

Rothia dentocariosa Septicemia without Endocarditis in a Neonatal Infant with Meconium Aspiration Syndrome

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Received 9 July 2003/Returned for modification 29 July 2003/Accepted 5 May 2004

***Rothia dentocariosa*, a gram-positive coccoid- to rod-shaped bacterium with irregular morphology, is a rare cause of bacteremia in patients without endocarditis. We report the first case of *R. dentocariosa* septicemia without endocarditis, which occurred in a neonatal infant with meconium aspiration syndrome.**

CASE REPORT

A female infant was delivered at term by spontaneous vaginal delivery with a birth weight of 3,500 g. Intrapartum monitoring revealed no evidence of fetal distress. Soon after delivery, the infant was admitted to an intensive care unit because of a meconium-stained anus, nonprojectile vomiting, and poor sucking and oral intake. On admission, her temperature was less than 36.0°C, her pulse was 148 beats/min, and her respiratory rate was 52 breaths/min. Her white blood cell count was 35.5×10^9 /liter, with 90% neutrophils, 5% lymphocytes, and 5% monocytes. The prothrombin time and the activated partial thromboplastin time were 20.7 and 54.6 s, respectively. Urine and blood were submitted for culture. Chest radiography showed patchy infiltrates and coarse streaking of the right lung field.

Meconium aspiration syndrome and sepsis were diagnosed, and intravenous fluids, ampicillin-sulbactam, and netilmicin were administered. On day 2 in the hospital, the fibrinogen degradation product was 2.79 μ g/ml, the D-dimer was 1.56 μ g/ml, and antithrombin III was 43.5%. Because of a suspicion of disseminated intravascular coagulopathy, fresh frozen plasma and antithrombin III were infused, and cefotaxime was added. On the fourth day of admission, the blood yielded a pure culture of a gram-positive bacillus, which was identified as *Rothia dentocariosa* by the API CORYNE system (bioMérieux, Marcy l'Etoile, France) with code number 7050125 (99.9%). On the ninth day of admission, the leukocyte count (8.7×10^9 /liter) and D-dimer value were normal. The infant was discharged on the 15th day of admission in good health with no detectable sequelae.

R. dentocariosa is an aerobic or facultatively anaerobic, non-spore-forming, nonmotile, pleomorphic, gram-positive, coccoid- to rod-shaped bacterium (8). Correct identification is difficult, and chemotaxonomic investigation is recommended. API CORYNE test strips are useful and typically yield codes 7050125

or 7052125 (2, 7). This test may be the most widely used and generally accepted method for the identification of the organism in a routine hospital laboratory. It was necessary to confirm the identification of the organism by an alternative method, because *R. dentocariosa* is an unusual source of infection in the neonatal infant and we could find no reports in the literature supporting vaginal colonization. We suspected the vaginal tract as the source of infection, but we could not validate the origin because the mother was already discharged.

Analysis of the cellular fatty acid composition by the Microbial Identification System (Microbial ID, Inc., Newark, Del.) revealed that the majority of the cellular fatty acids were of two types, anteiso-C15:0 (anteisopentadecanoic acid) and anteiso-C17:0 (anteisoheptadecanoic acid), but they were not clearly identified by the MIDI database and we could not verify the isolate as *R. dentocariosa*. The identity of the organism was confirmed by sequencing the 16S rRNA gene (rDNA).

After PCR amplification of the 16S rDNA with the primers 27F (5'-AGA GTT TGA TCM TGG CTC AG-3') and 1492R (5'-TAC GGY TAC CTT GTT ACG ACT T-3'), the purification amplicon was ligated into the pGEM-T Easy vector (Promega, Madison, Wis.). The ligation mixture was transformed into *Escherichia coli* DH5 α competent cells. The recombinant plasmid DNA was used as a template for sequencing. Sequencing was conducted with ChDC-GEM-F (5'-TTC CCA GTC ACG ACG TTG TAA AA-3'), Seq-F1 (5'-CCT ACG GGA GGC AGC AG-3'), Seq-R2 (5'-GAC TAC CAG GGT ATC TAA TCC-3'), F16 (5'-TAG ATA CCC YGG TAG TCC-3'), and ChDC-GEM-R (5'-GTG TGG AAT TGT GAG CGG ATA AC-3') primers, a Big Dye Terminator Cycle Sequencing kit (Applied Biosystems, Foster City, Calif.), and an ABI PRISM 310 genetic analyzer (Applied Biosystems). All sequences were compared with similar sequences of the reference organisms by using BLAST (a genome database of the National Center for Biotechnology Information). Our sequences showed 99% conformity with the 16S rDNA sequences of *R. dentocariosa*, such as *R. dentocariosa* ChDC OS32 (GenBank accession number AF543284) and *R. dentocariosa* ATCC BAA-907 (accession number AY546095).

As a common inhabitant of the human oral cavity, *R. dentocariosa* has rarely been reported to cause significant infection in humans (12). The serious infections ascribed to this organ-

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ism are endocarditis (1, 4–6, 10, 12), pneumonia (11, 13), endophthalmitis (9), and peritonitis (3), with endocarditis, mainly in adults, being the most common. To our knowledge, the present case is the first of *R. dentocariosa* sepsis in a patient with meconium aspiration syndrome associated with neither bacterial endocarditis nor problems in the oral cavity or heart.

Nucleotide sequence accession number. The GenBank accession number for the 16S rDNA sequence of the strain of *R. dentocariosa* identified in the present study is AY594189.

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