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Changing Epidemiology of MRSA Clones in Argentina: Community Associated MRSA Strains as Main Responsible of Hospital Onset Infections

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Background: The emergence of community-associated (CA) methicillin-resistant *Staphylococcus aureus* (MRSA) has transformed the epidemiology of MRSA over the last 15 years. In Argentina, the spread of the CA-ST5-IV and CA-ST30-IV clones in the community and, hospital-associated (HA)-ST5-I in the hospital setting has been reported. We aimed to investigate the molecular epidemiology of MRSA infections in both community and hospital setting in Argentina.

Materials/methods: Consecutive *S.aureus* clinical isolates were collected during May-2015 from 61 hospitals in 21 Argentinian provinces and BA city and subjected to antimicrobial susceptibility testing. Healthcare-onset (HO)/community-onset (CO) infections were defined when MRSA was obtained after/before 48 hours of hospitalization. MRSA strains were genetically typed as CA-MRSA and HA-MRSA by SCCmec, spa-typing, PVL, PFGE and MLST.

Results: A total of 668 *S.aureus* were collected; 471 (70%) were from CO infections and 341 (51%) were MRSA (45.2% CA- and 5.8% HA-). Of all patients, 251 were children (<19 years) (38%) and 394 were female (59%). MRSA percentages were higher in pediatric (59%) than adult patients (46.3%), $p=0.0015$. The proportion of MRSA differed from Northern (72.9%) to Centre (48.4%) and Southern (25.6%) regions of Argentina ($p<0.0001$). In contrast, no differences were found in the MRSA proportion among CO- (50.7%) and HO- (51.8%) infections. Among MRSA infections, 159 (47%) were invasive and 176 (52%) were non-complicated skin and soft-tissue infections. CO-MRSA infections were mainly associated to CA-ST30-SCCmecIVc-t019-PVL+ (South-West Pacific) (72%), CA-ST5-SCCmecIVa-t311-PVL+(12.6%) and CA-ST8-SCCmecIVc-t008-PVL+-ACME⁻ (USA300-LA, Latin-American variant) (4.6%). In the other side, HO-MRSA infections were mainly associated with CA-ST30-SCCmecIVc-t019-PVL+(40.2%), HA-ST5-SCCmecI-t149 (Cordobes/Chilean) (17.6%), CA-ST5-SCCmecIVa-t311-PVL+(15.7%), HA-ST100-SCCmecIVNv-t002-PVL⁻ (Pediatric) (7.8%), CA-ST97-SCCmecIVa (Livestock-Associated) (7.8%) and CA-ST8-SCCmecIVc-t008-PVL+-ACME⁻ (6.9%) clones.

Conclusions: The epidemiology of MRSA is continuously changing in Argentina, particularly due to the spread of CA-ST30-IV and CA-ST5-IV clones. CA-MRSA clones are responsible of the 95% of the CO- and 75% of HO-MRSA infections. The replace of HA- by CA-MRSA clones in the hospital setting along with an important reservoir of CA-MRSA clones in the community, strongly suggest to the community as the main source of MRSA in the hospitals.

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