9-2015

Recurrent *Streptococcus equi* subsp. *zooepidemicus* Bacteremia in an Infant

Joshua R. Watson  
*Ohio State University*

Amy Leber  
*Ohio State University*

Sridhar Velineni  
*University of Kentucky, sridharvelineni@uky.edu*

John F. Timoney  
*University of Kentucky, jtimoney@uky.edu*

Monica I. Ardura  
*Ohio State University*

[Click here to let us know how access to this document benefits you.](https://uknowledge.uky.edu/gerc_facpub)

Follow this and additional works at: [https://uknowledge.uky.edu/gerc_facpub](https://uknowledge.uky.edu/gerc_facpub)

Part of the [Large or Food Animal and Equine Medicine Commons](https://uknowledge.uky.edu/gerc_facpub)

Repository Citation


[https://uknowledge.uky.edu/gerc_facpub/9](https://uknowledge.uky.edu/gerc_facpub/9)

This Article is brought to you for free and open access by the Gluck Equine Research Center at UKnowledge. It has been accepted for inclusion in Gluck Equine Research Center Faculty Publications by an authorized administrator of UKnowledge. For more information, please contact UKnowledge@lsv.uky.edu.
Recurrent *Streptococcus equi subsp. zooepidemicus* Bacteremia in an Infant

Notes/Citation Information
Published in *Journal of Clinical Microbiology*, v. 53, no. 9, p. 3096-3099.

Copyright © 2015, American Society for Microbiology. All Rights Reserved.

The copyright holders have granted the permission for posting the article here.

Digital Object Identifier (DOI)
http://dx.doi.org/10.1128/JCM.01306-15

This article is available at UKnowledge: https://uknowledge.uky.edu/gerc_facpub/9
Recurrent *Streptococcus equi* subsp. *zooepidemicus* Bacteremia in an Infant

Joshua R. Watson, Amy Leber, Sridhar Velineni, John F. Timoney, Monica I. Ardura

Department of Pediatrics, Infectious Diseases and Immunology, Nationwide Children's Hospital, and The Ohio State University, Columbus, Ohio, USA; Departments of Pathology and Laboratory Medicine, Nationwide Children's Hospital, Columbus, Ohio, USA; Gluck Equine Research Center, University of Kentucky, Lexington, Kentucky, USA

We describe a case of an infant with recurrent bacteremia caused by *Streptococcus equi* subsp. *zooepidemicus*, likely transmitted from mother to infant. Our case highlights the importance of an epidemiological history and molecular diagnostics in ascertaining insights into transmission, pathogenesis, and optimal management.

CASE REPORT

A male infant was born via spontaneous vaginal delivery to a gravida 1, para 1 female at 32 weeks and 6 days of gestation because of preterm labor with Apgar scores of 7 at 1 min and 8 at 5 min. The mother’s group B streptococcal colonization status was unknown, and she received 2 doses of ampicillin prior to delivery. Artificial rupture of membranes occurred approximately 1 h prior to delivery. Placental pathology was normal. The infant required continuous positive airway pressure for respiratory distress and received 1 dose of surfactant. He was admitted to the neonatal intensive care unit at the delivery hospital and received ampicillin and gentamicin until a blood culture was negative at 48 h. On day of life (DOL) 12, the infant developed apnea, bradycardia, and hypoxemia. Physical examination revealed poor perfusion, poor tone, and skin erythema on the right side of his neck, chest, and abdomen. Neck ultrasound demonstrated parotitis and cellulitis, and blood culture yielded Gram-positive cocci identified by the outside hospital as group C streptococcus (GCS). He received intravenous ampicillin for 10 days with clinical improvement and clearance of bacteremia. He was discharged home on DOL 23.

The infant did well until DOL 28, when his parents noted nasal congestion, poor feeding of expressed human milk and infant formula, and decreased activity. On DOL 29, he developed altered breathing and central cyanosis after a feeding. Transient skin erythema on the right side of the neck was also noted. Review of systems was negative for fever, cough, emesis, and seizures. At the Nationwide Children’s Hospital emergency department, he developed apnea, bradycardia, and hypoxemia requiring intubation and mechanical ventilation. Laboratory studies and cultures were obtained, and empirical ampicillin and cefotaxime administration was initiated. In the pediatric intensive care unit, he required intravenous fluid resuscitation, vasopressors, and stress dose corticosteroids for hypotension and poor perfusion. A complete blood count, hepatic panel, and cerebrospinal fluid analysis were unremarkable. Chest X-ray, echocardiogram, and computed tomography of the head and neck were normal. Rhinovirus was detected in a nasopharyngeal sample by PCR (1). Peripheral blood cultures were obtained, and the aerobic blood culture was positive for Gram-positive cocci in pairs and chains at 14 h of incubation (BactAlert FN; bioMérieux, Durham, NC). Initial subculture revealed colonies that were 1 to 2 mm in diameter with a large zone of beta-hemolysis on sheep blood agar (Fig. 1) and were identified as GCS based on a negative catalase test and a latex agglutination result positive for group C antigen (Streptex; Remel, Lenexa, KS). The initial blood isolate from the outside hospital was also obtained, and the identification of GCS was confirmed by the aforementioned methods. Results of antimicrobial susceptibility testing (2) of both isolates were as follows: susceptible to penicillin (MIC, 0.03 µg/ml; Etest; bioMérieux, Durham, NC), resistant to clindamycin (disk diffusion), and a rifampin MIC of 0.023 µg/ml (Etest). Culture from the endotracheal tube aspirate also yielded rare GCS; urine and cerebrospinal fluid cultures were negative. The infant was extubated on hospital day 6 and demonstrated continued clinical improvement. He had documented clearance of bacteremia within 24 h and received 18 days of intravenous ampicillin. Evaluation for primary immunodeficiency was negative.

Additional history revealed that 48 h prior to the patient’s first episode of GCS sepsis, his mother had developed fever and malaise requiring hospitalization. Her blood and urine cultures were negative, and her symptoms resolved. Days before the patient’s second episode of GCS sepsis, the mother developed pharyngitis. A throat culture yielded GCS, for which she was prescribed azithromycin. Epidemiological history revealed that the family lived on a farm in Ohio where the father cared for approximately 100 horses, none of which were ill.

Throat cultures obtained from both parents during the second hospitalization were negative for GCS carriage. The infant and his parents were treated with a 2-day course of rifampin prior to hospital discharge. At a 6-week follow-up appointment, the infant was clinically well. Throat cultures from the infant and father at...
that time were negative. The mother’s throat culture yielded an isolate that was identified as described above as GCS susceptible to penicillin (MIC, 0.03 μg/ml), resistant to clindamycin (disk diffusion), and with a rifampin MIC of 0.023 μg/ml. Concern that maternal GCS pharyngeal colonization could serve as a source of re-exposure of the infant to GCS prompted treatment of the mother with oral penicillin for 10 days combined with rifampin during the final 4 days. At an appointment 3 months following the second hospitalization, the infant continued to do well and had negative throat and rectal cultures. Maternal throat culture was also negative at that time. At 16 months of age, the infant has had no further recurrences of GCS bacteremia or sepsis.

Further phenotypic characterization was performed with the two blood isolates from the infant and the throat isolate from the mother (from the 6-week follow-up appointment). The isolates were identified as Streptococcus equi subsp. zooepidemicus by Vitek 2 (bioMérieux, Durham, NC) by using the Gram-positive identification card with 99% probability and excellent identification confidence. The isolates fermented lactose and sorbitol but not trehalose, consistent with S. equi subsp. zooepidemicus (3). Matrix-assisted laser desorption ionization–time of flight mass spectrometry (Vitek MS; bioMérieux, Durham, NC) was performed and identified all of the isolates as S. equi subsp. zooepidemicus with a confidence value of 99.9 (Vitek MS IVD version 2.0, unclaimed identification).

Sequencing of the 16S rRNA genes (MicroSEQ 500 16S rDNA Bacterial Identification System; Life Technologies, Grand Island, NY) of the three isolates revealed identical 499-bp consensus sequences. Comparison to sequences available in databases at the National Center for Biotechnology Information, MicroSEQ v2.1, and SmartGene (Lausanne, Switzerland) showed that our isolates clustered closely with S. equi subsp. equi and zooepidemicus, but the sequence length was not sufficient to reliably distinguish between the two subspecies.

Analysis of the isolates by pulse-field gel electrophoresis (PFGE) with Smal revealed that the two blood isolates from the infant were indistinguishable from one another. The PFGE pattern of the isolate from the mother’s throat culture had two bands different from the infant’s blood isolates, a difference that may be explained by a single genetic event (4). The PFGE results indicate that the mother’s isolate was closely related to the infant’s isolates and was probably the same strain.

Additional molecular characterization of the isolates is shown in Table 1. The S. equi subsp. zooepidemicus _szm_ and _szp_ genes were detected and sequenced (5) and were identical in the three isolates. Molecular detection of S. equi subsp. _eqbN_ and _se18.9_ was also attempted (6, 7). Absence of _eqbN_ and _se18.9_ (as found in S. equi subsp. _equi_), together with the presence of identical _szm_ and _szp_ sequences typical of S. equi subsp. _zooepidemicus_, in all three isolates confirmed the identification and supported the conclusion that the isolates from the infant and the mother were the same strain of S. equi subsp. _zooepidemicus_. Multilocus sequence typing (MLST) (5) revealed that all three isolates had the same novel sequence type, 190 (ST190) (http://pubmlst.org/szooepidemicus/). As may be seen in S. equi subsp. _zooepidemicus_, _szeN_ and _szeP_, but not _szeF_, were detected by PCR (8).

This report describes, to our knowledge, the first case of recurrent S. equi subsp. _zooepidemicus_ infection in a young infant. Epidemiological history prompted a detailed molecular characterization that identified the bacterial isolates as S. equi subsp.

---

**TABLE 1** Molecular characterization of _S. equi_ subsp. _zooepidemicus_ clinical isolates from infant and mothera

<table>
<thead>
<tr>
<th>Source of bacterial isolate</th>
<th>MLST result</th>
<th>S. equi subsp. <em>zooepidemicus</em></th>
<th>S. equi subsp. <em>equi</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>Infant’s blood</td>
<td>ST190</td>
<td><em>SzP</em> protein&lt;sup&gt;b&lt;/sup&gt; 190 <em>SzM</em> protein&lt;sup&gt;c&lt;/sup&gt; A3(b), B2 tandem repeats Absent Present Present Absent Absent</td>
<td></td>
</tr>
<tr>
<td>Initial episode</td>
<td>ST190</td>
<td>N2HV5, 5PEPK A3(b), B2 tandem repeats Absent Present Present Present Absent</td>
<td></td>
</tr>
<tr>
<td>Recurrent episode</td>
<td>ST190</td>
<td>N2HV5, 5PEPK A3(b), B2 tandem repeats Absent Present Present Present Absent</td>
<td></td>
</tr>
<tr>
<td>Mother’s throat at 6-wk follow-up</td>
<td>ST190</td>
<td>N2HV5, 5PEPK A3(b), B2 tandem repeats Absent Present Present Present Absent</td>
<td></td>
</tr>
</tbody>
</table>

<sup>a</sup> _SzP_, protective protein; _SzM_, M-like protein; _szeF_, _szeN_, and _szeP_, superantigen genes; _eqbN_, equibactin gene of _S. equi_ subsp. _equi_; _se18.9_, gene for factor H binding protein of _S. equi_ subsp. _equi_; _N2HV5_, _N2HV5_, N-terminal _N2_ and hypervariable _5_ sequence motifs; _5PEPK_, five carboxy-terminal _PEPK_ repeats.

<sup>b</sup> The _N_, _HV_, and _PEPK_ regions of _SzP_ are variable among isolates of _S. equi_ subsp. _zooepidemicus_. The genes were completely sequenced and were identical in all three isolates (18).

<sup>c</sup> The _A_ and _B_ regions of _SzM_ are variable among isolates of _S. equi_ subsp. _zooepidemicus_. The genes were completely sequenced and were identical in all three isolates (19).
S. equi subsp. zooepidemicus and its clonal derivative S. equi subsp. equi share high DNA homology but differ in their pathogenicity (9). S. equi subsp. equi is the causative agent of a highly contagious respiratory tract infection of horses called strangles. S. equi subsp. zooepidemicus, in contrast, is a commensal organism of equine mucosal surfaces that may cause invasive infections in horses during times of viral infection, heat stress, or tissue injury (8, 9).

The production of superantigens may be important in the pathogenesis of S. equi subsp. zooepidemicus infections. Similar to Streptococcus pyogenes, three genes encoding superantigens (szeF, szeN, and szeP) have been described in the S. equi subsp. zooepidemicus genome (8). Of 165 S. equi subsp. zooepidemicus isolates examined by Paillot et al. (8), one or more superantigens were detected in 49%. The three superantigens possess a characteristic amino acid sequence signature, and their amino acid sequences are 34 to 59% identical to those of superantigens produced by S. pyogenes. The presence of szeN and szeP was associated with mitogenic activity, but the presence of szeF was not. In our case, both szeN and szeP, but not szeF, were detected.

Cases of S. equi subsp. zooepidemicus infections in adults with close and continuous contact with horses and dogs have been described previously (10, 11). A search of the MEDLINE database for English-language publications of infections in infants ≤3 months of age with the key words “Group C Strep*,” “S. equi,” and “S. zooepidemicus” yielded three prior reports that identified S. equi subsp. zooepidemicus causing meningitis and sepsis (12–14). Two of the cases occurred during outbreaks related to the consumption of unpasteurized cow’s milk but without confirmation of infection in family members of the infants (12, 13). Another report of S. equi subsp. zooepidemicus infection described a 14-week-old infant whose family owned a horse (15). In that case, the mother had a lower respiratory tract infection 3 weeks before the infant’s illness, but she was not tested for S. equi subsp. zooepidemicus colonization. In the case of our infant, results of molecular analysis supported mother-to-infant transmission. Although we questioned the possibility of an equine reservoir, we were unable to test the horses to confirm a zoonosis. No cases of recurrent S. equi subsp. zooepidemicus infection during the first 3 months of life were found in the published literature.

Because of concern that the patient’s mother was a chronic pharyngeal carrier of S. equi subsp. zooepidemicus, she was treated with penicillin and rifampin according to guidelines for chronic S. pyogenes carriage (16, 17). We believed this was a necessary intervention given the infant’s recurrent episodes of sepsis, prematurity, and immature immune system. This strategy appeared to be successful at least temporarily, as evidenced by a negative maternal throat culture at the 3-month follow-up visit and lack of disease recurrence in the infant.

In conclusion, this report describes the first case of recurrent bacteremia in a young infant caused by S. equi subsp. zooepidemicus, likely transmitted from mother to infant. Molecular characterization of bacterial isolates was essential to determine the precise identity of the pathogen and to identify modifiable risk factors for recurrent infection. Additionally, molecular techniques detected superantigen genes that may explain the organism’s pathogenicity. Clinicians should be aware that S. equi subsp. zooepidemicus may cause invasive infections in young infants and that recurrence is possible.

**Nucleotide sequence accession numbers.** The nucleotide sequences of the S. equi subsp. zooepidemicus szm and szp genes have been deposited in the GenBank database and assigned accession numbers KP735516 (szm) and KP735515 (szp).

**ACKNOWLEDGMENT**

We thank Susi Miller, medical librarian at Nationwide Children’s Hospital, for her assistance with the literature search.

**REFERENCES**


