

O407

Abstract (oral session)

Molecular epidemiology of methicillin-resistant *Staphylococcus aureus* in 13 European intensive care units

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Objective: The European epidemiology of methicillin-resistant *Staphylococcus aureus* (MRSA) is changing with the emergence of community-associated MRSA (CA-MRSA) and livestock-associated MRSA (LA-MRSA). In this study we investigated the molecular epidemiology of MRSA during two-years in 13 ICU's in eight European countries. **Methods:** Surveillance cultures for MRSA from nose and wounds were obtained on admission and twice weekly of all patients admitted for at least 3 days. First MRSA isolates per patient were confirmed in a reference laboratory and genotyped by multi locus sequence typing (MLST), spa-typing and SCCmec (sub)typing. **Results:** In all, 14,390 patients were screened of whom 8,519 stayed in ICU for >3 days. Overall MRSA admission prevalence was 3.9% and ranged from 1.0% to 6.4% for individual ICUs. Overall MRSA acquisition rate was 2.5/1,000 patient days at risk, and ranged from 0.2 to 8/1,000 patient days at risk per ICU. In all, 631 patients were colonized with MRSA, 550 isolates (87%) were submitted to the reference lab and presence of the *mecA* gene was confirmed in 510 isolates (93%). Each country had a distinct epidemiology, with ST8-IVc (UK-EMRSA -2/-6, USA500) being most prevalent (106 of 510 isolates, 21%), being dominant in France and Spain, and being detected in ICUs in six of eight countries. ST239-III and ST368-III (the Brazilian/ Hungarian clone) were dominant in Latvia and Greece. Fifteen (3%) and three isolates (0,6%) were categorized as CA-MRSA and LA-MRSA, respectively. **Conclusions:** The molecular epidemiology of MRSA in 13 European ICUs in eight countries was homogeneous within, but heterogeneous between countries. CA-MRSA and LA-MRSA genotypes and PVL-producing isolates were detected sporadically.