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Abstract (poster session)

Clonal complex 398 MSSA: a frequent unrecognised human pathogen and a probable reservoir for clonal complex 398 livestock-associated MRSA emergence

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Background: Clonal complex 398 Livestock-Associated-MRSA (CC398 LA-MRSA) clone has been described as major animal pathogen, that can also colonize and infect humans. Little is known about its CC398 Methicillin susceptible *Staphylococcus aureus* (CC398 MSSA) counterpart. Here, we investigated the clinical, phenotypic, genotypic characteristics of a large CC398 MSSA collection of human isolates. Materials and methods: One hundred and twenty six CC398 MSSA strains of human origin were identified within the collection of the French National Reference Centre for Staphylococci. They were extensively characterized using antimicrobial susceptibility testing, spa typing, DNA microarrays (StaphyType, Alere), specific CC398-specific sequence PCR, ermT (encoding macrolides resistance) PCR. Fifty-three CC398 LA-MRSA collected from French pigs and veals were used as comparators. Phylogenetic relation between human CC398 MSSA and animal CC398 MRSA populations were explored on the basis of spa-typing and DNA microarrays. Results-discussion: CC398 MSSA was able to induce a large spectrum of infections (especially skin, bloodstream and respiratory tract infections) and so appeared as an unspecialized pathogen. Surprisingly, its prevalence rate was high in MSSA population, i.e., 24.7% (n=21/85) in a local prospective study on nasal colonization, and 7.5% (n=10/132) in a national prospective study on infective endocarditis. CC398 MSSA isolates frequently (89 %, 112/126) presented an isolated erythromycin resistance, due to the presence of the ermT gene. Of note, the ermT gene was never detected in erythromycin resistant CC398 LA-MRSA strains. CC398 MSSA and CC398 LA-MRSA populations were closely related based on spa-typing and DNA microarrays. Genetic variability was associated with the acquisition of antibiotic resistance genes, including bla genes and a type IV or V SCCmec. Noteworthy, 26 CC398 MSSA strains isolated outside of mainland France (Switzerland, Algeria, Denmark, Dominican Republic, India, Madagascar, US, French Islands) showed similar features and clustered with French isolates. Conclusion: In human, CC398 MSSA is a frequent colonizing bacteria and unspecialized pathogen, that has specific phenotypic and genotypic signatures. The genetic background of this population appears homogenous, and close to CC398 LA-MRSA population. It may constitute the reservoir from which LA-MRSA CC398 emerged.