Bacteriology of deep neck abscesses: a retrospective review of 96 consecutive cases

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ABSTRACT

Introduction: This study aimed to review the microbiology of deep neck abscesses and identify the factors that influence their occurrence.

Methods: A retrospective chart review was done of patients diagnosed with deep neck abscesses at the Department of Otorhinolaryngology, Tan Tock Seng Hospital, Singapore between 2004 and 2009. The data of 131 deep neck abscess patients were reviewed, and those with positive pus culture were included in the study. Logistic regression was applied to analyse and compare the incidence of common organisms in various conditions (age, gender, aetiology and effects of diabetes mellitus).

Results: Of the 96 patients recruited, 18 had polymicrobial cultures. The leading pathogens cultured were *Klebsiella (K.) pneumoniae* (27.1 percent), *Streptococcus milleri* group (SMG) bacteria (21.9 percent) and anaerobic bacteria–not otherwise specified (NOS) (20.8 percent). *K. pneumoniae* (50.0 percent) was over-represented in the diabetic group. SMG bacteria (68.8 percent) and anaerobic bacteria–NOS (43.8 percent) were most commonly isolated in patients with odontogenic infections. *K. pneumoniae* was found more commonly among female patients (39.3 percent). The distribution of the three leading pathogens between patients aged below 50 years and those 50 years and above was comparable. *K. pneumoniae* was the commonest organism cultured in parapharyngeal space abscesses, while the submandibular space and parotid space most commonly isolated SMG bacteria and *Staphylococcus aureus*, respectively.

Conclusion: Broad-spectrum antibiotics are recommended for treating deep neck abscesses. Empirical antibiotic coverage against *K. pneumoniae* infection in diabetic patients, and SMG and anaerobic bacteria in patients with an odontogenic infection, is advocated. Routine antibiotic coverage against Gram-negative bacteria is not paramount.

Keywords: diabetes mellitus, *Klebsiella pneumoniae*, neck abscesses, odontogenic infections, upper respiratory tract infections

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INTRODUCTION

A deep neck abscess is defined as a collection of pus in the facial planes and spaces of the head and neck. The widespread availability of antibiotics has drastically reduced the incidence of deep neck abscess. However, it remains an important condition, as it may potentially lead to life-threatening complications such as airway compromise, pneumonia, pericarditis, jugular vein thrombosis, mediastinal involvement and arterial erosion.[1,2] Adequate antimicrobial coverage, surgical drainage and appropriate management of complications remain the cornerstone of treatment for deep neck abscesses. Although culture-guided antimicrobial therapy is advocated, empirical antibiotics play a critical role in alleviating the clinical course of the disease. This study aimed to review the microbiology of deep neck abscesses and identify the factors that impact their pattern of occurrence.

METHODS

A retrospective chart review of patients diagnosed with deep neck abscesses at the Department of Otorhinolaryngology, Tan Tock Seng Hospital between 2004 and 2009 was conducted. Superficial infections, limited intraoral abscesses, peri-tonsillar abscesses, cervical necrotising fasciitis, deep neck space cellulitis alone and infections due to penetrating or surgical neck trauma were excluded from this study. Patients who failed to complete the treatment were also excluded. A total of 131 patients met the above requirements. 125 patients underwent either surgical drainage or needle aspiration, of which 96 (76.8%) yielded positive culture results from the pus collected via these methods. Logistic regression was

Table I. Results of pus cultures in 96 patients with microbial growth.

Organisms	No. of patients		
	Diabetic (n = 44)	Non-diabetic (n = 52)	Total (n = 96)
Aerobic Gram-positive bacteria			
Streptococcus milleri group	5	16	21
Non-haemolytic *Streptococcus*	0	3	3
Alpha-haemolytic *Streptococcus*	2	1	3
Beta-haemolytic *Streptococcus*	1	1	2
Group C beta-haemolytic *Streptococcus*	0	1	1
Staphylococcus aureus	6	4	10
Coagulase-negative *Staphylococcus*	1	1	2
Streptococcus agalactiae (Group B)	3	0	3
Gram-positive cocci	0	2	2
Aerobic Gram-negative bacteria			
Klebsiella pneumoniae	22	4	26
Neisseria species	0	1	1
Salmonella enteritidis	2	0	2
Pseudomonas aeruginosa	1	1	2
Acinetobacter baumannii	1	1	2
Anaerobic bacteria			
Anaerobic bacteria–NOS	3	17	20
Peptostreptococcus	1	1	2
Eikenella	0	2	2
Bacteroides fragilis group	0	1	1
Propionibacterium species	1	0	1
Enterobacter species	1	0	1
Coliform	1	1	2
Fusobacterium necroforum	0	1	1
Miscellaneous			
Mycobacterium species	0	3	3
Mixed growth	0	3	3
Normal flora of the upper respiratory tract	6	0	6
Polymicrobial growth	5	13	18

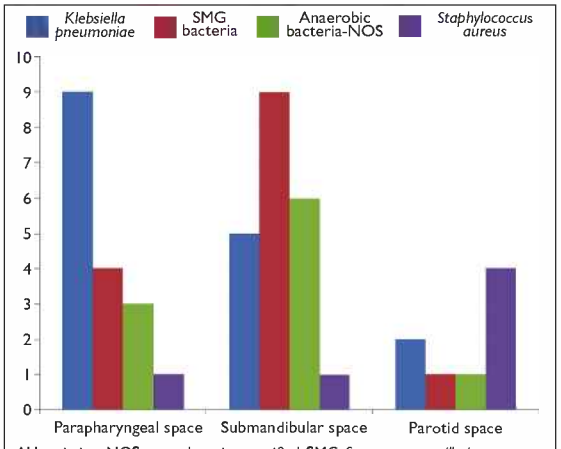
NOS: not otherwise specified

applied to analyse and compare the incidence of common organisms in various conditions such as age, gender, aetiology and effects of diabetes mellitus.

RESULTS

The cultured pathogens and their incidence are shown in Table I. As 18 patients had polymicrobial cultures, the total number of organisms cultured (n = 12) was more than the number of patients with positive cultures (n = 96). 80 (83.3%) patients had positive cultures for aerobic organisms, while 30 (31.3%) had anaerobic organisms. Apart from *Klebsiella (K.) pneumoniae*, the other Gram-negative bacteria appeared to play a minimal role in our study population. The distribution of common pathogens in the most commonly involved spaces is shown in Fig 1.

Upper airway infections and odontogenic infections were the most common causes of deep neck abscesses in our study. We found that *Streptococcus milleri* group (SMG) bacteria ($p < 0.001$) and anaerobic bacteria–NOS ($p = 0.047$) were isolated more frequently from deep neck abscesses with a dental source. The results of the pus cultures from the different sources of infections are shown in Table II.



Abbreviation: NOS: not otherwise specified; SMG: *Streptococcus milleri* group
The definitions for the analysed spaces are as follows: the parapharyngeal space is conical in shape, with its base at the petrous portion of the temporal bone and its apex at the hyoid bone. Medially, it extends to the lateral pharyngeal wall and is bounded laterally by the mandible, parotid gland and the internal pterygoid muscle. The submandibular space is bounded superiorly by the lingual mucosa and inferiorly by the anterior layer of the deep fascia. The parotid space is formed by splitting of the anterior layer of the deep cervical fascia and contains the parotid gland.

Fig. 1 Distribution of common organisms in different spaces.

The incidence of causative pathogens in both the diabetic and non-diabetic groups is shown in Table I.

Table II. Results of pus cultures from different sources of infection.

Organisms	URTI (n = 16)	Odontogenic (n = 16)	Others (n = 64)
Aerobic Gram-positive bacteria			
Streptococcus milleri group	1	11	9
Non-haemolytic *Streptococcus*	0	0	3
Alpha-haemolytic *Streptococcus*	0	2	1
Beta-haemolytic *Streptococcus*	0	0	2
Group C beta-haemolytic *Streptococcus*	0	0	1
Staphylococcus aureus	1	0	9
Coagulase-negative *Staphylococcus*	0	1	1
Streptococcus agalactiae (Group B)	0	0	3
Gram-positive cocci	1	0	1
Aerobic Gram-negative bacteria			
Klebsiella pneumoniae	9	0	17
Neisseria species	0	0	1
Salmonella enteritidis	0	0	2
Pseudomonas aeruginosa	1	0	1
Acinetobacter baumannii	0	0	2
Anaerobic bacteria			
Anaerobic bacteria–NOS	2	7	11
Peptostreptococcus	1	0	1
Eikenella	0	1	1
Bacteroides fragilis group	0	0	1
Propionibacterium species	0	0	1
Enterobacter species	0	0	1
Coliform	0	0	2
Fusobacterium necroforum	0	0	1
Miscellaneous			
Mycobacterium species	0	0	3
Mixed growth	0	2	1
Normal flora of the upper respiratory tract	1	0	5
Polymicrobial growth	1	5	12
Combined total	18	23	79

URTI: upper respiratory tract infection; NOS: not otherwise specified

K. pneumoniae was the most commonly cultured organism in the diabetic groups, and its culture rate was significantly higher than that in the non-diabetic group (50% vs. 7.7%, p = 0.002). Although not statistically significant, both anaerobic bacteria–NOS (32.7% vs. 6.8%, p = 0.054) and SMG bacteria (30.8% vs. 11.4%, p = 0.066) showed a trend toward higher culture rates in the non-diabetic group than in the diabetic group.

The incidences of the three most common organisms (*K. pneumoniae*, SMG and anaerobic bacteria–NOS) in male and female patients as well as those aged ≥ 50 years and those < 50 years were compared in Tables III and IV. Our data revealed that the culture rate for *K. pneumoniae* was significantly higher in female patients (39.4% vs. 20.6%, p = 0.0431). The distribution of these three pathogens between the age groups was comparable.

DISCUSSION

A wide spectrum of aerobic, microaerophilic and anaerobic pathogens are involved in deep neck abscesses. It is notable that there appear to be geographical differences in the microbiological pattern. In several Western studies,[3,4] the *Staphylococcus* (*S.*) species was a major causative pathogen of deep neck infections, while *K. pneumoniae* had a limited role. In Asian studies, however, the importance of *K. pneumoniae* in deep neck infections was emphasised while *S. aureus* isolations were much lower.[5,6] This disparity could be attributed to the lower rates of violence and substance abuse as well as higher diabetic rates in Asian societies.

Our study showed a bacteriological pattern similar to the Asian studies, with *K. pneumoniae* (27.1%) being the most commonly cultured organism, followed by SMG bacteria (21.9%) and anaerobic bacteria–NOS (20.8%). While 31.3% of our patients had positive cultures for anaerobes, this culture rate could be underestimated owing to its fastidious nature and the difficulty in isolating these organisms.[7] No organism

Table III. Results of logistic regression (*Klebsiella pneumoniae*).

Parameter	p-value
Age (≥ 50 years)	0.378
Gender (female)	0.043
Diabetes mellitus	0.002
URTI	0.196

URTI: upper respiratory tract infection

Table IV. Results of logistic regression (SMG and anaerobic bacteria–NOS).

Parameter	p-value	
	SMG	Anaerobic bacteria–NOS
Age (< 50 years)	0.661	0.215
Gender (male)	0.374	0.862
Non-diabetes mellitus	0.054	0.066
Odontogenic infection	< 0.001	0.047

SMG: *Streptococcus milleri* group; NOS: not otherwise specified

was isolated in 23.2% of the pus samples in this study. This rate was comparable to the reports of Huang et al[5] and Eftekharian et al.[8] This high proportion of nil growth is probably due to the prompt use of high-dose antimicrobials early in the course of the disease.[5]

Contemporary literature on deep neck infections has consistently described odontogenic infections to be an important cause.[2-5] Similarly, odontogenic infections were one of the two leading causes of deep neck abscesses in our study; thus, its impact on the bacteriology pattern must be analysed. SMG bacteria (68.8%) and anaerobic bacteria–NOS (43.8%) were significantly over-represented in deep neck abscesses with an odontogenic origin. This could be explained by the fact that SMG (21.9%) and anaerobic bacteria (20.8%) are common inhabitants of the oropharyngeal and gastrointestinal tracts. The close relationship between these organisms and dental infections has also been reported in other studies.[3,11] As such, there should be adequate empirical antibiotic coverage for SMG and anaerobic bacteria–NOS in deep neck abscess patients with a highly suspicious odontogenic source of infection.

As reported in many Asian studies,[6,11] diabetes mellitus was the most common systemic disease among our deep neck abscess patients. These same studies have also shown a close association between diabetes mellitus and *K. pneumoniae* infection. Similarly, in our study, 50% of diabetic patients had positive pus culture results that isolated *K. pneumoniae*. This culture rate was significantly higher than that in non-diabetic patients (7.7%, $p < 0.001$). Diabetic patients are known to have impaired neutrophilic functions and complement activation.[12] This reduced immunity, coupled with the increased oropharyngeal *K. pneumoniae* colonisation in immunocompromised hosts,[3] could possibly explain the predominance of *K. pneumoniae* in the pus cultures of deep neck abscesses among the diabetic group. To our current knowledge, there has not been any study reporting that gender influences the bacteriology of adult deep neck infections. Albeit an interesting finding, more studies are required to support the association of *K. pneumoniae* with female patients.

SMG bacteria were the most commonly isolated bacteria in the submandibular and floor of mouth abscesses, as many of these abscesses originated from an odontogenic infection. Notably, *S. aureus*, which played a minimal role in the earlier three most commonly involved spaces, was now the leading pathogen isolated in the pus cultures of parotid space abscesses ($p = 0.059$). This was also reported by Huang et al.[11] It suggests that parotid space abscess has a different cause and tract for infection to the other spaces.

As shown in our study, a wide variety of pathogens are involved in deep neck abscesses. Thus, it is advisable to start patients on broad-spectrum empirical antibiotics. With *K. pneumoniae* being the most commonly isolated organism in our study, its role in deep neck abscesses cannot be over-emphasised. *K. pneumoniae* is widely known as a nosocomial pathogen, and hospital outbreaks with new strains of extended spectrum beta-lactamase producers have been documented.[14] However, all our patients with *K. pneumoniae* infection had community-acquired strains that were sensitive to second- and third-generation cephalosporins as well as amoxicillin-clavulanic acid. All of these patients were treated with amoxicillin-clavulanic acid. Eight patients were given second- or third-generation cephalosporins, six were given metronidazole and two were given piperacillin concurrently. All responded well to the antimicrobial therapy.

SMG bacteria are known to consist of *Streptococcus intermedius*, *Streptococcus anginosus* and *Streptococcus constellatus*. It can be an aggressive pathogen, causing abscess formation in various sites of the body.[9] Hirai et al reported a 100% sensitivity of SMG to second-, third- and fourth-generation cephalosporins but only 71% sensitivity to ampicillin.[9] On the other hand, Fujiyoshi et al described a resistance to second-generation cephalosporins of up to 50% in their study, which also found ampicillin and third-generation cephalosporins to be less sensitive but without any resistant strains.[15] In our study, all cultured strains of SMG bacteria were sensitive to penicillin and

erythromycin. All patients infected with SMG bacteria responded well to amoxicillin-clavulanic acid. Five of these patients were treated with metronidazole as well.

Routine susceptibility testing for anaerobes was not available under current testing standards at our centre. Nevertheless, anaerobic bacteria–NOS were expected to respond to available anti-anaerobic antibiotics like amoxicillin-clavulanic acid, piperacillin-tazobactam, clindamycin, metronidazole or carbapenems. All our patients from whom we isolated anaerobic bacteria–NOS were treated with amoxicillin-clavulanic acid, and three with metronidazole as well. All showed satisfactory results. All three leading pathogens in our study were sensitive to amoxicillin-clavulanic acid. Gram-negative aerobic bacteria, apart from *K. pneumoniae*, played a minor role in our study. Thus, we do not recommend routine antibiotic coverage against these organisms. However, they should be considered only in patients with nosocomial infections and those with unsatisfactory response to the current treatment.

A large variety of pathogens may be involved in deep neck abscesses; broad-spectrum empirical antimicrobials such as amoxicillin-clavulanic acid are thus recommended. Empirical antibiotic coverage should recognise the high rate of *K. pneumoniae* infection in diabetic patients with deep neck abscesses. Given the predominance of SMG bacteria and anaerobic bacteria–NOS in deep neck abscesses with an obvious odontogenic source, it is advisable to provide empirical antibiotic overage against these organisms for patients with a highly suspicious dental source of infection. Patients with parotid space abscesses should receive antibiotic coverage against *S. aureus* in view of their high propensity in isolating this organism. Gram-negative bacteria other than *K. pneumoniae* played a limited role in our study. As such, routine antibiotics against these organisms are not necessary.

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