Does FESS alter the sinonasal microbiome

Original Article

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ABSTRACT

Introduction: Chronic rhinosinusitis is a common health problem.However few studies comparing pre and post-FESS microorganisms and efficacy of FESS are present.The present study aims to analyze the alteration in sinonasal microbiome in patients of chronic rhinosinusitis with and without nasal polyposis after functional endoscopic sinus surgery.

Patients and Methods: The prospective observational study was conducted in the Department of Otorhinolaryngology and Head Neck Surgery, SRMS IMS from November 2017 to April 2019 after the approval by the Research/Ethics Committee. All patients clinically diagnosed as Chronic Rhinosinusitis (CRS) with and without Nasal Polyposis posted for Functional Endoscopic Sinus Surgery (FESS) formed the study group.Culture analysis of specimen from middle meatus region was done twice first, prior to FESS and second 6 weeks post-FESS.The changes in the microbiome were then analysed.

Results: In 31.4% patients methicillin resistant staphylococcus aureus was cultured prior to FESS. Other organisms cultured were Staphylococcus aureus, Pseudomonas, Aspergillus, E.coli, Rhizopus and E.Faecalis. Post-FESS cultures were obtained at 6 weeks. Staphylococcus aureus was cultured in 77% cases. No fungal microbes or MRSA were cultured post operatively. In 11.4 % cultures no microorganisms were detected. No statistical correlation was observed between the diagnosis and organisms cultured.

Conclusion: The preoperative culture of MRSA and its absence in post-FESS cultures points to role in the pathogenesis of CRS. Fungal organisms Aspergillus and Rhizopus were cultured pre-operatively which were present in combination with bacteria supporting the co-infection theory. Effective role of FESS as surgical management is also consolidated.

Key Words: Biofilm, culture, MRSA, staphylococcus aureus, swab.

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INTRODUCTION

Chronic rhinosinusitis is the preferred term to describe the inflammation of the nose and paranasal sinuses and is a health problem worldwide affecting approximately 15% of the human population[1,2]. Several environmental and host mechanisms have been implicated in the etiology of chronic rhinosinusitis including presence of microbes (bacteria,fungus), allergy, ciliary dysfunction, derangements in innate and adaptive immunity, biofilm formation and osteitis[3].

There have been several studies about microorganisms implicated in CRS. On review of literature very few studies comparing pre and post-FESS microorganisms were obtained. Also the studies regarding efficacy of FESS were few in number. The most frequent microorganisms implicated in chronic rhinosinusitis were Staphylococcus aureus, Coagulase - negative Staphylococcus and Streptococcus pneumonia. According to some authors as chronicity develops the aerobic and facultative species are gradually replaced by anaerobes[4,5]. Often polymicrobial colonization is found. In an Indian subcontinental cross-sectional study Staphylococcus aureus was the most common isolate accounting for 43% of patients followed by Klebsiella sp. 9% and MRSA 3 %[6]. Fungal organisms identified were Aspergillus and Candida sp. isolated from 9% of patients. The presence of intracellular Staphylococcus aureus in epithelial cells of nasal mucosa has been suggested as a significant risk factor for recurrent episodes of rhinosinusitis. It is also emerging as a prominent disease modifying organism in sinusitis and its presence in patients has important clinical implications Anaerobes commonly found were Peptostreptococcus sp.[7,8].

Other microorganisms implicated are Haemophilus influenzae, Enterobacter aerogenes, Peptostreptococcus magnus, Peptostreptococcus sp.and Propionibacterium acnes[8].

Functional endoscopic sinus surgery (FESS) is a minimally invasive technique in which sinus air cells

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and sinus ostia are opened under direct visualization. The goal of this procedure is to restore sinus ventilation and normal function[9]. FESS aims to clear diseased air cells a particulary at the osteomeatal complex. Ventilation and drainage of maxillary and frontal sinuses are thus re-established through their natural ostia. It has been considered as an efficient and safe modality with minimum morbidity and complication rates[10].

Coagulase-negative staphylococci, diphtheroids and S.aureus constitute the predominant flora of the healthy post-ESS sinus cavity and probably represent colonization of the cavity by nasal flora from the contiguous nasal mucosa[4]. Post surgical patients with acute exacerbations of chronic rhinosinusitis most commonly grew S. aureus, coagulase-negative staphylococci and pseudomonal species[5]. The study aimed to analyze the sinonasal microbiome in patients of chronic rhinosinusitis with and without nasal polyposis and to assess the changes in the sinonasal microbiome after functional endoscopic sinus surgery (FESS).

Microbial diagnostics in CRS has traditionally been culture dependant however nowadays molecular detection techniques have also gained prominence[11]. However studies have found the results to be more or less in agreement with a higher diversity of anaerobes in molecular techniques[8].

Both aspirate and swab techniques have been utilized for endoscopically guided cultures[12]. It has also been found that there is no significant difference between mucosal tissue and swab samples and both methods showed strong correlation[13,14].

PATIENTS AND METHODS:

The prospective observational study was conducted in the Department of Otorhinolaryngology and Head Neck Surgery at SRMS Institute of Medical Sciences, Bareilly, India from November 2017 to April 2019 after the approval by the Research/Ethics Committee of Shri Ram Murti Smarak Institue of Medical Sciences, Bareilly. All patients clinically diagnosed as Chronic Rhinosinusitis with and without nasal polyposis posted for Functional Endoscopic Sinus Surgery (FESS) formed the study group. These patients had no improvement with conservative treatment like antibiotic usage taken earlier. Written informed consent was taken from all patients. Patients having any concomitant pathology in the nose and paranasal sinuses such as neoplasms (benign or malignant) and immunocompromised states were excluded. All patients included in study underwent complete ENT evaluation including clinical examination, Diagnostic nasal endoscopy (DNE), baseline haematological investigations and a CT Nose and PNS.

Swab/tissue specimens were taken twice. First specimen was taken just before functional endoscopic sinus surgery. The second specimen was taken 6 weeks later when patient came for followup.

Strict adherence to proper technique to avoid contamination from the nasal vestibule or the anterior nasal cavity was done. A nasal endoscope was placed into the nose and under endoscopic visualization, a standard culture swab was placed through the nasal cavity reaching the middle meatus. No contact was allowed between the swab and the nasal vestibular skin, septum, and lateral nasal wall. When such contact did occur, the culture swab was discarded and a new culture drawn. Where ever deemed necessary tissue sample was also taken.

Each properly obtained swab was send for aerobic, anaerobic, fungal culture analysis and gram staining. Second sample was taken after 6 weeks.Postoperatively patients were prescribed third generation intravenous cephalosporins during period of hospital stay.Saline nasal washes were also prescribed routinely to all post –op patients. Diagnostic nasal endoscopy was performed and specimen was taken from post- operative FESS cavity. For aerobic culture all swabs were inoculated on Mac Conkey agar, blood agar and chocolate agar. Fungal pathogens were found after inoculation on SDA and SCA. For anaerobic culture, all samples were inoculated on Mac Conkey agar and blood agar immediately after sampling and incubated in McIintosh Filde's Jar.

Descriptive statistics was analyzed with SPSS version 17.0 software. Continuous variables are presented as mean ± SD. Categorical variables are expressed as frequencies and percentages. The Pearson's chi-square test or the chi-square test of association was used to determine if there is a relationship between two categorical variables.

RESULTS:

A total of 35 patients were included in the study. 54.3% were males and 45.7% were females. Age of the patients ranged from 12-76 yrs with mean age of 40 years. Majority of patients were in the age group 41 to 50 years.

Most patients posted for FESS were having bilateral Chronic Rhinosinusitis with nasal polyposis (CRSwNP-37.1%) followed by unilateral Chronic Rhinosinusitis without nasal polyposis (U/L CRSnNP-31.4%), unilateral Chronic Rhinosinusitis with nasal polyposis (U/L CRSwNP-20%) and bilateral Chronic Rhinosinusitis without nasal polyposis (B/L CRSnNP-11.45%). As shown in table 1 prior to FESS 31.4% patients had methicillin resistant staphylococcus aureus (MRSA). Other organisms cultured were (Table 1) Staphylococcus aureus(25.7%) and Pseudomonas(11.4%) Aspergillus (8.6%), E. coli (8.6%), Rhizopus (5.7%),

ESBL (2.9%) and E.Faecalis (2.9%). Post-operative microbes were cultured at 6 weeks after FESS. It was observed that in 77 % cases staphylococcus aureus was cultured (Table 2). No fungal microbes were cultured post operatively. Other microorganisms cultured were E.Coli (5.7%), Pseudomonas (2.9%), ESBL (2.9%) and E. Faecalis (2.9%) (Table 2). Rest of the cultures were sterile. Post FESS MRSA was not cultured (Table 2). MRSA was cultured predominantly in unilateral Chronic rhinosinusitis with and without nasal polyposis preoperatively (Table 3). However, no statistical correlation was observed between the diagnosis preoperatively and organisms cultured (Table 3). Most cases of bilateral chronic rhinosinusitis with nasal polyposis yielded Staphylococcus aureus post FESS. However no statistical correlation was found between the diagnosis of patients and the post-FESS microorganisms cultured (Table 4).

Table 1: Pre-Fess Cultures Obtained in CRS Patients

Pre-op microorganisms	No. of patients	%
ASPERGILLUS	3	8.6%
E. COLI	3	8.6%
MRSA	11	31.4%
E. FAECALIS	1	2.9%
RHIZOPUS	2	5.7%
ESBL	1	2.9%
PSEUDO	4	11.4%
S.A	9	25.7%
None	11	31.4%

Table 2: Post –Fess Cultures Obtained In CRS Patients

Post- op microorganisms	No. of patients	%
PATIENT EXPIRED	1	2.9%
S. A	27	77.1%
E. COLI	2	5.7%
PSEUDO	1	2.9%
ESBL	1	2.9%
None	8	22.8%
E. FAECALIS	1	2.9%

Table 3: Correlation of Type of CRS with Microorganisms Cultured Pre-Fess

Diagnosis	No. of patients	Pre-op microorganisms (only n – not significant) (n*- significant)							
		AG	E. COLI	MRSA	E. FAECALIS	RHIZOPUS	ESBL	PSEUDO	S.A
B/L CRSnNP	4	0	1	2	0	1	0	2	1
B/L CRSwNP	13	1	0	2	0	0	0	1	3
U/L CRSnNP	11	2	1	4	1	1	1	1	4
U/L CRSwNP	7	0	1	3	0	0	0	0	1
TOTAL	35	3	3	11	1	2	1	4	9

(AG-Aspergillus, S.A.-Staphylococcus aureus,Pseudo-Pseudomonas, CRSwNP-Chronic Rhinosinusitis with Nasal Polyposis, CRSnNP-Chronic Rhinosinusitis without Nasal Polyposis, U/L-Unilateral, B/L-Bilateral)

Table 4: Corelation of Type of CRS with Post-Fess Microorganisms

Diagnosis	No. of patients	S. A	E. COLI	PSEUDO	ESBL	E.FAECALIS
B/L CRSnNP	4	3	0	0	0	0
B/L CRSwNP	13	11	2	0	0	0
U/L CRSnNP	11	8	0	1	1	1
U/L CRSwNP	7	5	0	0	0	0
TOTAL	35	27	2	1	1	1

(only n – not significant) (n*- significant)

(S.A-Staphylococcus aureus, K.Pn-Klebsiella Pneumonie, Pseudo-Pseudomonas)

DISCUSSION

Chronic rhinosinusitis is defined as the persistent inflammation of the nasal and sinus mucosa. Although insights into the pathophysiology of CRS have expanded greatly over the last few decades but many of the mechanisms involved in the disease process are still under research[15]. Majority of patients were in there late forties thus pointing to the incidence of CRS more in this age group.CRS was rarely present in extremes of age[16].

CRS predlication was slightly more for males than female.Perhaps less females approached the healthcare system in our study group because of low socio-economic status and neglect of their diseases unlike in the west[17,18,19]. Higher incidence of nasal polyposis patients in our series could be attributed to the willingness to get polyps operated more commonly.

Pre-operative cultures in our study yielded MRSA predominately followed by Staphylococcus aureus. Other microorganisms cultured were gram-negative bacteria like Pseudomonas, E.Coli, E.Faecalis. As per study by Brook Staphylococcus aureus and anaerobic organisms (Prevotella and Porphyromonas, Fusobacterium, and Peptostreptococcus spp.) are the commonest isolates in chronic rhinosinusitis (CRS). In his study aerobic and anaerobic beta lactamase-producing bacteria (BLPB) were recovered from over a third of these patients. Methicillin-resistant S. aureus (MRSA) accounted for over 60 % of S. aureus isolates[20]. Over the years there has been a rise in MRSA as was reported in a 20 year period Stanford study[21]. The presence of MRSA in large amount can be attributed to either the prevalence of MRSA which was acquired from the community. The increase in MRSA may partially be attributed due to the indiscriminate use of antibiotics which are prescribed to patients without adequate culture analysis reports. Gram negative bacteria and fungi were also cultured however no anaerobes were obtained which is similar to study by Rujanavej V *et al*[22]. The dysbiotic communities obtained in CRS patients in study by Hoggart *et al* were mostly composed of members from genera Staphylococcus, Streptococcus Haemophilus, Pseudomonas, Moraxella, or Fusobacterium[23]. It was observed in our study that several cultures were negative in case of Chronic rhinosinusitis with nasal polyposis thus pointing to a decreased diversity of bacteria in nasal polyposis which may be a contributing factor in its pathogenesis. However this role of dysbiosis in chronic rhinosinusitis with nasal polyposis requires further validation. Postoperative FESS microbiome analysis shows no growth of MRSA (Methicillin Resistant Staphylococcus aureus) in the present study thus pointing to its involvement in pathogenesis of Chronic rhinosinusitis.Possibilty of biofilm formation and MRSA strains cannot be overlooked[24,25]. The presence of Staphylococcus aureus in cases of chronic rhinosinusitis with nasal polyposis is similar to the 10 year study done in France, however the specimens were taken from ethmoid sinuses.Moreover in our study MRSA were equally present[26]. Postoperatively MRSA was absent and only Staphylococcus was present in our study as in study by Day N *et al*[27]. Our study reaffirms the effective role of FESS as a good option for eradication of diseased mucosa as seen by the micro-organisms cultured post-operatively.

Limitations in our study are the small sample size taken. Another weakness of the study is the use of antibiotics after FESS which may have added a bias and may have some role in the change of the microbiome. The employemt of newer techniques like PCR could have probably yielded a better stratification of microbes especially anaerobic bacteria. However, nasal swab still remains the option in many institutes as PCR techniques are costlier.

CONCLUSION

After analysis of the observations and results of our study the following conclusions were drawn. MRSA was cultured in one third patients of CRS with and without nasal polyposis preoperatively.However, it was totally absent in post-FESS cultures thus emphasising its role in the pathogenesis of CRS. Possible targeted antibiotic therapy against MRSA after appropriate culture analysis may play an added role in CRS management. Fungal organisms Aspergillus and Rhizopus were cultured pre-operatively which were present in combination with bacteria supporting the co-infection theory. Also the indequate and non culture directed use of antibiotics should be avoided. Our study also emphasis the role of FESS in surgical management of CRS.

CONFLICT OF INTEREST

There are no conflicts of interest.

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