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**Influence of the genetic background of *Staphylococcus aureus* strains in the study of their virulence on the *Galleria mellonella* model**

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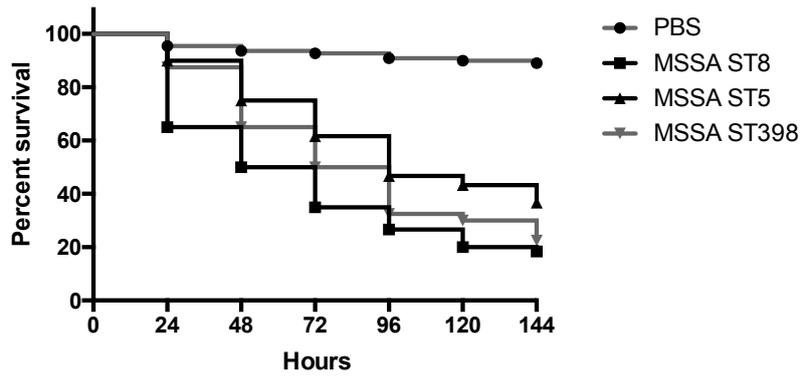
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**Background:** *Staphylococcus aureus* is an important human pathogen. While understanding its virulence mechanisms seems essential, impact of genetic background of strains remains unclear. The aim of our study was to evaluate the influence of the genetic background of *S. aureus* on strain's virulence using the recent non-vertebrate screening model *Galleria mellonella*.

**Material/methods:** 20 strains of methicillin susceptible *Staphylococcus aureus* (MSSA) and methicillin resistant *Staphylococcus aureus* (MRSA) isolated from bacteremia and identified by multilocus sequence typing (MLST) and spa typing had been selected: 8 ST8 (4 MSSA and 4 MRSA), 8 ST5 (4 MSSA and 4 MRSA) and 4 MSSA ST398. These strains had been characterized with respect to *agr*, SCCmec cassette and main *S. aureus* virulence factors. *Galleria mellonella* larvae were infected with three inocula ( $10^4$ ,  $10^5$  and  $10^6$  CFU/mL) and larval mortality was checked daily during a six days period.

**Results:** Larvae survival at the  $10^6$  CFU/mL inoculum was chosen to compare strain virulence. The MSSA ST8 isolates exhibited a higher virulence than the MSSA ST5 isolates in the *G. mellonella* model ( $p=0.0026$ ). The clone ST398 had an intermediate virulence. Among MRSA, ST8 strains shown a greater virulence compare to the ST5 strains but this difference was not significant.



Survival of *Galleria mellonella* larvae infected with MSSA ST8, MSSA ST5 and MSSA ST398 at the  $10^6$  CFU/ml inoculum

**Conclusions:** Our study suggests a role of the *S. aureus* genetic background on its virulence. Even if this study needs to be confirmed on a mammalian model such mouse pneumonia or infective endocarditis in rabbits, it demonstrates the importance of knowing the genetic background of *S. aureus* strains used in scientific studies