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Spread of methicillin-susceptible *Staphylococcus aureus* ST398 in patients, health care workers and environment in an intensive care unit

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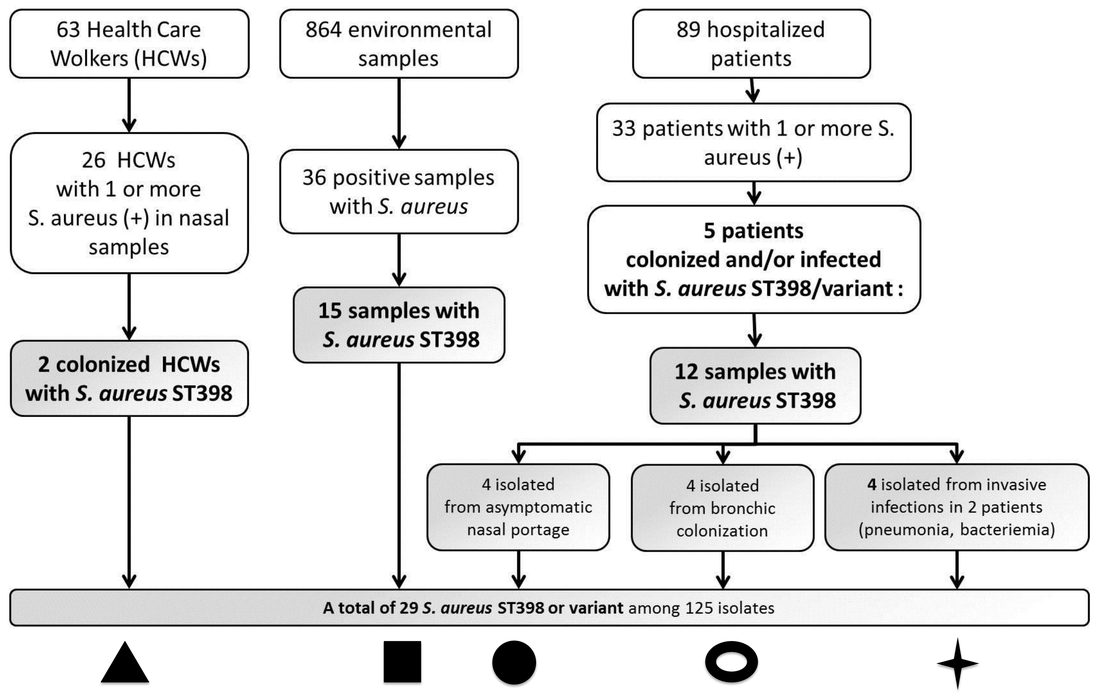
Introduction and Purpose

Staphylococcus aureus (S. aureus) is both human commensal and an important human pathogen, responsible for community-acquired and nosocomial infections. An increasing number of human infections with livestock-associated *S. aureus* sequence type (ST) 398 has been recently reported (1), sometimes without contact with livestock (2), suggesting that this strain is emerging in community and health care settings. *S. aureus* ST398 isolated from patients, health care workers (HCW) and environmental samples in an Intensive Care Unit (ICU) of Montpellier Hospital were characterized with the aim to understand the circulation of this pathogen into the ICU.

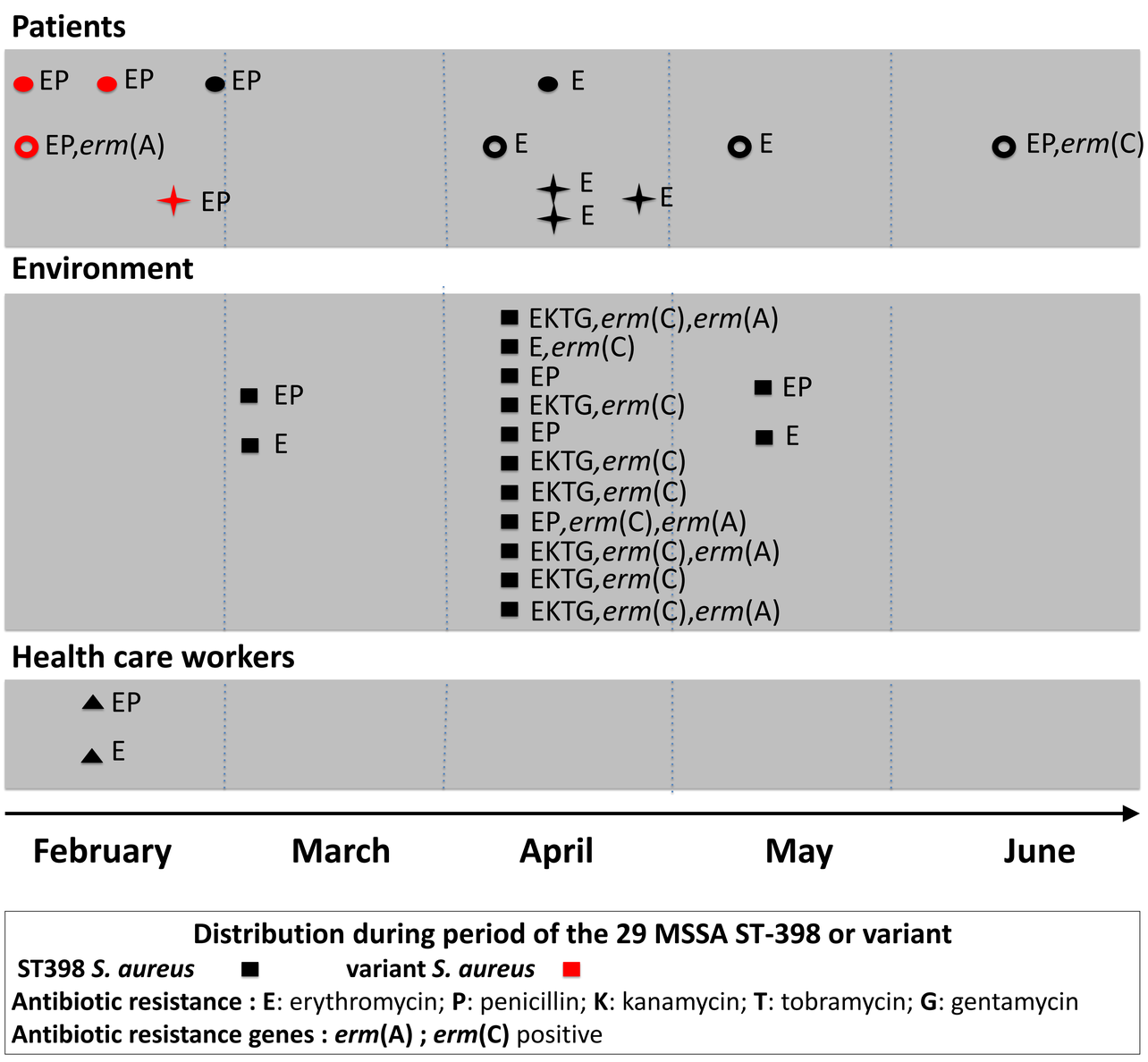


Materials and Methods

125 *S. aureus* were isolated between February and June 2011 in the ICU from patients, HCWs and environment, and typed by MultiLocus Sequence typing (MLST). *S. aureus* ST398 strains and variant (belonging to clonal complex 398) were analyzed by Double-Locus Sequence Typing (DLST) (3) and accessory gene regulation (*agr*) typing. Resistance to antibiotics was detected by disk-diffusion method. Macrolide-Lincosamide-Streptogramin type B (MLS_B) resistant strains were screened by PCR for *erm*(A), *erm*(C), *erm*(T) (4) and *msr*(A) genes. Virulence genes encoding to Panton Valentin Leucocidin PVL (*lukS-PV)*, to Toxic Shoc Syndrom Toxin TSST-1 (*tst*), and to Staphylococcal Enterotoxin A or SEA (*sea)* were detected by specific PCRs.

Results

Out of the 125 isolates, 29 methicillin-susceptible *S. aureus* (MSSA) ST398 or variant were isolated in nasal carriage and invasive diseases in 5 patients (n=12), nasal colonization of 2 HCWs (n=2) and environmental samples (n=15). For the first time, 4 isolates were identified as variant of ST398 with a unique mutation in the *pta* gene. All isolates were *agr*1 and DLST-type 144-186 (DLST-*spa* 186 corresponding to *spa*-type t571). Erythromycin resistance and inducible MLS_B phenotype were observed for 100% of the isolates. Resistant to β-Lactam was limited to Penicillin for only 41.3% of strains (12/29). Seven environmental isolates showed additional resistance to Kanamycin, Tobramycin and Gentamicin. All strains harbored the *erm*(T) gene and different combinations of *erm*(A) and *erm*(C) and the absence of *msr*(A). No isolate contained the genes encoding the PVL, TSST-1 and SEA. No history of contact with livestock was identified in patients and HCWs. Two patients presented nosocomial pneumonia after acquired-nasal colonization, associated with a bacteremia for one of them.



Conclusion

Isolation of MSSA ST398 or variant strains, sharing similarity with Chinese-type strains (2), in patients, HCWs and environment in an ICU during short time period underlines the capacity of this emerging pathogen to rapid person-to-person transmission and the role of the environment as potential reservoir. Despite the absence of large antibiotic resistance and virulence traits, MSSA ST398 can lead to severe infections in critically ill patients. Evolutionary capacity of ST398 genotype is underlined here by description of a mutated genotype, the impact of the mutation on the phenotypic and spreading properties of ST398 genotype has to be investigated.

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