O412

Abstract (oral session)

Unexpectedly high prevalence of the emerging CC398 methicillin-susceptible Staphylococcus aureus clonal complex in bone and joint infections

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Objectives: To describe the prevalence of the emerging CC398 methicillin-susceptible S. aureus (MSSA) clone in bone and joint infections (BJI). Methods: Retrospective study including patients with MSSA BJI (n=271) in 3 French Hospital centers (HCL Lyon, Novecia, Hôpitaux de Montpellier) from 2009 to 2012. BJI MSSA collection was screened using a specific CC398 PCR. CC398 MSSA strains from HCL Lyon (n=91) were extensively characterized by antimicrobial susceptibility testing, spa-typing, and DNA microarray analyses targeting 332 genes or alleles. Clinical description could be retrospectively obtained for 61 patients of our institution. A control population was constituted by colonizing MSSA strains isolated from nasal swabbing of patients admitted in orthopedic surgery and intensive care units from June to December 2010 (n=74) and from April to July 2012 (n=80). Results: Among the 271 BJI isolates included, 43 (15.9%) belonged to CC398 (HCL Lyon, 8.8%; Novecia, 9.7%, Montpellier, 24.6%). For comparison, only 6 strains (3.9%) belonged to CC398 among nasal colonizing isolates ($p<0.001$). Of note, only 1 CC398 was identified during the 2001-2008 period in HCL Lyon. Among the 91 MSSA strains from HCL Lyon, a great diversity of clonal complex was observed (n=16) among which CC398 was the fifth most common. Except the penicillin resistance (50%), the only antibiotic-resistance profile of the 8 CC398 strains was an isolated resistance to erythromycin detected in 7 strains (87.5%) due to ermT. DNA microarray analysis confirmed this multi-susceptible profile with no usual antibiotic-resistance genes. Other virulence genes were negative with the exception of one strain bearing enterotoxin C and L. All strains were positive for the chp and scn genes, associated with the immune evasion complex. No difference was observed between CC398 and other strains regarding demographic characteristics of patients and clinical presentation of BJI. CC398 BJI were associated with a lower biological inflammatory syndrome ($p<0.05$). Treatment failure rate tended to be lower for CC398 BJI (0% vs 31.0%, $p=0.095$). Conclusion: In these last 4 years, we report the unexpected high prevalence of MSSA CC398 clone in BJI, compared to colonizing MSSA strains, suggesting a higher capacity of this emerging clonal complex to cause BJI. Further studies are underway to explore and understand this specific feature. Preliminary results indicate that these isolates are less cytotoxic and invasive regarding human osteoblasts.