Microbiology of Postoperative Infections after Third Molar Surgery: A Systematic Review of Case Reports

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ABSTRACT

Background: Antibiotic treatment for a clinical infection should be based on a thorough knowledge of the causative organisms involved in the infection. Methods used to evaluate microbiology should provide a comprehensive and accurate assessment of the microbiological spectrum. Currently, there is limited evidence on the microbiology of postoperative infection after third molar surgery, leading to inappropriate antibiotic prescription.

Aim: The objective of this review was to summarize the current documented evidence on bacteriology of postoperative infection samples after third molar surgery with a systematic search of the literature.

Results: A systematic search was performed in three databases (PubMed, Web of Science, and Medline-Ovid) on March 17, 2017 with no filters applied. After exclusion of duplicates, 142 records were screened, based on predetermined exclusion criteria and finally, 11 case reports recording microbiological data for clinical infection samples were selected. The most common genus of organisms isolated from third molar infections was Streptococcus. Anaerobic species dominated in cases where prior antibiotic treatment was initiated. However, documented microbiological data are only culture based and predominantly report fascial space infections after third molar surgery.

Conclusion: Culture-based methods may not be accurately representing the true microbial profile of postoperative infections. There is an urgent need for comprehensive microbiological data employing next-generation sequencing techniques on postoperative infections to prevent inappropriate antibiotic prescription.

Clinical significance: Prescribing broad spectrum antibiotics to treat postoperative infections with inadequate information on the microbiology is a questionable clinical practice that propagates antibiotic resistance. Clinicians should utilize recent advances in microbiological diagnosis to reduce unsuitable antibiotic prescription.

Keywords: Case reports, Extraction, Review, Surgical wound infection, Third molar.

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BACKGROUND

Odontogenic infections are infections arising from teeth that have the potential to spread locally and ultimately generate complications systemically. Infections associated with second and third molar teeth are the second most common causes of deep neck infection. The potential of infections following third molar extractions to spread into adjoining anatomical spaces, obstruct the airway, and create life-threatening conditions has been well documented. In addition, the occurrence and enhanced aggressiveness of these infections in systemically compromised patients (diabetes, human immunodeficiency virus) highlight the need for rapid microbiological diagnosis for possible emergency management of such infections.

The rate of infection reported after extraction of third molars is less than 5%. In a study examining the need for surgical and medical management of postoperative infections, 71.8% required antibiotic treatment. Hence, when managing these postoperative infections, the appropriate prescription of antibiotics clinically should comprise a thorough understanding of the likely organisms involved in the infection, which in turn will avoid the prescription of unsuitable antibiotics, reducing the possibility of developing antibiotic resistance.

The purpose of this review was to evaluate the present evidence on the microbiology of postoperative infections after third molar surgery through a systematic search of the literature.

RESULTS

Three databases, PubMed, Web of Science, and Medline-Ovid, were searched on March 17, 2017 using the following keywords: (Third Molar) and (Extraction or Surgery) and (Bacteremia or Bacteria or Microbiome). After exclusion of duplicates among the three databases searched, articles were excluded based on the following criteria: No microbiological findings related to third molar infections, studies reporting the microbiology of pericoronar inflammation and localized alveolar osteitis (dry socket), studies evaluating transient bacteremia following third molar surgery, reviews, comments, and others. Search strategy and results is depicted in Flow Chart 1.
The detailed search results and all excluded articles with the specified reasons for each database is available on request (Supplementary material, S1). Data extraction was performed from the selected articles for: Author/year of publication, whether antibiotic prophylaxis was given before surgery, type of sample collected, the site and time of sample collection, bacterial isolation method, and microbiological findings.

Eleven studies (2–5, 15–21) were identified which isolated bacteria from the postoperative infection samples following third molar extractions (Table 1).

Case reports documenting microbiological data from postoperative purulent infections from 1990 until 2013 report *Streptococcus* as the most frequently identified

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Table 1: Case reports with documented microbiological data of postoperative infection after third molar extraction

<table>
<thead>
<tr>
<th>Author</th>
<th>Antibiotic</th>
<th>Sample</th>
<th>Site/space</th>
<th>Time of sample collection</th>
<th>Method</th>
<th>Bacteria</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yun et al5</td>
<td>No</td>
<td>Pus</td>
<td>Periauricular buccal</td>
<td>Baseline 15 days</td>
<td>Culture</td>
<td><em>Pseudomonas aeruginosa</em></td>
</tr>
<tr>
<td>Moses et al3</td>
<td>No</td>
<td>I/oral</td>
<td>Pterygomaseteric</td>
<td>1 week</td>
<td>Culture</td>
<td><em>Streptococcus anginosus, Streptococcus viridans, coagulase-negative</em></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pus</td>
<td></td>
<td></td>
<td></td>
<td><em>Staphylococci</em> gram-negative, pleomorphic bacilli, Gram-positive cocci</td>
</tr>
<tr>
<td></td>
<td></td>
<td>E/oral</td>
<td></td>
<td></td>
<td></td>
<td><em>S. anginosus</em></td>
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<td></td>
<td></td>
<td>TMJ fluid</td>
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<td></td>
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<tr>
<td>Ricalde et al15</td>
<td>No</td>
<td>Pus</td>
<td>Facial Periorbital Submandibular Mediastinal</td>
<td>2 days</td>
<td>Culture</td>
<td>Group I beta-hemolytic <em>Streptococcus</em></td>
</tr>
<tr>
<td>Sakkas et al4</td>
<td>No</td>
<td>Pus</td>
<td>Orbital Submandibular</td>
<td>1 week</td>
<td>Culture</td>
<td><em>Streptococcus intermedius</em></td>
</tr>
<tr>
<td>Al-Muharraqi et al16</td>
<td>No</td>
<td>Pus</td>
<td>Blood Submandibular</td>
<td>2 days</td>
<td>Culture</td>
<td>Alpha-hemolytic *Streptococci, Staphylococci, anaerobic Gram-positive cocci</td>
</tr>
<tr>
<td>de Oliveira Neto et al2</td>
<td>Yes</td>
<td>Pus</td>
<td>Temporal pterygomandibular</td>
<td>1 week</td>
<td>Culture</td>
<td><em>Prevotella oralis, Bacteroides ureolyticus, Peptostreptococcus micros, Parvimonas mira, Gemella morbilorum</em></td>
</tr>
<tr>
<td>Yuvaraj et al17</td>
<td>No</td>
<td>Pus</td>
<td>Submandibular submental Pterygomandibular sublingual Anterior chest wall</td>
<td>10 days</td>
<td>Culture</td>
<td><em>Streptococcus sanguis, Streptococcus mitis, Peptostreptococci, Propionibacterium</em></td>
</tr>
<tr>
<td>Hobson et al18</td>
<td>No</td>
<td>Pus</td>
<td>Left pterygoid muscle Brain</td>
<td>2 weeks</td>
<td>Culture</td>
<td><em>Streptococcus viridans, Nongroupable Streptococci</em></td>
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<tr>
<td></td>
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<td></td>
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<td></td>
<td></td>
<td>Recurrent abscess at day 13</td>
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<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
<td><em>Bacteroides fragilis, Veillonella species, Campylobacter gracilis, Prevotella buccae</em></td>
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<td></td>
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<td></td>
<td></td>
<td>Most common <em>Fusobacterium</em></td>
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<td></td>
<td></td>
<td><em>Prevotella</em></td>
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<td></td>
<td><em>Peptostreptococcus</em></td>
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<td></td>
<td></td>
<td></td>
<td>Group I <em>Streptococci</em></td>
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<tr>
<td>Figueiredo et al19</td>
<td>Yes</td>
<td>Pus</td>
<td>Distal area of second molar</td>
<td>After 1 week 16–79 days</td>
<td>Culture</td>
<td><em>Most common Fusobacterium</em></td>
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<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td><em>Prevotella</em></td>
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<td></td>
<td><em>Peptostreptococcus</em></td>
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<td></td>
<td>Group I <em>Streptococci</em></td>
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<tr>
<td>Leavitt and Van Ess20</td>
<td>No</td>
<td>Pus</td>
<td>Mandibular third molar extraction site Masseteric pterygomandibular extension to the left deep temporal region and the skull base</td>
<td>1–3 days</td>
<td>Culture</td>
<td>Coagulase-negative <em>Staphylococcus, Group III Streptococcus, Acinetobacter baumannii</em></td>
</tr>
</tbody>
</table>
A genus in all cases where the patient did not have a recent antibiotic treatment/prophylaxis. In two cases, one in which the patient had a prophylactic treatment with amoxicillin (2) and the other in which amoxicillin was prescribed on onset of symptoms (20), the pus cultures were similar, showing the presence of *Fusobacterium, Prevotella,* and *Peptostreptococcus.*

One study (5) classically deviated from the results with the presence of *Pseudomonas aeruginosa* in the clinical infection samples with the patient in this case report suffering from uncontrolled diabetes mellitus. Recurrent abscess showed a distinct microbiological picture with the predominance of *Bacteroides* and *Prevotella.*

With regard to the studies that cultured the postoperative infection after third molar surgery, all the infections subsided with incision and drainage along with antibiotic treatment, with *Clindamycin* being the most commonly used.

**DISCUSSION**

The results of this review of case reports identify *Streptococcus* as the most isolated bacterial genus from postoperative infectious discharge after third molar surgery. Aside from the third molar infections, *Streptococcus* is also the most frequently isolated organism from odontogenic infections,*22,33* as well as from pericoronitis.*24,25* *Streptococcus* is an oral commensal microorganism commonly associated with a healthy oral cavity.*26,27* The presence of *Streptococcus* in infection samples might not represent the causative organisms of an infection, and might be a depiction of the culturing techniques employed to identify organisms. However, the limitations of culture-based techniques to identify microorganisms in samples have been questioned by extensive next-generation sequencing research. Majority of the bacteria are now proved to be uncultivable and hence a culture-based assessment of microbiology might be providing biased evidence to a clinician.*28* Two techniques that may be used to provide comprehensive microbiological information to a clinician are 16S ribosomal ribonucleic acid (rRNA) gene sequencing and shotgun metagenomic sequencing, which have been extensively employed in oral microbiome studies.*28,29* The 16S rRNA gene sequencing identifies even uncultivable bacteria from clinical specimens by amplifying a specific gene sequence which is common to the bacterial kingdom, however, unique to specific bacteria. Shotgun metagenomics amplifies all the gene content from a clinical sample and can help identify causative bacteria including additional genes and functions (like antibiotic resistance). This information is critical in the clinical decision of antibiotic prescription and may help in curbing the widespread and rampant use of broad spectrum antibiotics.

From the results, it is evident that most of the infections are reported within a period of 10 days and are resolved by rescue measures. Hence, it might be prudent method to monitor patients closely after extractions and treat with antibiotics based on microbiological data if and when needed, as opposed to prophylactic prescription of antibiotics. The efficiency of antibiotics in preventing postoperative infections after third molar extractions has been thoroughly evaluated by previous randomized controlled trials. The Cochrane review suggests judicious use of antibiotics and restricting antibiotic use to patients at risk.*30* In the current systematic review, the presence of an altered microflora and the predominance of anaerobic species could be identified in patients pretreated with amoxicillin. This result is expected, as the spectrum of amoxicillin would have resulted in selection toward the anaerobic species. Amoxicillin is the preferred antibiotic worldwide among dentists.*31-50* Numerous randomized controlled trials have investigated the effectiveness of amoxicillin use in preventing postoperative infections after third molar surgery.*51-57* However, a summary of the evidence presented in these studies indicates that the solo use of amoxicillin might not be effective in preventing infections.*58* Moreover, there is recent evidence utilizing next-generation sequencing techniques that the use of amoxicillin is associated with a prolonged alteration in the human microflora in healthy volunteers.*26,29*

**CLINICAL SIGNIFICANCE**

Prescription of broad spectrum antibiotics in third molar surgery to prevent infections with inadequate information on the causative organisms should be reassessed. The questionable efficacy of the most preferred antibiotic (amoxicillin), possible long-term effects on the microflora, and the one-dimensional (culture-based) assessment of postoperative infections should alert clinicians. Microbiological evidence (utilizing next-generation sequencing techniques) from case reports reporting postoperative infections might build up an evidence base for clinicians in developing treatment guidelines for postoperative infections instead of resorting to broad spectrum antibiotic use. Development of novel techniques for rapid microbiological diagnosis may diminish the time factor in microbiological diagnosis, aiding in making clinical decisions.

**CONCLUSION**

Considering the limited information on the microbiology of postoperative infection, future research and case reports in third molar infections should utilize
next-generation sequencing techniques to identify the microbiome of postoperative infections.

REFERENCES


32. Dar-Odeh NS, Abu-Hammad OA, Khraisat AS, El Maaytah MA, Shehabi A. An analysis of therapeutic, adult antibiotic