sup>(c)</sup>All strains in this group showed SCC*mec* type-II. <sup>(d)</sup>Positive PCR amplification for the *cp8* gene.

The *mecA* gene was detected in the 90 MRSA strains. Nevertheless, 3 out of the 90 strains displayed oxacillin inhibition zone diameters  $\geq 13$  mm (OS-MRSA??)

# StaphNET South America: Establishing a network for genomic surveillance of *Staphylococcus aureus* in South America. Buenos Aires, 2018.

Isolates of pulsotype A exhibited a band pattern identical to those isolates identified previously by Ma et al. being the most frequently found in Uruguay (UR 06 and ST30) during the 2002-2003 period.

Visually, the pulsotype A band pattern closely resembles to a community-associated MRSA clone reported in the South West Pacific region. (USA 1100)



## StaphNET South America: Establishing a network for genomic surveillance of *Staphylococcus aureus* in South America. Buenos Aires, 2018.

In summary, three years after of the first finding of CA-MRSA isolates in Uruguay these strains are still producing SSTI. We identified two major groups of CA-MRSA strains (1 and 2) defined according to phenotypic and genotypic characteristics. The most prevalent group, **G1**, showed a *Sma*I- PFGE pattern identical to CA-MRSA strains previously isolated in Uruguay and Brazil corresponding with (USA 1100).

## StaphNET South America: Establishing a network for genomic surveillance of *Staphylococcus aureus* in South America. Buenos Aires, 2018.

Between 2004-2005 we studied 125 *S. aureus* isolates recovered from 125 children  $\leq 15$  years who sought medical attention at the HP-CHPR (28d-15y).

89 were recovered from invasive infections (e.g., bone, blood, cerebrospinal, pleural, and synovial samples).

36 MRSA isolates were recovered from children with superficial infections.

# StaphNET South America: Establishing a network for genomic surveillance of *Staphylococcus aureus* in South America. Buenos Aires, 2018.

Pardo *et al.* – CA-MRSA infections in Uruguayan children

*J Infect Dev Ctries* 2013; 7(1):010-016.

**Table 2.** Microbiological characteristics of 125 *S. aureus* isolates recovered from children with invasive and superficial infections treated at the HP-CHPR between 2003 and 2006

Genotypic or phenotypic characteristic	CA-MRSA		HA-MRSA	MSSA
	Invasive (n=65) Nº. (%) of isolates with positive result to:	Superficial (n=36) Nº. (%) of isolates with positive result to:	Invasive (n=3) Nº. of isolates with positive result to:	Invasive (n=21) Nº. (%) of isolates with positive result to:
<i>LukS-F</i> genes	57 (87.6)	30 (83.3)	0	6 (28.5)
<i>cna</i> gene	55 (84.6)	29 (80.5)	1	3 (14.2)
SCCmec cassette type IV	65 (100)	36 (100)	0 <sup>a</sup>	NA <sup>b</sup>
Pulsotype A (USA1100)	52 (80)	29 (80.5)	0	4 (19)
iMLS <sub>B</sub> phenotype	29 (44.6)	11 (30.5)	0	0 (0)
TMP-SMX susceptibility	65 (100)	36 (100)	1	21 (100)

<sup>a</sup> One isolate carried SCCmec cassette type I and the other two isolates carried SCCmec cassette type III; <sup>b</sup> Not applicable

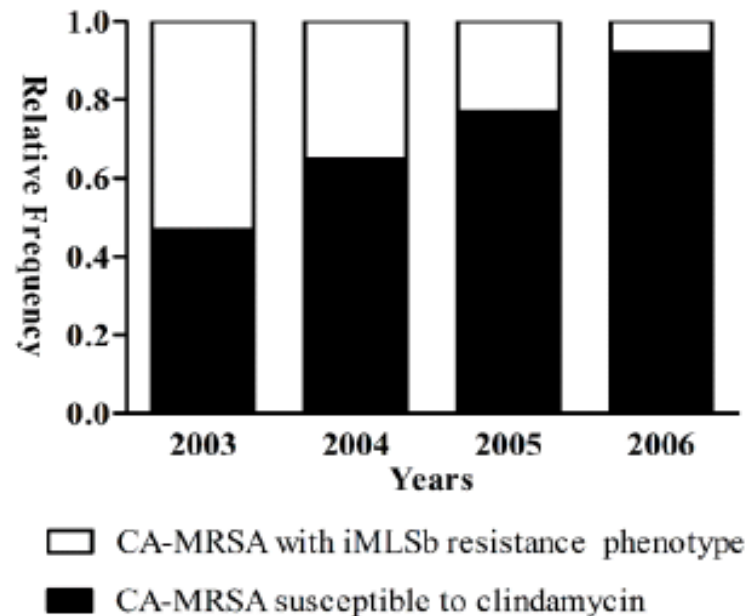
Two CA-MRSA isolates analyzed by MLST belonged to ST30.

One HA-MRSA isolate was susceptible to TMP-SMX, carried SCCmec type I, and visually its PFGE profile closely resembled the previously described MRSA “Cordobés clone”.

## StaphNET South America: Establishing a network for genomic surveillance of *Staphylococcus aureus* in South America. Buenos Aires, 2018.

In this study 40 out of 101 CA-MRSA isolates showed the iMLSB phenotype. However, the prevalence of the iMLSB phenotype decreased over time despite the increased use of clindamycin during the study period in the HP-CHPR.

**Figure 2.** Evolution of the iMLSB phenotype in CA-MRSA isolates recovered from children treated at the HP-CHPR between 2003 and 2006



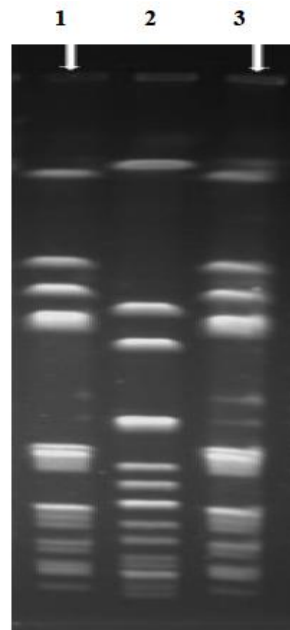


# StaphNET South America: Establishing a network for genomic surveillance of *Staphylococcus aureus* in South America. Buenos Aires, 2018.

## Case

From a girl with joint infection, 2 bacterial isolates were obtained, one from the joint fluid and another from blood. Both were identified as *S. aureus* and classified one as methicillin-sensitive [MSSA] (joint) and the other as methicillin-resistant [MRSA] (blood culture) using the VITEK 2® 7.01 version. Both showed inhibition halos for OXA > 15 mm and for FOX of 19 and 17 mm, respectively. The presence of the *mecA* gene was demonstrated by PCR in 2 isolates and both carried the SCC*mec* type V. Both isolates showed identical profiles by *Sma*I-PFGE.

This report describes the detection of an OS-MRSA culture in Uruguay and highlights the limitations of some laboratory procedures to correctly identify resistance phenotypes associated with the *mecA* gene in clinical isolates of *S. aureus*.



# StaphNET South America: Establishing a network for genomic surveillance of *Staphylococcus aureus* in South America. Buenos Aires, 2018.

One-hundred non-duplicates *S. aureus* isolates obtained from July 2012 to December 2013 were collected from distinct clinical samples. The antibiotic resistance profile was determined and the presence of resistance genes was detected using PCR.

**Table 1.** Distribution of  $MLS_B$  phenotypes in all *S. aureus* isolates analyzed using the D-zone test.

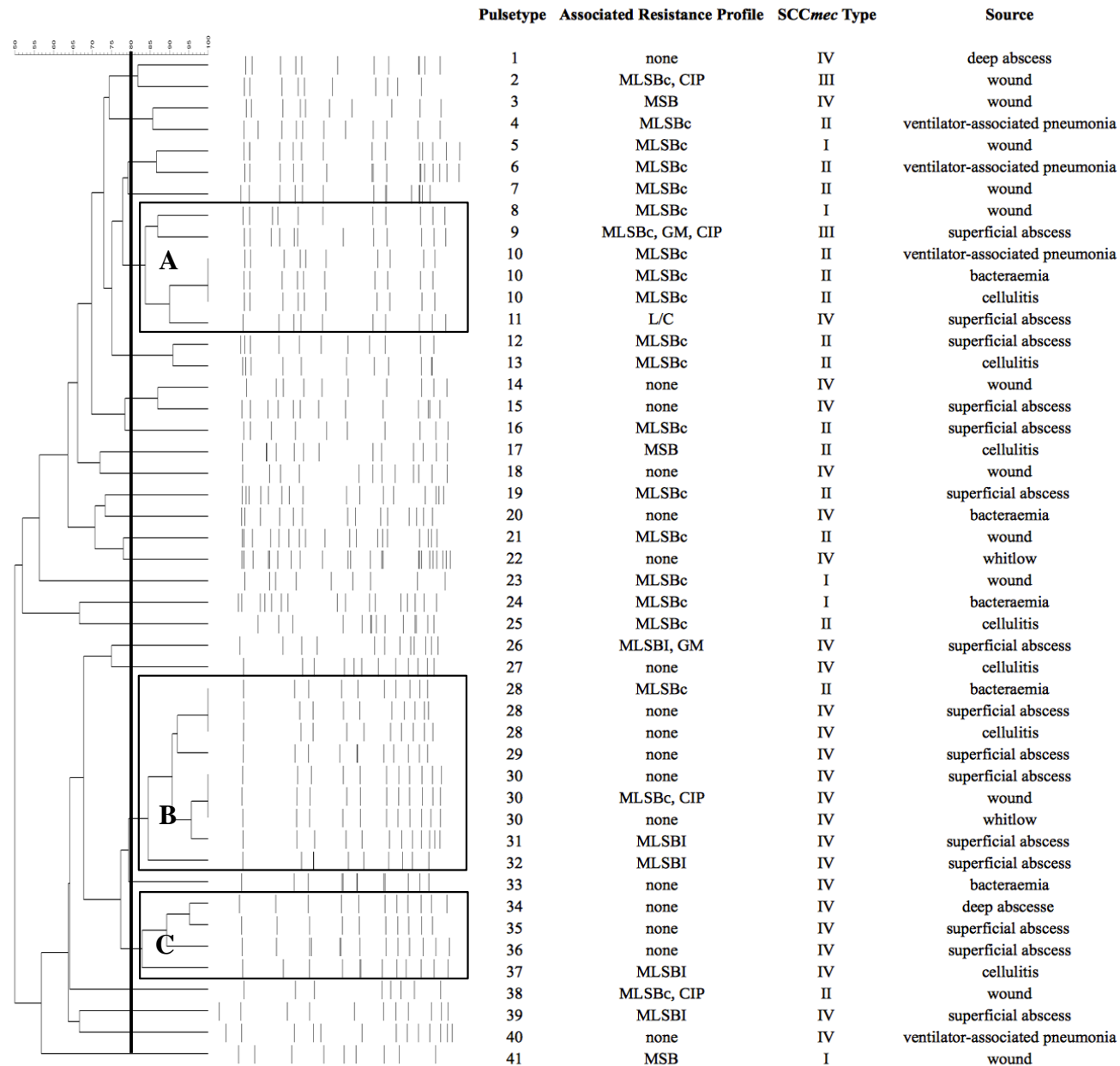
	$MLS_B$ phenotype in disk D-zone test					Total
	$MLS_{B\ i}$ (n)	$MLS_{B\ c}$ (n)	$MS_B$ (n)	LC (n)	S (n)	
MSSA	5	1	2	0	45	53
CA-MRSA	5	1	1	1	17	25
HA-MRSA	0	20	2	0	0	22
Total (%)	10 (10%)	22 (22%)	5 (5%)	1 (1%)	62 (62%)	100

# StaphNET South America: Establishing a network for genomic surveillance of *Staphylococcus aureus* in South America. Buenos Aires, 2018.

**Table 2.** SCC*mec* type, MIC<sub>100</sub> to oxacillin, vancomycin and teicoplanin found in the analyzed MRSA isolates.

		MRSA isolates					
		MIC <sub>100</sub> in µg/ml to:		MLSB resistance phenotype in D-Test			
SCC <i>mec</i> type	N° of studied isolates/N° with MLSB resistance	Oxacillin	Vanco/Teico	MLSBi	MLSBc	MS	L/C
I	5/5	256	1/1	---	4	1	--
II	15/15	64	1/1	---	14	1	--
III	2/2	16	1/1	---	2	---	---
IV	25/8	32	1/1	5	1	1	1
Total	47/30	-		5	21	3	1

# StaphNET South America: Establishing a network for genomic surveillance of *Staphylococcus aureus* in South America. Buenos Aires, 2018.



N=47

# StaphNET South America: Establishing a network for genomic surveillance of *Staphylococcus aureus* in South America. Buenos Aires, 2018.




## MLST results

Adults, n=15 isolates, 2011-2013

ST (n° of isolates)	SCCmec	Antibiotype	Grupo
5 (3)	I II II	OX CIP cMLSb OX CIP GN cMLSb OX CIP GN cMLSb	1
8 (2)	I MSSA	OX CIP cMLSb	1
868	III	OX CIP cMLSb	1
72	IV	OX iMLSb	1
15	MSSA	iMLSb	1
83	MSSA	GN	1
2770*	I	OX cMLSb CIP	1
1279	MSSA	-	1
30 (2)	IV MSSA	OX iMLSb iMLSb	2
508 (2)	II MSSA	OX GN iMLSb	3

NY-J and SWP clones were also recovered from children

ST 8 in Brasil, MSSA  
ST 72 in Brasil, IV, MRSA  
ST 508 MSSA in Brasil

 Cordobés Clone
  NY-Japón Clone
  EMRSA 7 Clone
   
 UR6/SWP Clone

## StaphNET South America: Establishing a network for genomic surveillance of *Staphylococcus aureus* in South America. Buenos Aires, 2018.

We study 66 butcher shops from Montevideo city between December 2012 and June 2013.

We take samples of four types of surfaces that are in contact with the meat products and the hands of the manipulators: work tables, tables, knife handles and mincer.

In 65% (n=44) butcher shops we demonstrate the presence of *S. aureus*. The most frequently contaminated surfaces were tables, mincers and knives handles.

In the 9.24% of the butcher shops we recovered *S. aureus* strains carrying the gen *mecA*.

StaphNET South America: Establishing a network for genomic surveillance of *Staphylococcus aureus* in South America. Buenos Aires, 2018.

Work team:

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**Thank you very much for your attention and apologies for destroying the English language**

