

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.¹ 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.²⁻⁴ 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.⁵

The rate of infection reported after extraction of third molars is less than 5%.⁶⁻¹⁴ In a study examining the need for surgical and medical management of postoperative infections, 71.8% required antibiotic treatment.¹ 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.

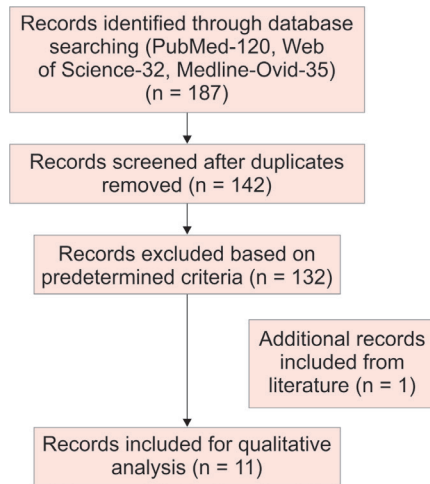
The purpose of this review was to evaluate the present evidence on the microbiology of postoperative infections after third molar surgery through a systematic search of the literature.

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 pericoronal 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.

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Flow Chart 1: Search strategy and results

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

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

Author	Antibiotic	Sample	Site/space	Time of sample collection	Method	Bacteria
Yun et al ⁵	No	Pus blood	Periauricular buccal	Baseline 15 days	Culture	<i>Pseudomonas aeruginosa</i>
Moses et al ³	No	I/oral Pus E/oral TMJ fluid	Pterygomasseteric	1 week	Culture	I/oral <i>Streptococcus anginosus</i> , <i>Streptococcus viridans</i> , coagulase-negative Staphylococci gram-negative, pleomorphic bacilli, Gram-positive cocci E/oral <i>S. anginosus</i>
Ricalde et al ¹⁵	No	Pus	Facial Periorbital Submandibular Mediastinal	2 days	Culture	Group I beta-hemolytic <i>Streptococcus</i>
Sakkas et al ⁴	No	Pus	Orbital	1 week	Culture	<i>Streptococcus intermedius</i>
Al-Muharraqi et al ¹⁶	No	Pus Blood	Submandibular	2 days	Culture	Alpha-hemolytic <i>Streptococci</i> , <i>Staphylococci</i> , anaerobic Gram-positive cocci
de Oliveira Neto et al ²	Yes	Pus	Temporal pterygomandibular	1 week	Culture	<i>Prevotella oralis</i> , <i>Bacteroides ureolyticus</i> , <i>Peptostreptococcus micros</i> , <i>Parvimonas micra</i> , <i>Gemella morbillorum</i>
Yuvaraj et al ¹⁷	No	Pus	Submandibular submental Pterygomandibular sublingual Anterior chest wall	10 days	Culture	<i>Streptococcus sanguis</i> , <i>Streptococcus mitis</i> , <i>Peptostreptococci</i> , <i>Propionibacterium</i>
Hobson et al ¹⁸	No	Pus	Left pterygoid muscle Brain	2 weeks	Culture	<i>Streptococcus viridans</i> , Nongroupable <i>Streptococci</i> Recurrent abscess at day 13 <i>Bacteroides fragilis</i> , <i>Veillonella</i> species, <i>Campylobacter gracilis</i> , <i>Prevotella buccae</i>
Figueiredo et al ¹⁹	Yes	Pus	Distal area of second molar	After 1 week 16–79 days	Culture	Most common <i>Fusobacterium</i> <i>Prevotella</i> <i>Peptostreptococcus</i>
Leavitt and Van Ess ²⁰	No	Pus	Mandibular third molar extraction site	1–3 days	Culture	Group I Streptococci
Gayle et al ²¹	No	Pus	Masseteric pterygomandibular extension to the left deep temporal region and the skull base	3 weeks	Culture	Coagulase-negative Staphylococcus, Group III Streptococcus, <i>Acinetobacter baumannii</i>

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,^{22,23} 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.^{28,29}

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.

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