Data on Whole-Genome Sequencing Are Insufficient to Rule Out Patient-to-Patient Transmission as a Significant Source of \textit{Staphylococcus aureus} Acquisition in an Intensive Care Unit

To the Editor—The recent publication by Price et al [1] uses novel methods to illustrate the complex dynamics involved in nosocomial transmission of \textit{Staphylococcus aureus} through the use of whole-genome sequencing. However, the claim that patient-to-patient transmission is a rare occurrence is not well justified by the presented data. The authors report 7 of 37 (18.7%) patient-to-patient transmission events based on whole-genome sequencing of isolates with available \textit{spa} typing results. Our calculated confidence intervals for these proportions range from 6.3\% to 31.5\%. Furthermore, if only methicillin-resistant \textit{S. aureus} transmission events in isolates with available \textit{spa} types are analyzed, the proportion increases to 5 of 14 (35.7\%), with confidence intervals of 10.6\%–60.8\%. These numbers are more consistent with existing data on rates of horizontal transmission of \textit{S. aureus} [2]. Although the study clearly shows the limitations of conventional methods of transmission assessment, the data are far from conclusive in exonerating patient-to-patient transmission as a major source of in-hospital \textit{S. aureus} acquisition.

Note

\textit{Potential conflicts of interest.} Both authors: No reported conflicts.

Both authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

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