

**P0230**

**Paper Poster Session**

**MRSA - one health worldwide**

**Molecular epidemiology of *Staphylococcus aureus* strains isolated from blood cultures in six tertiary care hospitals, Italy, 2012**

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**Background:** bacteremias due to *Staphylococcus aureus* (SA) represent a serious challenge for clinicians, particularly because of the problem of resistance to methicillin. In Italy methicillin resistant *S. aureus* (MRSA) accounted for more than 35% of the isolates involved in invasive infections, according to ECDC (35,2% and 35,6% in 2012 and 2013, respectively). The aim of this study was to investigate the epidemiology of SA bacteremias in six different Tertiary Care Hospitals located in Northern and Central Italy (approximately 5700 acute care beds) during the year 2012.

**Material/methods:** all the SA strains isolated from blood cultures (a single isolate per patient) were analyzed with molecular techniques to determine the presence/absence of the *mecA* gene and of the Panton-Valentine leukocidin (PVL). The MRSA strains were further characterized through the evaluation of the *SCCmec* cassette (typing and subtyping) and *spa*-typing using *in house* molecular methods.

**Results:** during the study period, 491 SA isolates have been collected and analyzed. 326 out of the 491 strains were *mecA* negative and PVL negative (66.40%), 160 were *mecA* positive and PVL negative (32.59%), 5 were *mecA* negative and PVL positive (1.02%). No *mecA* and PVL positive strains were found. Some kind of variability in the methicillin resistance was documented among the different centers, varying from 24.74 to 43,01%. Among the MRSA strains, the two *SCCmec* present throughout all the hospitals were the IVc (51 out the 160 isolates analyzed, 31.88%) and the IVh (again, 51 out the 160 isolates, 31.88%), followed by the *SCCmec* cassettes I (21 isolates in four different centers, 13.13%) and II (18 strains from four different hospitals, 11.25%). Less represented was the *SCCmec* IVa, whereas the cassettes IVf and V occurred sporadically (single isolates). 8 out of the 160 isolates (5%) were *SCCmec* non-typeable with the method we used. *Spa*-typing was

performed on all the MRSA strains and is currently in evaluation. Preliminary results on more than an half of the isolates allowed us to demonstrate an overall circulation of the *spa*-type t008, followed by other *spa*-types (clusterization in progress).

**Conclusions:** our study demonstrated a very low prevalence of strains harbouring PVL, all found in methicillin susceptible isolates. The percentage of MRSA was in agreement with the ECDC data (32.6% in this study vs 35.6%) with variability from center to center. Two major clonal types, as indicated by the association of *SCCmec* and *spa*-typing, were identified (accounting for both of the 31.88% of the isolates), together with less prevalent sporadic clones. The first of these two clones was IVc, which comprised the t008 and single *spa*-types (which could probably be ST-8, USA500-like), whereas the second one was IVh, comprising different *spa*-types (which could probably be ST-22, EMRSA-15).