Review of: "Everybody Nose: Molecular and Clinical Characteristics of Nasal Colonization During Active Methicillin-Resistant Staphylococcus Aureus Bloodstream Infection"

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Potential competing interests: The author(s) declared that no potential competing interests exist.

The manuscript reports a study on nasal MRSA colonization in patients with MRSA blood stream infection (BSI). It was performed from July 2018 until May 2019 at the Mount Sinai Hospital, NYC. 63 patients with BSI were enrolled, finally data on demographic and clinical characteristics as well as results from bacteriology were available for 53 of them. Primary cultures were carefully examined by colony morphology for probably heterogeneous colonization. Representative isolates were subjected to molecular typing by means of *spa*-typing.

Background of this study is the widely accepted concept that nasal colonization with *Staphylococcus aureus* is a substantial reservoir for infections with this pathogens in these carriers. This had also been demonstrated for methicillin resistant *S.aureus* (MRSA) by studies performed nearly 20 years ago.

The study is aimed to analyse the diversity of colonizing MRSA within hosts and of the demographic and clinical features associated with concomitant nasal MRSA colonization in patients suffering from MRSA BSI.

The reported data on heterogeneous nasal colonization, on the frequency of concomitant nasal MRSA colonization (70%) and the congruence of results from typing nasal and blood stream isolates (95%) largely confirm results from studies in Europe where at that time MRSA epidemiology was different from that in the USA at present. Furthermore, these previous studies did not include such a broad analysis of clinical patient characteristics.

From my side there are following comments/suggestions:

1. Abstract; conclusions a little bit more concrete explanations on the consequences of the findings for prevention/treatment would be desirable.
2. Introduction: For those who are not active in the field of MRSA infections a short description of the changing MRSA epidemiology including the discrimination of HA-MRSA, CA-MRSA and discrimination of widely disseminated epidemic strains of both categories would be helpful.
3. Methods:
    1. Either here or at the beginning of the results section more details on the study setting with respect to prevalence of MRSA infections, and, if performed, on results from MRSA screening at admission would be of interest.

2. 3.2.The study is based on 53 patients (37 colonized and 16 noncolonized), for which at least different 12 clinical variables had been recorded. I am concerned about the statistical power. Was a power calculation carried out when designing the study ?

4. Results. Starting point is the widely accepted concept that nasal colonization with *Staphylococcus aureus* is a substantial reservoir for infections with this pathogens in these carriers. This had also been demonstrated for methicillin resistant *S.aureus* (MRSA) by studies performed nearly 20 years ago. We should, however, keep in mind, that nosocomial infections (e.g. surgical wound infections) can result from direct transmission to the site of infection and must not necessarily start from nasal colonization. With respect to the comparatively low prevalence of MRSA BSI it would have been a tremendous effort to screen each patient before medical procedures which may result in an infection for MRSA colonization. One of the results is the observation that 38% of the colonized and 2 from 14 of the noncolonized patients had a history of previous MRSA colonization (Table 2). Were the corresponding isolates typed or are they still available for typing ?
5. The authors assume that spa-type t002 is indicative for MRSA CC5 “USA100” which is widely disseminated as HA-MRSA in the USA and t008 for the “notorious” CA-MRSA “USA300”. There are however, nosocomial MRSA that also exhibit t008. Therefor it would be highly advisable to perform at least PCR for *luk*-PV, better in addition also for *arc*A. (We have to keep in mind that high resolution typing based next generation sequencing [core genome MLST represents the state of the art).
6. Discussion. It would not be revealing to discuss the differences observed for MRSA CC8 and CC5 against the background of HA-MRSA and CA-MRSA epidemiology.