P0211
Paper Poster Session
MRSA - one health worldwide

Major clones of Staphylococcus aureus circulating in Ecuador

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Background: The regional spread of the different *Staphylococcus aureus* epidemic clones has to be surveyed in order to assemble an accurate epidemiologic analysis at a local level. In Ecuador, the prevalence of the USA300 Latin American variant clone (USA300-LV) is well known, however there is scarce information about other clones that could be circulating in our country. In order to identify the clones of a *S. aureus* present in Ecuador, we applied an $MLVA_{14Orsay}$ genotyping approach to a heterogeneous strain collection including both, MRSA and MSSA isolates.

Material/methods: We studied a total of 178 *S. aureus* from different sources: 80 isolates consecutively recovered from bloodstream infections between 2010 and 2013 of three hospitals in Quito (P1); 32 nonconsecutive isolates from different infection sites recovered between 2011 and 2013 from 11 different clinical setting in Quito (P2); 20 isolates randomly selected from a MRSA archive collection recovered between 2005 and 2007 (P3); and 46 isolates from nasal carriers of swine farms workers from 2014 (P4). We identified by PCR the presence of *mecA* and *lukS/F-PV* genes, and the SCC*mec* cassette type. The MLVA 14-loci approach was resolved by electrophoresis. We identify the sequence type (ST) related by querying the MLVA genotypes in the MLVAbank for Bacterial Genotyping on-line database (http://mlva.u-psud.fr/).

Results: The *mecA* gene was detected in all 69 MRSA (38.76%) isolates identified previously by Vitek®2 System. The PVL genes were identified in 61 (34.27%) isolates, most of them MRSA (39/61 isolates). The prevalent SCC*mec* cassette was IV (50 isolates); the remaining cassettes were III, II and V (11, 5 and 1 isolates respectively). Two isolates remains with indeterminate cassette. We found seven epidemic clones: the Latin America USA300 variant (ST8-MRSA-IV-PVL+) as the predominant clone (37 isolates). The Brazilian clone (ST239-MRSA-III-PVL-) was found in 11 isolates. The Pediatric clone (ST5-MRSA-IV-PVL-) in 5 isolates. The NY/Japan clone (ST5-MRSA-II-PVL-) in two isolates. The UK-EMRSA-15 (ST22-MRSA-IV-PVL-) and the USA600 clones in one isolate each. Furthermore, we found 9 isolates related with the Livestock associated clone ST398 (LA-ST398); all of them but one recovered from P4. Between the MSSA isolates the most prevalent ST was ST8 (27 isolates), followed by ST30 (16 isolates), ST22 (11 isolates), ST45 and 121 (9 isolates each). The minimum spanning tree analysis exhibited 13 clonal complexes (Figure 1)

Conclusions: We detect a wide variety of STs in both, MRSA and MSSA, identifying the presence in Ecuador of different clones. We analyzed different population of S*. aureus* through the years, and we confirmed that LV-USA300 is the main clone in Ecuador, as previously reported. Furthermore, other clones less frequent in the region also were detected in this study. In addition we made the first description of LA-ST398 clone in Ecuador.

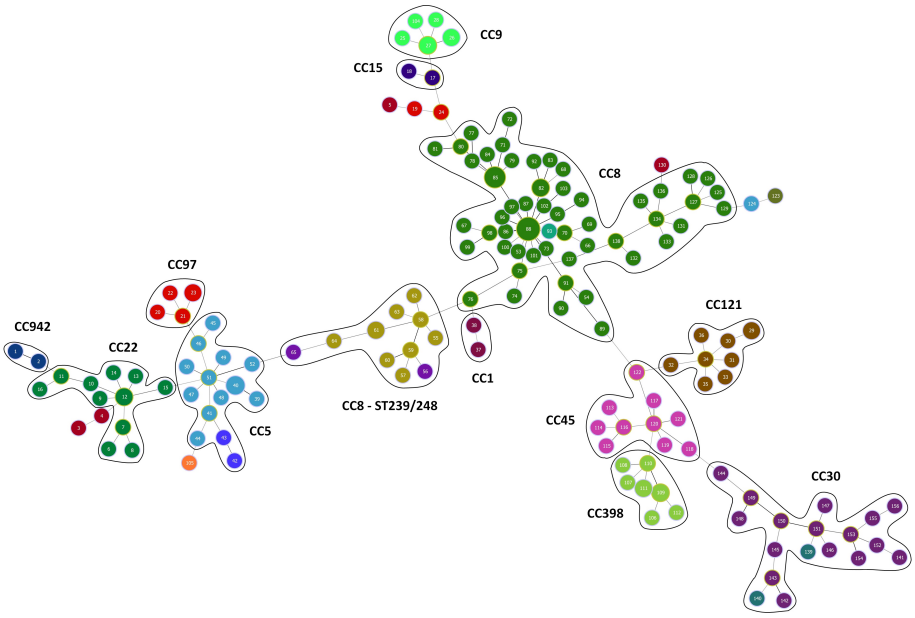

Figure 1. Minimum spanning tree of the 178 *S. aureus* isolates using MLVA$_{14Orsay}$. It represent the relationship of all the isolates analyzed in the study. The colors represent the diverse STs identified. We use the phyloviz v.1.1 software in the analysis.