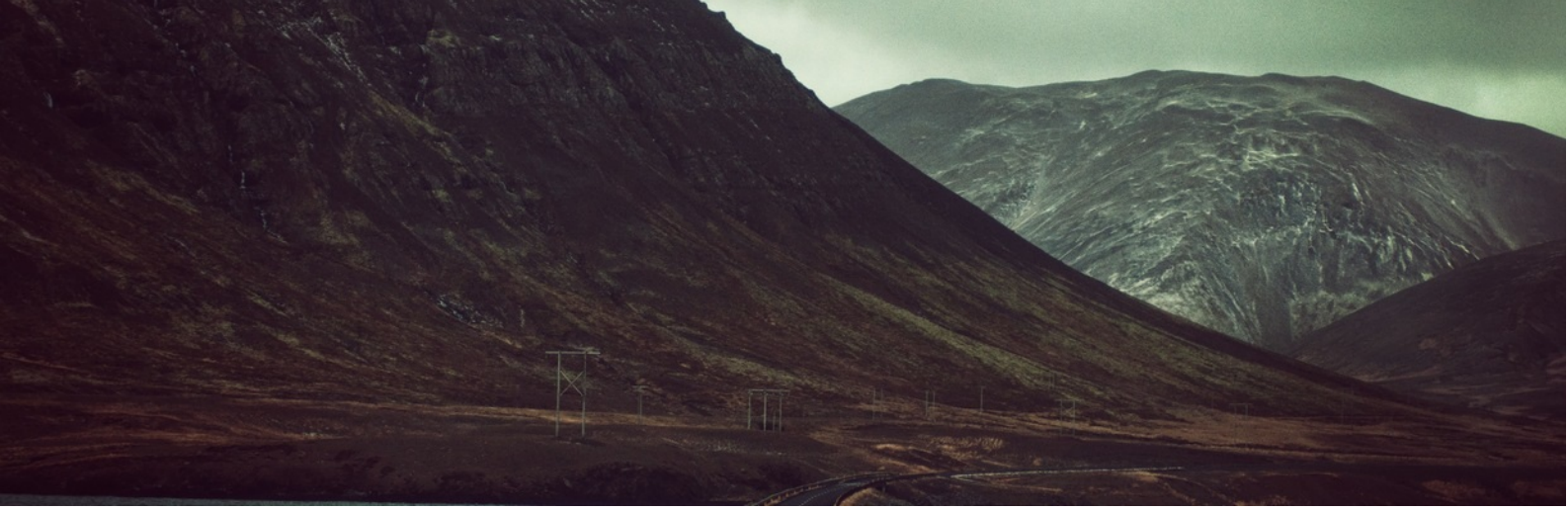

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Authors: Marta Mollerach
Submitted: 27. April 2015
Published: 4. May 2015
Volume: 2
Issue: 3
Keywords: CA-MRSA, methicillin-resistance, Staphylococcus aureus, infection, multicenter studies
DOI: 10.17160/josha.2.3.33

Current trends in Community-acquired methicillin-resistant *Staphylococcus aureus* in Argentina

Dr. Marta Mollerach,
University of Buenos Aires
Adjunct Professor of Microbiology
Department of Microbiology, Immunology and Biotechnology
School of Pharmacy and Biochemistry
E-Mail: mmollera@ffyb.uba.ar

Community-acquired methicillin-resistant *Staphylococcus aureus* (CA-MRSA) infections have become a major concern worldwide. Different from hospital-acquired MRSA, CA-MRSA usually is staphylococcal cassette chromosome (SCCmec) type IV, carries genes for Panton-Valentine leukocidin (PVL) and is susceptible to several non ß-lactam antibiotics. The epidemic of CA-MRSA is evolving. A specific clone that is initially propagating and causing CA-MRSA infections can be displaced by a more successful one. In Argentina, previous studies have identified sequence type 5 (ST5), SCCmec IV, spa type 311 as the predominant CA-MRSA clone causing infections and colonizing children.

We conducted two prospective observational multicenter studies in adolescent and adult patients in Argentina. The specific aims were: a) to evaluate clinical features and genotype of strains in **invasive CA-MRSA** infections (Invasive CA-MRSA study), b) to establish the prevalence, clinical and molecular characteristics of CA-MRSA in patients with **skin and skin structure infections** (SSSI study).

A total of 55 patients with invasive CA-MRSA infections were included. Most patients (60%) had bloodstream infections, 42% required admission to intensive care unit and 16% died. No CA-MRSA isolates were multiresistant (resistant ≥3 classes of antibiotics). All isolates carried PVL genes and SCCmec type IV. The majority CA-MRSA strains belonged to ST30 and had identical pulsed-field gel electrophoresis (PFGE) patterns, qualifying as clone dissemination of a highly transmissible strain.

The SSSI study of CA-MRSA provided several findings. Firstly, CA-MRSA has become the most common cause of skin and soft tissue infections in our patient without healthcare contact. From the total of 311 patients enrolled with SSSI 70% had CA-MRSA. The occurrence of CA-MRSA as the predominant pathogen prompted an urgent change in the empirical therapy used to treat our community patients with SSSI. In addition, results from this study encouraged physicians to obtain cultures in patients with SSSI, most importantly in those areas where the prevalence of CA-MRSA or its antibiotic susceptibility was unknown. Second, SSSI caused by CA-MRSA have some characteristics that can be easily detected at the initial clinical evaluation. In our community population CA-MRSA is more common in patients < 50 years old and presenting with purulent lesion such as abscesses or furuncles. Third, consistent with the finding of ST-30 SCCmec IV, PVL+ spa t019 among patients with invasive CA-MRSA infections in Argentina, we revealed the predominance of the same clone among our patients suffering SSSI from the community. This clone which was previously considered as an uncommon

clone in Argentina appears to have displaced the previously predominant clone (ST5, SCCmec IV, PVL+).

In a posterior analysis, we observed a significant association between the presence of CA-MRSA ST30 clone and the occurrence of invasive disease. This observation led us to hypothesize that ST30-SCC*mec*IVc-*spa*t019 clone could be more virulent than the previous predominant clone (ST5-SCC*mec*IVa-t311), perhaps due to an enhanced ability to survive in the infection site or a better capacity of dissemination. To investigate the apparent enhanced clinical virulence of the new predominant clone we conducted three animal models of infection and molecular characterization of virulence factors.