



Case report

Endocarditis caused by *Thalassospira* sp.

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ABSTRACT

We report a case of an infective endocarditis caused by a *Thalassospira* sp. in a 53-year-old man with pre-existing valvular lesions and living in French Polynesia as a fisherman. The strain was identified with DNA-sequencing methods while it was not by mass spectrometry.

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Introduction

Infective endocarditis (IE) refer to the infections of the inner surface of the heart. They are mostly caused by bacteria, typically staphylococci, streptococci, enterococci and HACEK-related organisms [1]. The microbiological diagnostic of IE relies on the culture of blood samples and infected tissues (when surgery is performed). In 10 % cases, no etiology for IE is found, and culture-independent, molecular methods such as broad-range PCR and more recently, metagenomic sequencing can be used [2].

Case report

A 53-year-old man living in Bora-Bora (French Polynesia) and working as a fisherman (apnea fishing, i.e. spending hours per day in sea water) presented at the Cardiology department of Papeete hospital (French Polynesia) in October 2020 with dyspnea of

progressive worsening over 6 months. He has a medical history of hypertension and rheumatic fever from childhood. Trans-thoracic and trans-esophageal echocardiography found a mixed calcific aortic valve disease combining severe stenosis and moderate regurgitation, dilatation of the ascending aorta at 49 mm and a circulating retro-aortic false aneurysm of 50 by 15 mm. Left ventricular ejection fraction was 40 %. The patient did not report any fever.

On admission, C-reactive protein was 25 mg/L with 9000/μL leukocytes. The patient was transferred to the Bichat-Claude Bernard Hospital (Paris, France) to undergo surgery. There, transoesophageal echocardiography and CT scan confirmed the posterior peri-aortic false aneurysm. A positron emission tomography (PET) scan showed no evidence of cardiac valve or vascular hypermetabolism, and did not reveal any embolic lesion. He developed cardiogenic shock and was operated on October 26th. Repeated blood cultures (total of three pairs before surgery) remained sterile. The surgery consisted of aortic valve replacement by bioprosthesis, reconstruction of the aortic ring by patch, placement of a supracoronary tube and tricuspid ring annuloplasty. The Gram stain examination of the aortic valve revealed a high number of Gram-negative, spiral and

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salmonicida endocarditis where the patient had rheumatic heart disease and bathed in well water [8] and in *Shewanella* endocarditis where the patient had bioprosthetic mitral and aortic valves and fished in saline waters [9].

Nonetheless unlike those reports and that of Marchese et al., our patient did not present any fever or significant biological inflammatory syndrome that could have led to the suspicion of endocarditis at presentation. Moreover, the strain was unable to grow on Bactec vials and the diagnostic of infective endocarditis was only possible by culturing valve specimens. In conclusion, we report here a case of aortic endocarditis caused by *Thalassospira* sp., an unusual bacterium only reported once in human infection. The bacterium has likely been acquired through bathing in saline water and has attached to pre-existing valvular lesions. While conventional methods were challenged by the absence of the strain in MALDI-TOF databases, we showed that rapid, low-cost (<100€) metagenomic and genomic sequencing using Nanopore Flongle flow-cells could help.

Declaration of Competing Interest

The authors declare no conflict of interest.

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Ethical approval

The patient authorized the publication of the case by a signed agreement on December 1.

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References

- [1] Hoen B, Duval X. Infective endocarditis. *N Engl J Med* 2013;368:1425–33, doi:<http://dx.doi.org/10.1056/NEJMcp1206782>.
- [2] Kolb M, Lazarevic V, Emonet S, Calmy A, Girard M, Gaïa N, et al. Next-generation sequencing for the diagnosis of challenging culture-negative endocarditis. *Front Med* 2019;6, doi:<http://dx.doi.org/10.3389/fmed.2019.00203>.
- [3] Li H. Minimap2: pairwise alignment for nucleotide sequences. *Bioinformatics* 2018;34:3094–100, doi:<http://dx.doi.org/10.1093/bioinformatics/bty191>.
- [4] Wood DE, Salzberg SL. Kraken: ultrafast metagenomic sequence classification using exact alignments. *Genome Biol* 2014;15:R46, doi:<http://dx.doi.org/10.1186/gb-2014-15-3-r46>.
- [5] Sunagawa S, Coelho LP, Chaffron S, Kultima JR, Labadie K, Salazar G, et al. Ocean plankton. Structure and function of the global ocean microbiome. *Science* 2015;348:1261359, doi:<http://dx.doi.org/10.1126/science.1261359>.
- [6] Marchese A, Santoriello L, Riccio G, Coppo E, Carrega G. First description of human invasive infection due to *Thalassospira profundimarum*. *Clin Microbiol Infect* 2019;25:1162–3, doi:<http://dx.doi.org/10.1016/j.cmi.2019.05.023>.
- [7] Diaz JH. Skin and soft tissue infections following marine injuries and exposures in travelers. *J Travel Med* 2014;21:207–13, doi:<http://dx.doi.org/10.1111/jtm.12115>.
- [8] Salehi MR, Shadvar S, Sadeghian M, Doomanlou M, Abdollahi A, Manshadi SAD, et al. Endocarditis with *Aeromonas salmonicida*. *IDCases* 2019;18:e00625, doi:<http://dx.doi.org/10.1016/j.idcr.2019.e00625>.
- [9] Davidson NL, Subedi S, Wilks K, Morgan J. A case of *Shewanella* algae endocarditis: an emerging pathogen with a diverse clinical spectrum. *BMJ Case Rep* 2018;2018, doi:<http://dx.doi.org/10.1136/bcr-2017-223396>.