

Get the Species Right: *Aerococcus viridans* is Likely not Responsible

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Received on: 16 June 2022; Accepted on: 12 July 2022; Published on: 30 September 2022

Keywords: *Aerococcus*, Bacteremia, Vitek2.

Indian Journal of Critical Care Medicine (2022): 10.5005/jp-journals-10071-24330

We read with interest the article “*Aerococcus viridans* bacteremia: A rare case report from India” published in your journal.¹ While we find new information on aerococci and aerococcal infection is much called for, such information needs to be correct. The authors of this report claim that the infection described was caused by *A. viridans* but they use a method for species identification, Vitek2, which is known to misidentify *Aerococcus sanguinicola* as *A. viridans*.^{1,2} Furthermore, *A. sanguinicola* is a more common cause of severe aerococcal infections^{3,4} and it is likely that the most reported cases of *A. viridans* infections, including the one by Varshini et al., actually represents infections with another bacterium, with *A. sanguinicola* being likely.^{2,4} Varshini et al. also claim that the isolated bacteria induced β -hemolysis on blood agar plates which is a very atypical feature for an *Aerococcus*. We, therefore, believe it very likely that the case report describes an infection, not with *A. viridans*, but with a yet undetermined bacterial species. A correct species determination of bacteria is a prerequisite in scientific reports as errors in species determination risks to add to confusion and not to knowledge. Both matrix-assisted laser desorption/ionization time-of-flight mass spectroscopy (MALDI-TOF MS) and methods based on 16S rDNA sequencing could have been used to determine species of the bacterium in this case.⁵

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How to cite this article: Rasmussen M, Sunnerhagen T. Get the Species Right: *Aerococcus viridans* is Likely not Responsible. *Indian J Crit Care Med* 2022;26(10):1158.

Source of support: Nil

Conflict of interest: None

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