

A Novel *Helcococcus*-like Organism Causing Endocarditis in an Injecting Drug User

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A case is presented of infective endocarditis caused by a previously undescribed *Helcococcus*-like organism, in a patient with human immunodeficiency virus infection. The organism, which could not be identified phenotypically in the routine laboratory,

was identified using partial 16S rRNA gene sequencing.

The Journal of Heart Valve Disease 2005;14:693-694

Helcococcus sp. is a catalase-negative, Gram-positive coccus that has been recently recognized (1,2) and isolated from clinical specimens including a breast abscess (3), an infected sebaceous cyst (4), as a co-isolate in skin and soft tissue infection, and as a skin colonizer (5,6). It has been identified using 16S rRNA gene sequencing techniques, and to date two species have been characterized: *Helcococcus kunzii* (5) from humans, and *Helcococcus ovis* (7) from sheep. Herein is reported a novel *Helcococcus*-like organism, identified using 16S rRNA gene sequencing, isolated in pure culture from the blood of a patient with infective endocarditis.

Case report

A 48-year-old female injecting drug user was admitted through the Emergency Department with a two-week history of exertional dyspnea, ankle edema, fatigue and feeling generally unwell. She was known to be infected with the human immunodeficiency (HIV) virus and was Hepatitis C virus (HCV) antibody positive. She had been treated three years previously for tricuspid valve endocarditis; at that time, *Staphylococcus aureus* and Group G streptococcus were isolated from blood cultures. In the intervening years, she was also treated for septic arthritis of the left knee, retroperitoneal abscess, extensive left iliofemoral deep venous thrombosis and methicillin-resistant

Staphylococcus aureus (MRSA) pneumonia. The patient gave a history of skin popping and intravenous drug injecting (six to eight times) during the month before admission, having not injected drugs for a year prior to that.

On examination, the patient was afebrile and hemodynamically stable. The jugular venous pressure was elevated and there was an apical systolic murmur consistent with mitral regurgitation. Auscultation of the chest revealed bilateral basal crepitations. There was moderate splenomegaly. Ankle edema was present to mid-calf. The white cell count was normal, hemoglobin was reduced at 10.7 mg/dl, the erythrocyte sedimentation rate was elevated at 46 mm/h, and C-reactive protein was raised at 32 mg/l. Renal and liver function tests were within normal limits. The CD4 count was 622 cells/mm³ and HIV viral load was 316 copies/ml. Hepatitis C virus RNA was not detected. Chest X-radiography showed moderate cardiomegaly and bilateral interstitial infiltrates consistent with pulmonary edema. Blood cultures were drawn. The admitting diagnosis was of probable infective endocarditis with associated pulmonary edema. Trans-thoracic echocardiography showed mitral and tricuspid valvular regurgitation with moderate left ventricular function. Multiple mobile vegetations were demonstrated on the atrial side of the mitral valve on the transesophageal echocardiogram. Ultrasound of the abdomen revealed moderate splenomegaly.

The patient was started on flucloxacillin, benzylpenicillin and gentamicin intravenously pending blood culture results. Four out of four sets of blood cultures yielded a Gram-positive, catalase-negative coccus which was slow-growing. The organism failed to be identified using the API20 Strep system

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(bioMerieux) and was forwarded for molecular identification employing partial sequencing of the 16S rRNA gene. Sensitivity testing was performed using E-test methodology on Mueller-Hinton agar supplemented with 5% (v/v) sheep blood. The minimum inhibitory concentrations (MICs) of penicillin, methicillin, gentamicin, vancomycin and teicoplanin were 0.064, 1.0, 3.0, 3.0 and 0.5 mg/l, respectively. Antibiotic treatment was changed to benzylpenicillin (i.v., high dose) for six weeks and gentamicin (i.v.) for four weeks. The patient made a good recovery and was discharged home. At present, she is being followed at the cardiology outpatient unit and was free of recurrence of infection at nine months post-discharge.

Discussion

Given the relatively poor phenotypic identification obtained, molecular identification through polymerase chain reaction amplification and direct sequencing of a large but partial region of the 16S rRNA gene, corresponding to base position of approximately 257-1304 of *Stenotrophomonas maltophilia* 16S rRNA (GenBank Accession number A Y169434) was undertaken. As the isolated organism's closest phylogenetic neighbors were two species within the genus *Helcococcus*, which lay at 91-92% similarity, it was concluded that the isolated organism was a novel *Helcococcus*-like organism.

Helcococcus sp. is one of the many recently described catalase-negative, Gram-positive cocci (2), arranged as Gram-positive pairs and tetrads. It is facultatively anaerobic, and grows on blood agar producing pinpoint colonies which are usually non- or slightly alpha-hemolytic. The genus *Helcococcus* is identified using 16S rRNA gene sequencing techniques, and to date two species have been described: *Helcococcus kunzii* (5) and *Helcococcus ovis* (7). *Helcococcus kunzii*, first described in 1993 by Collins et al. (1), is an opportunist pathogen and is also recognized as part of the normal skin flora. *Helcococcus ovis*, described by Collins et al. in 1999 as a novel species, to date however has only been

described in sheep and its pathogenic potential is unclear (7).

In conclusion, we describe the case of an active injecting drug user with HIV infection who presented with endocarditis caused by a novel *Helcococcus*-like organism. As *Helcococcus kunzii* has been recognized previously as part of the normal flora of the skin, and the infection occurred in an active injecting drug user, the bacterium may have been endogenously acquired from the patient's own skin or normal oral flora. Molecular methods are an essential tool in the laboratory investigation of difficult cases of infective endocarditis.

References

1. Collins MD, Facklam RR, Rodrigues UM, Ruoff KL. Phylogenetic analysis of some *Aerococcus*-like organisms from clinical sources: Description of *Helcococcus kunzii* gen. nov., sp. nov. *Int J Syst Bacteriol* 1993;43:425-429
2. Facklam R, Elliott JA. Identification, classification and clinical relevance of catalase-negative, Gram-positive cocci, excluding the streptococci and enterococci. *Clin Microbiol Rev* 1995;8:479-495
3. Chagla AH, Borczyk AA, Facklam RR, Lovgren M. Breast abscess associated with *Helcococcus kunzii*. *J Clin Microbiol* 1998;36:2377-2379
4. Peel MM, Davis JM, Griffin KJ, Freedman DL. *Helcococcus kunzii* as sole isolate from an infected sebaceous cyst. *J Clin Microbiol* 1997;35:328-329
5. Caliendo AM, Jordan CD, Ruoff KL. *Helcococcus*, a new genus of catalase-negative, Gram-positive cocci isolated from clinical specimens. *J Clin Microbiol* 1995;33:1638-1639
6. Haas J, Jernick SL, Scardina RJ, Teruya J, Caliendo AM, Ruoff KL. Colonization of skin by *Helcococcus kunzii*. *J Clin Microbiol* 1997;35:2759-2761
7. Collins MD, Falsen E, Foster G, Monasterio LR, Dominguez L, Fernandez Garazabal JF. *Helcococcus ovis* sp. nov., a Gram-positive organism from sheep. *Int J Syst Bacteriol* 1999;49:1429-1432