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P2845 Genotype-phenotype correlation in *Staphylococcus lugdunensis*: a comprehensive comparative WGS study of 70 French isolates associated with various infection types

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Background: *Staphylococcus lugdunensis* (SLU) is particularly virulent coagulase negative staphylococcus. Like *S. aureus*, it is predominantly associated with community-acquired soft-tissue and skin infections including Hidradenitis Suppurativa (HS) skin abscesses and is a rare cause of life threatening infective endocarditis (IE). Paradoxically, few virulence factors have been described in *S. lugdunensis*. The aim of this study was to investigate the genomics traits of 70 SLU clinical isolates obtained from 8 French University Hospitals including 19 IE, 30 skin abscesses (15 from in Hidradenitis Suppurativa patients), 19 osteoarticular infections (native n=7; prosthetic joint infections (PJI) n=12), and 1 urosepsis by Whole-Genome sequencing (WGS).

Materials/methods: WGS of strains was performed using HiSeq2500 technology (Illumina, San Diego, USA). Obtained genomes were *de novo* assembled using Spades and mapped against a reference strain (SLU-HKU09-01; NC_013893.1). In addition, a phylogeny based on single nucleotide polymorphism (SNP) was accessed using Bowtie2 and analysis was performed using Gubbins software. Molecular types as Multi-Locus Sequence Typing (MLST) and virulence genes were extracted from assembled sequences using databases available on Center for Genomic Epidemiology.

Results: Seven distinct clusters were defined by our SNP phylogenic analysis. MLST type ST3, the predominant clonal group (n = 24/70), was found in strains mainly isolated from patients suffering of skin abcesses in HS context (n = 9/15) and PJI (n = 7/19).

Previously described virulence factors were found in all strains except for *fbl* (fibrinogen binding protein), lug operon (lugdunin secretion) and *vwbl* (von Willebrand binding protein) which were found in 91,5%, 90% and 98,5%, respectively. Interestingly, CRISPR-Cas system was found in only 29,5% of strains.

Eight types of plasmids (already described in *Staphylococcus aureus*) were also found in our study.

Conclusions: Our data suggest heterogeneity in clinical strains of SLU without a clearly established link between virulence factors and clinical presentation. To our knowledge, this is the first genomic study concerning SLU with a consistent number of well documented clinical strains and need to be completed by other clinical and microbiological studies.