Endophthalmitis Caused by *Enterococcus mundtii*

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*Enterococcus mundtii* has rarely been isolated from environmental or human sources. We report the identification of *E. mundtii* as a pathogen of human infectious disease by DNA sequencing of 16S rRNA and sodA genes in a case of endophthalmitis developed in a 66-year-old immunocompetent gardener.

**CASE REPORT**

A 66-year-old gardener presented with a 1-day history of blurred vision in the right eye. He had no history of ocular trauma, surgery, uveitis, or systemic disease. Vision in the right eye was limited to being able to count fingers, while vision in the left eye was 20/20 with no abnormality. Moderate conjunctival injection and 2+ anterior chamber cells were present in the right eye. The right fundus was hardly visible due to severe vitreous opacity, but extensive sheathing of retinal vessels and retinal hemorrhage could be seen in the superior quadrant.

He was afebrile, and standard blood tests and physical examination were unremarkable, except for a mild liver dysfunction due to regular alcohol consumption. Therefore, blood cultures were not performed. Systemic betamethasone (8 mg daily) and acyclovir (1,500 mg daily) doses were started with an initial diagnosis of acute retinal necrosis. While sheathing of retinal vessels gradually decreased, marked hypocupon and increased vitreous opacity were noted 2 days later.

With a provisional diagnosis of bacterial endophthalmitis, vitrectomy and intravenous imipenem (1 g daily) were immediately implemented, and systemic steroid and acyclovir administration was terminated. An infusion solution containing imipenem (5 μg/ml) and acyclovir (1,500 mg daily) doses were started with an initial diagnosis of acute retinal necrosis. While sheathing of retinal vessels gradually decreased, marked hypocupon and increased vitreous opacity were noted 2 days later.

The species identification of the enterococcal isolate was not conclusive by phenotypic methods. The isolate was identified as *Enterococcus faecium* by the API 20 Strep (bioMerieux, Marcy-l’Etoile, France), with the results of all panel tests consistent with the biochemical characteristics of *E. faecium*. However, nonmotility in semisolid agar and yellow pigmentation on 5% sheep blood agar suggested *Enterococcus mundtii* rather than *E. faecium* (1). The inability of API 20 Strep to indicate the possibility of *E. mundtii* may have resulted from the absence of this species in the API database (version 6.0). Therefore, we compared the API results for the isolate with the reported characteristics of *E. mundtii* (9). Of the 20 tests included in the API 20 Strep, the isolate did not ferment raffinose, while the majority of the reported strains did. However, other biochemical test results for the isolate were highly consistent with those for other *E. mundtii* strains. Thus, the biochemical characteristics that can be tested by the API 20 Strep may not distinguish *E. mundtii* from *E. faecium*. Accordingly, DNA sequencing of the 16S rRNA gene using a pair of primers corresponding to the nucleotide sequence (sense nucleotides, 4 to 25; antisense, 1174 to 1194) of the *Escherichia coli* 16S rRNA gene (GenBank-EMBL accession number J01859) was undertaken (10). The 1,167-bp amplified fragment had the highest degree of sequence identity (99.9%, with 1 base mismatch) with the *E. mundtii* 16S rRNA gene (GenBank-EMBL accession number AB066266) by a homology search using BLAST software (National Center for Biotechnology Information, Bethesda, Md.). However, the 16S rRNA gene sequence of the isolate also showed a high sequence identity (99.1%, 11 base mismatches) with the *E. faecium* 16S rRNA gene (GenBank-EMBL accession number AJ17257) as reported by Patel et al. (11). Therefore, DNA sequencing of the sodA gene,
which was reported to be more discriminative for species identification of enterococci than the 16S rRNA gene (12), was undertaken. The sodA gene sequence of the isolate had the highest identity to that of E. mundtii (97%) compared to that of other Enterococcus species (less than 85%), confirming that the isolate was E. mundtii.

Poyart et al. (12) reported the presence of two major clusters, the E. faecium group and the E. avium group, within the phylogenetic tree of enterococcal species, which were established by sodA gene sequences. In addition to E. mundtii, E. faecium, E. durans, and E. hirae belong to the E. faecium group. The 16S rRNA gene sequences exhibit more than 99% sequence identity within each group (12), which was also observed between the isolate from our case and E. faecium. Other yellow-pigmented species, including E. casseliflavus, E. flavescens, and E. sphaericus, do not belong to the E. faecium group and are phylogenetically more distant from E. mundtii than E. faecium.

E. mundtii was discovered in 1986 as nonmotile, yellow-pigmented enterococci isolated from cow teats, the hands of milkers, soil, and plants (1). The species has rarely been isolated from environmental (7) or human sources (4) since then. Misidentification by commercial biochemical assays, which also happened in our case, may account for the scarcity of reports on the organism (8). With regard to the pathogenicity of E. mundtii in humans, no clear evidence of virulence has been undertaken. The sodA gene sequence of the isolate had the sequence identity within each group (12), which was also observed between the isolate from our case and E. faecium. Other yellow-pigmented species, including E. casseliflavus, E. flavescens, and E. sphaericus, do not belong to the E. faecium group and are phylogenetically more distant from E. mundtii than E. faecium.

In conclusion, E. mundtii was identified as a pathogen of human infectious disease by DNA sequencing of the 16S rRNA and sodA genes in a case of endophthalmitis. The correct identification of the minor enterococcal species by molecular analysis in more cases of human infection may reveal its clinical significance.

REFERENCES