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We aimed assess the genetic relationship between CA-MRSA epidemic clones and MSSA strains identified in Argentina to investigate the possible local origin or its spread from other countries of these international CA-MRSA clones A total of 132 MSSA clinical isolates collected during Nov-2009 from 66 hospitals (20 provinces and Bs. As. City) were analyzed by *S. aureus* Protein A (spa) typing, Pantón Valentin Leukocidin (PVL), Pulsed Field Gel Electrophoresis (PFGE) and Multilocus Sequence Typing (MLST). Molecular analysis by spa typing; showed 65 different spa types (t) grouped into 12 CC according MLST (%): CC5 (21), CC30 (16), CC1 (15), CC121 (10), CC8 (8), CC45 (8) CC12 (1), CC97 (8), CC25 (4) CC101 (2), CC15 (1), CC88 (1) distributed throughout the country. The proportion of isolates belonging to CC5 (t311 and t002) and CC30: (t012, t021 and t018) differed significantly between North and South of Argentina: 36% and 6% vs. 12% and 32 %, respectively. Based Upon Repeat Pattern (BURP) analysis showed that MRSA (previously analyzed) and MSSA isolates belonging to CC5 shared the same spa type (t311 and t002), suggesting that these were closely related. Contrary, no common spa type was shared between MSSA and MRSA belonging the CC30 (ST30). The remaining CCs also showed a closely genetic relation between the MSSA and MRSA by PFGE type, spa type and Sequence Type , sharing the spa type and the ST, such us: ST72 and t148 (CC8), ST1 and t127 (CC1), ST88 and t186 (CC88), ST97 and t359 (CC97) and ST121 and t159. We also detect MRSA and MSSA belonging to ST8 with spa t008, genetic characteristics of the major epidemic CAMRSA clone spread in EEUU: USA300. However as many as four different SCCmec (sub) types in five MRSA isolates with spa t008, indicating independent acquisitions in the MSSA ancestor. These results support the hypothesis about the local and continuous emergence of new CA-MRSA clones from successful MSSA lineages in addition to the dissemination of them is an important process of increasing resistance to betalactam antibiotics. However, only the whole genome sequence of these strains will clarify this hypothesis.

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PROKARYOTIC DIVERSITY IN ECOSYSTEMS ASSOCIATED TO MINERALS FROM THE HYPERSALINE LAKE TEBENQUICHE IN THE ATACAMA DESERT

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The Salar de Atacama is located in the Chilean central Andes and it is a huge evaporitic system with a large number of saline water bodies in its interior. Lake Tebenquiche is one of the largest and prokaryotic microorganisms inhabiting this lake are subjected to severe conditions as high solar radiation due to a lower barometric pressure at high altitude, extreme daily temperature fluctuations, intense changes in salinity caused by net evaporation and high arsenic concentrations in the water due to volcanic events. Therefore, we decided to analyse the prokaryotic diversity of microbial mats, microbialites and one evaporite by pyrosequencing of the V4 hypervariable region of the 16S rRNA gene. In addition, the total metagenomic DNA of a microbial mat was sequenced to study the genetic and metabolic diversity for understanding the microbial processes associated to minerals in a system at high altitude. Five different samples were collected from lake Tebenquiche: two microbial mats, TebMa1 and TebMa2; two microbialites, TebMi1 and TebMi2; and one evaporite, TebEv1. The total metagenomic DNA of each sample was extracted and pyrosequenced the V4 hypervariable region of the prokaryotic 16S rRNA gene. The prokaryotic 16S rRNA amplicons were analysed using the QIIME software package. The total metagenomic DNA from microbial mat, TebMa1, was sequenced using paired-end Hi-Seq 1500 Illumina Technology and the raw reads obtained were filtered, assembled into contigs and annotated. Euryarchaeota is one of the most abundant phyla in all samples studied, especially in TebEv1 with 97 % of 16S rRNA sequences. Most of the euryarchaeal OTUs are classified within the class Halobacteria or anaerobic and methanogenic archaea. Specific genes as indicators of particular biogeochemical cycles were searched in the assembled contigs of TebMa1. Nitrogenase gene sequences are found in a high amount and these sequences were aligned with a range of 70%-89% identity to known nitrogenase sequences. Phosphate is mainly obtained by two mechanisms when there is a reduced availability of phosphorus: polyphosphate metabolism and phosphate recycling. Cytoplasmic arsenate reduction and arsenite oxidation are clearly present in the arsenic-rich habitat TebMa1. The high conductivity measured in TebMa2 and TebEv1 must be promoting the growth of members belonging to the class Halobacteria due to the dominance of this taxon in both samples. In TebMa1, we suggest could be carried out an active biological nitrogen fixation by bacteria and archaea and due to the low percentage identity to the closest relative an important part could be novel diazotrophic microorganisms. This ecosystem is rich in arsenic and its inhabitants use arsenic resistance strategies as cytoplasmic arsenate reduction and arsenite oxidation but a possible mechanism employed by these microorganisms could be through chelation of this metalloids using polyphosphates.