

High frequency of Panton-Valentine leukocidin genes in invasive methicillin-susceptible *Staphylococcus aureus* strains and the relationship with methicillin-resistant *Staphylococcus aureus* in Córdoba, Argentina

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RESUMEN

In the study presented here, the genetic characteristics of methicillin-susceptible *Staphylococcus aureus* (MSSA) strains isolated from patients attending hospitals in the city of Córdoba, Argentina, during 1999-2002 were evaluated to determine their genetic relationship with methicillin-resistant *S. aureus* (MRSA) clones as part of an effort to control the potential emergence of new epidemic MRSA strains. The results showed there is a high frequency of MSSA strains carrying Panton-Valentine leukocidin genes in invasive infections in Córdoba, Argentina, particularly in those occurring in hospital settings. Panton-Valentine leukocidin genes were found in the genomic background of one clone (ST30-N pulsotype) belonging to a successful internationally distributed MSSA lineage (clonal complex 30), which is closely related to the EMRSA-16 pandemic clone. These genes were also detected in the ancestral clone (ST5-M pulsotype) of the most prevalent MRSA epidemic clone causing healthcare-associated infections in this region, known as the Cordobes/Chilean clone. The molecular characterization of circulating MSSA strains, including the detection of Panton-Valentine leukocidin genes, is thus a useful marker for investigating the evolving epidemiology of hospital- and community-acquired MRSA clones.

TIPO DE DOCUMENTO:

Artículo

DOI:

<https://doi.org/10.1007/s10096-007-0278-4>

PALABRAS CLAVE:

Panton Valentine leukocidin.

TEMAS:

R Medicina > R Medicina (General)

UNIDAD ACADÉMICA:

[Universidad Católica de Córdoba > Facultad de Ciencias de la Salud](#)