[LETTERS TO THE EDITOR]

Additional Bacteriological Examinations Might be Required for the Correct Identification of *Staphylococcus warneri*

Key words: Staphylococcus warneri, Staphylococcus pasteuri, matrix-assisted laser desorption ionisation time-of-flight mass spectrometry, rRNA restriction fragment length polymorphism analysis, 16S rRNA gene sequencing

(Intern Med 60: 821, 2021) (DOI: 10.2169/internalmedicine.5675-20)

To the Editor We read with great interest the article, "Native valve endocarditis due to *Staphylococcus warneri* developing in a patient with type 1 diabetes," by Yamamoto et al. (1). This article described the patient's clinical course in detail, as well as the clinical decision making that was involved, the deductive interpretation of underlying heart disease, the pathogenicity of coagulase-negative Staphylococci, including *Staphylococcus warneri*, and diabetes as an accelerating factor. We appreciate the authors' contribution to furthering our understanding of infective endocarditis caused by the extremely rare pathogen *S. warneri*.

However, an Australian case report described an elderly man suffering from native valve endocarditis caused by *S. pasteuri*, which has been frequently misidentified as *S. warneri* because of the strong phenotypic similarity (2). This pathogen was detected by both a biochemical procedure (VITEK[®]) and matrix-assisted laser desorption ionisation time-of-flight mass spectrometry (MALDI-TOF MS). In addition, an article published by a European microbiological laboratory group revealed that four of the nine *S. warneri* strains were correctly identified based on their phenotype and molecular methods (3). An rRNA restriction fragment

length polymorphism analysis (ribotyping) correctly identified all nine *S. warneri* strains. Furthermore, partial 16S rRNA gene sequencing correctly identified coagulasenegative Staphylococci, which included *S. warneri* and *S. pasteuri* (4).

Therefore, we wonder if an additional analysis, such as MALDI-TOF MS, ribotyping or 16S rRNA gene sequencing, was performed for the identification of this rarely isolated microorganism. Although, to our knowledge, no article has yet determined the difference in the clinical course between *S. warneri* and *S. pasteuri*, the correct identification of the pathogen is ultimately the most important point when treating infectious diseases.

The authors state that they have no Conflict of Interest (COI).

Takahiko Fukuchi and Hitoshi Sugawara

References

- 1. Yamamoto J, Endo A, Sugawara H, et al. Native valve endocarditis due to *Staphylococcus warneri* developing in a patient with type 1 diabetes. Intern Med **59**: 2269-2274, 2020.
- Ramnarain J, Yoon J, Runnegar N. *Staphylococcus pasteuri* infective endocarditis. A Case Report Case Reports ID Cases 18: e00656, 2019.
- **3.** Carretto E, Barbarini D, Couto I, et al. Identification of coagulasenegative Staphylococci other than *Staphylococcus epidermidis* by automated ribotyping. Clin Microbiol Infect **11**: 177-184, 2005.
- **4.** Ayeni FA, Andersen C, Nørskov-Lauritsen N. Comparison of growth on mannitol salt agar, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry, VITEK 2 with partial sequencing of 16S rRNA gene for identification of coagulase-negative staphylococci. Microb Pathog **105**: 255-259, 2017.

The Internal Medicine is an Open Access journal distributed under the Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License. To view the details of this license, please visit (https://creativecommons.org/licenses/ by-nc-nd/4.0/).

Division of General Medicine, Saitama Medical Center, Jichi Medical University, Japan Received: June 21, 2020; Accepted: August 3, 2020; Advance Publication by J-STAGE: September 30, 2020 Correspondence to Dr. Takahiko Fukuchi, chicco@f.email.ne.jp

© 2021 The Japanese Society of Internal Medicine. Intern Med 60: 821, 2021